

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
10 October 2002 (10.10.2002)

PCT

(10) International Publication Number
WO 02/079243 A2

- (51) International Patent Classification⁷: C07K 14/22
- (21) International Application Number: PCT/IB02/02069
- (22) International Filing Date: 12 February 2002 (12.02.2002)
- (25) Filing Language: English
- (26) Publication Language: English
- (30) Priority Data:
0103424.8 12 February 2001 (12.02.2001) GB
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- (81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW.
- (84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).
- Published:**
- without international search report and to be republished upon receipt of that report
 - with sequence listing part of description published separately in electronic form and available upon request from the International Bureau
- For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.*

(54) Title: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS

(57) Abstract: The invention provides proteins from gonococcus (*Neisseria gonorrhoeae*), including amino acid sequences, the corresponding nucleotide sequences, expression data, and serological data. The proteins are useful antigens for vaccines, immunogenic compositions, and/or diagnostics. They are also useful for distinguishing between gonococcus and meningococcus and, in particular, between gonococcus and serogroup B meningococcus.

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GONOCOCCAL PROTEINS AND NUCLEIC ACIDS

All documents cited herein are incorporated by reference in their entirety.

TECHNICAL FIELD

This invention relates to proteins from the bacterium *Neisseria gonorrhoeae*, and more particularly to
5 such proteins which do not have corresponding homologs or orthologs in serogroup B *N.meningitidis*.

BACKGROUND ART

Neisseria gonorrhoeae is a bacterial pathogen. There is currently no effective vaccine against *N.gonorrhoeae* infection. It is an object of the invention to provide proteins and nucleic acid useful in vaccine study and/or manufacture.

10 *N.gonorrhoeae* is related to *N.meningitidis*. Sequence data are now available for serogroup B of meningococcus [e.g. WO99/24578; WO99/36544; WO99/57280; WO00/22430; WO00/66791; Tettelin *et al.* (2000) *Science* 287:1809-1815] and also for serogroup A [Parkhill *et al.* (2000) *Nature* 404:502-506]. It is a further object of the invention to provide proteins and nucleic acid useful in distinguishing between gonococcus and meningococcus and, in particular, between gonococcus and serogroup B meningococcus.

15 DISCLOSURE OF THE INVENTION

The invention provides proteins comprising the *N.gonorrhoeae* amino acid sequences disclosed in the examples (the even-numbered SEQ IDS 2 to 8622). 159 of these have no homolog in serogroup B meningococcus and these have been given a name in the form "NGSn".

It also provides proteins comprising amino acid sequences having sequence identity to the *N.gonorrhoeae*
20 amino acid sequences disclosed in the examples. Depending on the particular sequence, the degree of sequence identity is preferably greater than 50% (e.g. 60%, 70%, 80%, 90%, 95%, 99% or more). These proteins include homologs, orthologs, allelic variants and functional mutants. Typically, 50% identity or more between two proteins is considered to be an indication of functional equivalence. Identity between proteins is preferably determined by the Smith-Waterman homology search algorithm as implemented in
25 the MPSRCH program (Oxford Molecular), using an affine gap search with parameters *gap open penalty=12* and *gap extension penalty=1*.

The invention further provides proteins comprising fragments of the *N.gonorrhoeae* amino acid sequences disclosed in the examples. The fragments should comprise at least *n* consecutive amino acids from the sequences and, depending on the particular sequence, *n* is 7 or more (e.g. 8, 10, 12, 14, 16, 18,
30 20, 30, 40, 50, 60, 70, 80, 90, 100 or more). Preferably the fragments comprise one or more epitopes from the sequence. Other preferred fragments are (a) the N-terminal signal peptides of the proteins disclosed in the examples, and (b) the proteins disclosed in the examples, but without their N-terminal signal peptides.

The proteins of the invention can, of course, be prepared by various means (e.g. recombinant expression, purification from *Neisseria*, chemical synthesis *etc.*) and in various forms (e.g. native, fusions *etc.*). They
35 are preferably prepared in substantially pure form (i.e. substantially free from other *N.gonorrhoeae* or host cell proteins).

The proteins of the invention are preferably *Neisserial* proteins, more preferably *N.gonorrhoeae* proteins.

The invention provides antibodies which bind to these proteins. These may be polyclonal or monoclonal and may be produced by any suitable means. The antibodies may include a detectable label.

The invention provides nucleic acid comprising the *N.gonorrhoeae* nucleotide sequences disclosed in the examples. In addition, the invention provides nucleic acid comprising nucleotide sequences having
5 sequence identity to the *N.gonorrhoeae* nucleotide sequences disclosed in the examples.

Furthermore, the invention provides nucleic acid which can hybridise to the *N.gonorrhoeae* nucleic acid disclosed in the examples, preferably under "high stringency" conditions (e.g. 65°C in a 0.1xSSC, 0.5% SDS solution).

Nucleic acid comprising fragments of these sequences are also provided. These should comprise at least *n*
10 consecutive nucleotides from the *N.gonorrhoeae* sequences and, depending on the particular sequence, *n* is 10 or more (e.g. 12, 14, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200 or more).

The invention also provides nucleic acid encoding the proteins and protein fragments of the invention.

The invention includes nucleic acid comprising sequences complementary to those described above (e.g. for antisense or probing purposes).

15 Nucleic acid according to the invention can be prepared in many ways (e.g. by chemical synthesis, from genomic or cDNA libraries, from the organism itself *etc.*) and can take various forms (e.g. single stranded, double stranded, vectors, probes *etc.*).

In addition, the term "nucleic acid" includes DNA and RNA, and also their analogues, such as those containing modified backbones, and also peptide nucleic acids (PNA) *etc.*

20 The invention provides vectors comprising nucleotide sequences of the invention (e.g. cloning or expression vectors) and host cells transformed with such vectors.

The invention provides compositions comprising protein, antibody, and/or nucleic acid according to the invention. These compositions may be suitable as immunogenic compositions, for instance, or as diagnostic reagents, or as vaccines.

25 The invention also provides nucleic acid, protein, or antibody according to the invention for use as medicaments (e.g. as vaccines) or as diagnostic reagents. It also provides the use of nucleic acid, protein, or antibody according to the invention in the manufacture of: (i) a medicament for treating or preventing infection due to *Neisseria*; (ii) a diagnostic reagent for detecting the presence of *Neisseria* or of antibodies raised against *Neisseria*; and/or (iii) a reagent which can raise antibodies against *Neisseria*. Said *Neisseria*
30 may be any species, but is preferably *N.gonorrhoeae*.

The invention also provides a method of treating a patient, comprising administering to the patient a therapeutically effective amount of nucleic acid, protein, and/or antibody of the invention.

According to further aspects, the invention provides various processes.

A process for producing proteins of the invention is provided, comprising the step of culturing a host cell
35 of to the invention under conditions which induce protein expression.

A process for producing protein or nucleic acid of the invention is provided, wherein the protein or nucleic acid is synthesised in part or in whole using chemical means.

A process for detecting polynucleotides of the invention is provided, comprising the steps of: (a) contacting a nucleic probe according to the invention with a biological sample under hybridising conditions to form duplexes; and (b) detecting said duplexes.

A process for detecting proteins of the invention is provided, comprising the steps of: (a) contacting an antibody of the invention with a biological sample under conditions suitable for the formation of an antibody-antigen complexes; and (b) detecting said complexes.

A process for distinguishing *N.gonorrhoeae* from *N.meningitidis* is provided, comprising the steps of: (a) contacting an antibody of the invention with a biological sample under conditions suitable for the formation of an antibody-antigen complexes; and (b) detecting said complexes. Alternatively, the steps may be (a) contacting nucleic acid of the invention with a biological sample under conditions suitable for the nucleic acid hybridisation; and (b) detecting any such hybridisation. Alternatively, the steps may be (a) contacting a protein of the invention with a biological sample (e.g. blood or serum) under conditions suitable for the formation of an antibody-antigen complexes; and (b) detecting said complexes.

A summary of standard techniques and procedures which may be employed in order to perform the invention (e.g. to utilise the disclosed sequences for vaccination or diagnostic purposes) follows. This summary is not a limitation on the invention, but gives examples that may be used, but are not required.

General

The practice of the present invention will employ, unless otherwise indicated, conventional techniques of molecular biology, microbiology, recombinant DNA, and immunology, which are within the skill of the art. Such techniques are explained fully in the literature eg. Sambrook *Molecular Cloning; A Laboratory Manual, Second Edition* (1989) or *Third Edition* (2000); *DNA Cloning, Volumes I and II* (D.N Glover ed. 1985); *Oligonucleotide Synthesis* (M.J. Gait ed, 1984); *Nucleic Acid Hybridization* (B.D. Hames & S.J. Higgins eds. 1984); *Transcription and Translation* (B.D. Hames & S.J. Higgins eds. 1984); *Animal Cell Culture* (R.I. Freshney ed. 1986); *Immobilized Cells and Enzymes* (IRL Press, 1986); B. Perbal, *A Practical Guide to Molecular Cloning* (1984); the *Methods in Enzymology* series (Academic Press, Inc.), especially volumes 154 & 155; *Gene Transfer Vectors for Mammalian Cells* (J.H. Miller and M.P. Calos eds. 1987, Cold Spring Harbor Laboratory); Mayer and Walker, eds. (1987), *Immunochemical Methods in Cell and Molecular Biology* (Academic Press, London); Scopes, (1987) *Protein Purification: Principles and Practice*, Second Edition (Springer-Verlag, N.Y.), and *Handbook of Experimental Immunology, Volumes I-IV* (D.M. Weir and C. C. Blackwell eds 1986).

Standard abbreviations for nucleotides and amino acids are used in this specification.

Definitions

A composition containing X is "substantially free of" Y when at least 85% by weight of the total X+Y in the composition is X. Preferably, X comprises at least about 90% by weight of the total of X+Y in the composition, more preferably at least about 95% or even 99% by weight.

The term "comprising" means "including" as well as "consisting" e.g. a composition "comprising" X may consist exclusively of X or may include something additional e.g. X + Y.

The term "heterologous" refers to two biological components that are not found together in nature. The components may be host cells, genes, or regulatory regions, such as promoters. Although the heterologous components are not found together in nature, they can function together, as when a promoter heterologous to a gene is operably linked to the gene. Another example is where a *Neisseria* sequence is heterologous to a mouse host cell. A further examples
5 would be two epitopes from the same or different proteins which have been assembled in a single protein in an arrangement not found in nature.

An "origin of replication" is a polynucleotide sequence that initiates and regulates replication of polynucleotides, such as an expression vector. The origin of replication behaves as an autonomous unit of polynucleotide replication within a cell, capable of replication under its own control. An origin of replication may be needed for a vector to
10 replicate in a particular host cell. With certain origins of replication, an expression vector can be reproduced at a high copy number in the presence of the appropriate proteins within the cell. Examples of origins are the autonomously replicating sequences, which are effective in yeast; and the viral T-antigen, effective in COS-7 cells.

A "mutant" sequence is defined as DNA, RNA or amino acid sequence differing from but having sequence identity with the native or disclosed sequence. Depending on the particular sequence, the degree of sequence identity between
15 the native or disclosed sequence and the mutant sequence is preferably greater than 50% (eg. 60%, 70%, 80%, 90%, 95%, 99% or more, calculated using the Smith-Waterman algorithm as described above). As used herein, an "allelic variant" of a nucleic acid molecule, or region, for which nucleic acid sequence is provided herein is a nucleic acid molecule, or region, that occurs essentially at the same locus in the genome of another or second isolate, and that, due to natural variation caused by, for example, mutation or recombination, has a similar but not identical nucleic acid
20 sequence. A coding region allelic variant typically encodes a protein having similar activity to that of the protein encoded by the gene to which it is being compared. An allelic variant can also comprise an alteration in the 5' or 3' untranslated regions of the gene, such as in regulatory control regions (eg. see US patent 5,753,235).

Expression systems

The *Neisseria* nucleotide sequences can be expressed in a variety of different expression systems; for example those
25 used with mammalian cells, baculoviruses, plants, bacteria, and yeast.

i. Mammalian Systems

Mammalian expression systems are known in the art. A mammalian promoter is any DNA sequence capable of binding mammalian RNA polymerase and initiating the downstream (3') transcription of a coding sequence (eg. structural gene) into mRNA. A promoter will have a transcription initiating region, which is usually placed proximal
30 to the 5' end of the coding sequence, and a TATA box, usually located 25-30 base pairs (bp) upstream of the transcription initiation site. The TATA box is thought to direct RNA polymerase II to begin RNA synthesis at the correct site. A mammalian promoter will also contain an upstream promoter element, usually located within 100 to 200 bp upstream of the TATA box. An upstream promoter element determines the rate at which transcription is initiated and can act in either orientation [Sambrook et al. (1989) "Expression of Cloned Genes in Mammalian Cells."
35 In *Molecular Cloning: A Laboratory Manual*, 2nd ed.].

Mammalian viral genes are often highly expressed and have a broad host range; therefore sequences encoding mammalian viral genes provide particularly useful promoter sequences. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter (Ad MLP), and herpes simplex virus promoter. In addition, sequences derived from non-viral genes, such as the murine metallothionein gene, also
40 provide useful promoter sequences. Expression may be either constitutive or regulated (inducible), depending on the promoter can be induced with glucocorticoid in hormone-responsive cells.

The presence of an enhancer element (enhancer), combined with the promoter elements described above, will usually increase expression levels. An enhancer is a regulatory DNA sequence that can stimulate transcription up to 1000-fold when linked to homologous or heterologous promoters, with synthesis beginning at the normal RNA start site. Enhancers are also active when they are placed upstream or downstream from the transcription initiation site, in either normal or flipped orientation, or at a distance of more than 1000 nucleotides from the promoter [Maniatis et al. (1987) *Science* 236:1237; Alberts et al. (1989) *Molecular Biology of the Cell*, 2nd ed.]. Enhancer elements derived from viruses may be particularly useful, because they usually have a broader host range. Examples include the SV40 early gene enhancer [Dijkema et al (1985) *EMBO J.* 4:761] and the enhancer/promoters derived from the long terminal repeat (LTR) of the Rous Sarcoma Virus [Gorman et al. (1982b) *Proc. Natl. Acad. Sci.* 79:6777] and from human cytomegalovirus [Boshart et al. (1985) *Cell* 41:521]. Additionally, some enhancers are regulatable and become active only in the presence of an inducer, such as a hormone or metal ion [Sassone-Corsi and Borelli (1986) *Trends Genet.* 2:215; Maniatis et al. (1987) *Science* 236:1237].

A DNA molecule may be expressed intracellularly in mammalian cells. A promoter sequence may be directly linked with the DNA molecule, in which case the first amino acid at the N-terminus of the recombinant protein will always be a methionine, which is encoded by the ATG start codon. If desired, the N-terminus may be cleaved from the protein by *in vitro* incubation with cyanogen bromide.

Alternatively, foreign proteins can also be secreted from the cell into the growth media by creating chimeric DNA molecules that encode a fusion protein comprised of a leader sequence fragment that provides for secretion of the foreign protein in mammalian cells. Preferably, there are processing sites encoded between the leader fragment and the foreign gene that can be cleaved either *in vivo* or *in vitro*. The leader sequence fragment usually encodes a signal peptide comprised of hydrophobic amino acids which direct the secretion of the protein from the cell. The adenovirus tripartite leader is an example of a leader sequence that provides for secretion of a foreign protein in mammalian cells.

Usually, transcription termination and polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. The 3' terminus of the mature mRNA is formed by site-specific post-transcriptional cleavage and polyadenylation [Birnstiel et al. (1985) *Cell* 41:349; Proudfoot and Whitelaw (1988) "Termination and 3' end processing of eukaryotic RNA. In *Transcription and splicing* (ed. B.D. Hames and D.M. Glover); Proudfoot (1989) *Trends Biochem. Sci.* 14:105]. These sequences direct the transcription of an mRNA which can be translated into the polypeptide encoded by the DNA. Examples of transcription terminator/polyadenylation signals include those derived from SV40 [Sambrook et al (1989) "Expression of cloned genes in cultured mammalian cells." In *Molecular Cloning: A Laboratory Manual*].

Usually, the above described components, comprising a promoter, polyadenylation signal, and transcription termination sequence are put together into expression constructs. Enhancers, introns with functional splice donor and acceptor sites, and leader sequences may also be included in an expression construct, if desired. Expression constructs are often maintained in a replicon, such as an extrachromosomal element (eg. plasmids) capable of stable maintenance in a host, such as mammalian cells or bacteria. Mammalian replication systems include those derived from animal viruses, which require trans-acting factors to replicate. For example, plasmids containing the replication systems of papovaviruses, such as SV40 [Gluzman (1981) *Cell* 23:175] or polyomavirus, replicate to extremely high copy number in the presence of the appropriate viral T antigen. Additional examples of mammalian replicons include those derived from bovine papillomavirus and Epstein-Barr virus. Additionally, the replicon may have two replicon systems, thus allowing it to be maintained, for example, in mammalian cells for expression and in a prokaryotic host

for cloning and amplification. Examples of such mammalian-bacteria shuttle vectors include pMT2 [Kaufman et al. (1989) *Mol. Cell. Biol.* 9:946] and pHEBO [Shimizu et al. (1986) *Mol. Cell. Biol.* 6:1074].

5 The transformation procedure used depends upon the host to be transformed. Methods for introduction of heterologous polynucleotides into mammalian cells are known in the art and include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

10 Mammalian cell lines available as hosts for expression are known in the art and include many immortalized cell lines available from the American Type Culture Collection (ATCC), including but not limited to, Chinese hamster ovary (CHO) cells, HeLa cells, baby hamster kidney (BHK) cells, monkey kidney cells (COS), human hepatocellular carcinoma cells (eg. Hep G2), and a number of other cell lines.

ii. Baculovirus Systems

15 The polynucleotide encoding the protein can also be inserted into a suitable insect expression vector, and is operably linked to the control elements within that vector. Vector construction employs techniques which are known in the art. Generally, the components of the expression system include a transfer vector, usually a bacterial plasmid, which contains both a fragment of the baculovirus genome, and a convenient restriction site for insertion of the heterologous gene or genes to be expressed; a wild type baculovirus with a sequence homologous to the baculovirus-specific fragment in the transfer vector (this allows for the homologous recombination of the heterologous gene in to the baculovirus genome); and appropriate insect host cells and growth media.

20 After inserting the DNA sequence encoding the protein into the transfer vector, the vector and the wild type viral genome are transfected into an insect host cell where the vector and viral genome are allowed to recombine. The packaged recombinant virus is expressed and recombinant plaques are identified and purified. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, *inter alia*, Invitrogen, San Diego CA ("MaxBac" kit). These techniques are generally known to those skilled in the art and fully described in Summers & Smith, *Texas Agricultural Experiment Station Bulletin No. 1555* (1987) ("Summers & Smith").

25 Prior to inserting the DNA sequence encoding the protein into the baculovirus genome, the above described components, comprising a promoter, leader (if desired), coding sequence, and transcription termination sequence, are usually assembled into an intermediate transplacement construct (transfer vector). This may contain a single gene and operably linked regulatory elements; multiple genes, each with its own set of operably linked regulatory elements; or multiple genes, regulated by the same set of regulatory elements. Intermediate transplacement constructs are often maintained in a replicon, such as an extra-chromosomal element (e.g. plasmids) capable of stable maintenance in a host, such as a bacterium. The replicon will have a replication system, thus allowing it to be maintained in a suitable host for cloning and amplification.

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Currently, the most commonly used transfer vector for introducing foreign genes into AcNPV is pAc373. Many other vectors, known to those of skill in the art, have also been designed. These include, for example, pVL985 (which alters the polyhedrin start codon from ATG to ATT, and which introduces a BamHI cloning site 32 basepairs downstream from the ATT; see Luckow and Summers, *Virology* (1989) 17:31.

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The plasmid usually also contains the polyhedrin polyadenylation signal (Miller et al. (1988) *Ann. Rev. Microbiol.*, 42:177) and a prokaryotic ampicillin-resistance (*amp*) gene and origin of replication for selection and propagation in *E. coli*.

Baculovirus transfer vectors usually contain a baculovirus promoter. A baculovirus promoter is any DNA sequence capable of binding a baculovirus RNA polymerase and initiating the downstream (5' to 3') transcription of a coding sequence (eg. structural gene) into mRNA. A promoter will have a transcription initiation region which is usually placed proximal to the 5' end of the coding sequence. This transcription initiation region usually includes an RNA polymerase binding site and a transcription initiation site. A baculovirus transfer vector may also have a second domain called an enhancer, which, if present, is usually distal to the structural gene. Expression may be either regulated or constitutive.

Structural genes, abundantly transcribed at late times in a viral infection cycle, provide particularly useful promoter sequences. Examples include sequences derived from the gene encoding the viral polyhedron protein, Friesen et al., (1986) "The Regulation of Baculovirus Gene Expression," in: *The Molecular Biology of Baculoviruses* (ed. Walter Doerfler); EPO Publ. Nos. 127 839 and 155 476; and the gene encoding the p10 protein, Vlak et al., (1988), *J. Gen. Virol.* 69:765.

DNA encoding suitable signal sequences can be derived from genes for secreted insect or baculovirus proteins, such as the baculovirus polyhedrin gene (Carbonell et al. (1988) *Gene*, 73:409). Alternatively, since the signals for mammalian cell posttranslational modifications (such as signal peptide cleavage, proteolytic cleavage, and phosphorylation) appear to be recognized by insect cells, and the signals required for secretion and nuclear accumulation also appear to be conserved between the invertebrate cells and vertebrate cells, leaders of non-insect origin, such as those derived from genes encoding human α -interferon, Maeda et al., (1985), *Nature* 315:592; human gastrin-releasing peptide, Lebacqz-Verheyden et al., (1988), *Molec. Cell. Biol.* 8:3129; human IL-2, Smith et al., (1985) *Proc. Nat'l Acad. Sci. USA*, 82:8404; mouse IL-3, (Miyajima et al., (1987) *Gene* 58:273; and human glucocerebrosidase, Martin et al. (1988) *DNA*, 7:99, can also be used to provide for secretion in insects.

A recombinant polypeptide or polypeptide may be expressed intracellularly or, if it is expressed with the proper regulatory sequences, it can be secreted. Good intracellular expression of nonfused foreign proteins usually requires heterologous genes that ideally have a short leader sequence containing suitable translation initiation signals preceding an ATG start signal. If desired, methionine at the N-terminus may be cleaved from the mature protein by *in vitro* incubation with cyanogen bromide.

Alternatively, recombinant polypeptides or proteins which are not naturally secreted can be secreted from the insect cell by creating chimeric DNA molecules that encode a fusion protein comprised of a leader sequence fragment that provides for secretion of the foreign protein in insects. The leader sequence fragment usually encodes a signal peptide comprised of hydrophobic amino acids which direct the translocation of the protein into the endoplasmic reticulum.

After insertion of the DNA sequence and/or the gene encoding the expression product precursor of the protein, an insect cell host is co-transformed with the heterologous DNA of the transfer vector and the genomic DNA of wild type baculovirus -- usually by co-transfection. The promoter and transcription termination sequence of the construct will usually comprise a 2-5kb section of the baculovirus genome. Methods for introducing heterologous DNA into the desired site in the baculovirus virus are known in the art. (See Summers & Smith *supra*; Ju et al. (1987); Smith et al., *Mol. Cell. Biol.* (1983) 3:2156; and Luckow and Summers (1989)). For example, the insertion can be into a gene such as the polyhedrin gene, by homologous double crossover recombination; insertion can also be into a restriction enzyme site engineered into the desired baculovirus gene. Miller et al., (1989), *Bioessays* 4:91. The DNA sequence, when cloned in place of the polyhedrin gene in the expression vector, is flanked both 5' and 3' by polyhedrin-specific sequences and is positioned downstream of the polyhedrin promoter.

The newly formed baculovirus expression vector is subsequently packaged into an infectious recombinant baculovirus. Homologous recombination occurs at low frequency (between about 1% and about 5%); thus, the majority of the virus produced after cotransfection is still wild-type virus. Therefore, a method is necessary to identify recombinant viruses. An advantage of the expression system is a visual screen allowing recombinant viruses to be distinguished. The polyhedrin protein, which is produced by the native virus, is produced at very high levels in the nuclei of infected cells at late times after viral infection. Accumulated polyhedrin protein forms occlusion bodies that also contain embedded particles. These occlusion bodies, up to 15 μm in size, are highly refractile, giving them a bright shiny appearance that is readily visualized under the light microscope. Cells infected with recombinant viruses lack occlusion bodies. To distinguish recombinant virus from wild-type virus, the transfection supernatant is plaqued onto a monolayer of insect cells by techniques known to those skilled in the art. Namely, the plaques are screened under the light microscope for the presence (indicative of wild-type virus) or absence (indicative of recombinant virus) of occlusion bodies. "Current Protocols in Microbiology" Vol. 2 (Ausubel et al. eds) at 16.8 (Supp. 10, 1990); Summers & Smith, *supra*; Miller et al. (1989).

Recombinant baculovirus expression vectors have been developed for infection into several insect cells. For example, recombinant baculoviruses have been developed for, *inter alia*: *Aedes aegypti*, *Autographa californica*, *Bombyx mori*, *Drosophila melanogaster*, *Spodoptera frugiperda*, and *Trichoplusia ni* (WO 89/046699; Carbonell et al., (1985) *J. Virol.* 56:153; Wright (1986) *Nature* 321:718; Smith et al., (1983) *Mol. Cell. Biol.* 3:2156; and see generally, Fraser, et al. (1989) *In Vitro Cell. Dev. Biol.* 25:225).

Cells and cell culture media are commercially available for both direct and fusion expression of heterologous polypeptides in a baculovirus/expression system; cell culture technology is generally known to those skilled in the art. See, eg. Summers & Smith *supra*.

The modified insect cells may then be grown in an appropriate nutrient medium, which allows for stable maintenance of the plasmid(s) present in the modified insect host. Where the expression product gene is under inducible control, the host may be grown to high density, and expression induced. Alternatively, where expression is constitutive, the product will be continuously expressed into the medium and the nutrient medium must be continuously circulated, while removing the product of interest and augmenting depleted nutrients. The product may be purified by such techniques as chromatography, eg. HPLC, affinity chromatography, ion exchange chromatography, etc.; electrophoresis; density gradient centrifugation; solvent extraction, etc. As appropriate, the product may be further purified, as required, so as to remove substantially any insect proteins which are also present in the medium, so as to provide a product which is at least substantially free of host debris, eg. proteins, lipids and polysaccharides.

In order to obtain protein expression, recombinant host cells derived from the transformants are incubated under conditions which allow expression of the recombinant protein encoding sequence. These conditions will vary, dependent upon the host cell selected. However, the conditions are readily ascertainable to those of ordinary skill in the art, based upon what is known in the art.

35 iii. Plant Systems

There are many plant cell culture and whole plant genetic expression systems known in the art. Exemplary plant cellular genetic expression systems include those described in patents, such as: US 5,693,506; US 5,659,122; and US 5,608,143. Additional examples of genetic expression in plant cell culture has been described by Zenk, *Phytochemistry* 30:3861-3863 (1991). Descriptions of plant protein signal peptides may be found in addition to the references described above in Vaulcombe et al., *Mol. Gen. Genet.* 209:33-40 (1987); Chandler et al., *Plant Molecular Biology* 3:407-418 (1984); Rogers, *J. Biol. Chem.* 260:3731-3738 (1985); Rothstein et al., *Gene* 55:353-356 (1987);

- Whittier et al., *Nucleic Acids Research* 15:2515-2535 (1987); Wirsal et al., *Molecular Microbiology* 3:3-14 (1989); Yu et al., *Gene* 122:247-253 (1992). A description of the regulation of plant gene expression by the phytohormone, gibberellic acid and secreted enzymes induced by gibberellic acid can be found in R.L. Jones and J. MacMillin, *Gibberellins*: in: *Advanced Plant Physiology*, Malcolm B. Wilkins, ed., 1984 Pitman Publishing Limited, London, pp. 21-52. References that describe other metabolically-regulated genes: Sheen, *Plant Cell*, 2:1027-1038(1990); Maas et al., *EMBO J.* 9:3447-3452 (1990); Benkel and Hickey, *Proc. Natl. Acad. Sci.* 84:1337-1339 (1987).

Typically, using techniques known in the art, a desired polynucleotide sequence is inserted into an expression cassette comprising genetic regulatory elements designed for operation in plants. The expression cassette is inserted into a desired expression vector with companion sequences upstream and downstream from the expression cassette suitable for expression in a plant host. The companion sequences will be of plasmid or viral origin and provide necessary characteristics to the vector to permit the vectors to move DNA from an original cloning host, such as bacteria, to the desired plant host. The basic bacterial/plant vector construct will preferably provide a broad host range prokaryote replication origin; a prokaryote selectable marker; and, for *Agrobacterium* transformations, T DNA sequences for *Agrobacterium*-mediated transfer to plant chromosomes. Where the heterologous gene is not readily amenable to detection, the construct will preferably also have a selectable marker gene suitable for determining if a plant cell has been transformed. A general review of suitable markers, for example for the members of the grass family, is found in Wilmink and Dons, 1993, *Plant Mol. Biol. Rept.*, 11(2):165-185.

Sequences suitable for permitting integration of the heterologous sequence into the plant genome are also recommended. These might include transposon sequences and the like for homologous recombination as well as Ti sequences which permit random insertion of a heterologous expression cassette into a plant genome. Suitable prokaryote selectable markers include resistance toward antibiotics such as ampicillin or tetracycline. Other DNA sequences encoding additional functions may also be present in the vector, as is known in the art.

The nucleic acid molecules of the subject invention may be included into an expression cassette for expression of the protein(s) of interest. Usually, there will be only one expression cassette, although two or more are feasible. The recombinant expression cassette will contain in addition to the heterologous protein encoding sequence the following elements, a promoter region, plant 5' untranslated sequences, initiation codon depending upon whether or not the structural gene comes equipped with one, and a transcription and translation termination sequence. Unique restriction enzyme sites at the 5' and 3' ends of the cassette allow for easy insertion into a pre-existing vector.

A heterologous coding sequence may be for any protein relating to the present invention. The sequence encoding the protein of interest will encode a signal peptide which allows processing and translocation of the protein, as appropriate, and will usually lack any sequence which might result in the binding of the desired protein of the invention to a membrane. Since, for the most part, the transcriptional initiation region will be for a gene which is expressed and translocated during germination, by employing the signal peptide which provides for translocation, one may also provide for translocation of the protein of interest. In this way, the protein(s) of interest will be translocated from the cells in which they are expressed and may be efficiently harvested. Typically secretion in seeds are across the aleurone or scutellar epithelium layer into the endosperm of the seed. While it is not required that the protein be secreted from the cells in which the protein is produced, this facilitates the isolation and purification of the recombinant protein.

Since the ultimate expression of the desired gene product will be in a eucaryotic cell it is desirable to determine whether any portion of the cloned gene contains sequences which will be processed out as introns by the host's

splicosome machinery. If so, site-directed mutagenesis of the "intron" region may be conducted to prevent losing a portion of the genetic message as a false intron code, Reed and Maniatis, *Cell* 41:95-105, 1985.

The vector can be microinjected directly into plant cells by use of micropipettes to mechanically transfer the recombinant DNA. Crossway, *Mol. Gen. Genet*, 202:179-185, 1985. The genetic material may also be transferred into
 5 the plant cell by using polyethylene glycol, Krens, et al., *Nature*, 296, 72-74, 1982. Another method of introduction of nucleic acid segments is high velocity ballistic penetration by small particles with the nucleic acid either within the matrix of small beads or particles, or on the surface, Klein, et al., *Nature*, 327, 70-73, 1987 and Knudsen and Muller, 1991, *Planta*, 185:330-336 teaching particle bombardment of barley endosperm to create transgenic barley. Yet another method of introduction would be fusion of protoplasts with other entities, either minicells, cells, lysosomes or
 10 other fusible lipid-surfaced bodies, Fraley, et al., *Proc. Natl. Acad. Sci. USA*, 79, 1859-1863, 1982.

The vector may also be introduced into the plant cells by electroporation. (Fromm et al., *Proc. Natl. Acad. Sci. USA* 82:5824, 1985). In this technique, plant protoplasts are electroporated in the presence of plasmids containing the gene construct. Electrical impulses of high field strength reversibly permeabilize biomembranes allowing the introduction of the plasmids. Electroporated plant protoplasts reform the cell wall, divide, and form plant callus.

15 All plants from which protoplasts can be isolated and cultured to give whole regenerated plants can be transformed by the present invention so that whole plants are recovered which contain the transferred gene. It is known that practically all plants can be regenerated from cultured cells or tissues, including but not limited to all major species of sugarcane, sugar beet, cotton, fruit and other trees, legumes and vegetables. Some suitable plants include, for example, species from the genera *Fragaria*, *Lotus*, *Medicago*, *Onobrychis*, *Trifolium*, *Trigonella*, *Vigna*, *Citrus*,
 20 *Linum*, *Geranium*, *Manihot*, *Daucus*, *Arabidopsis*, *Brassica*, *Raphanus*, *Sinapis*, *Atropa*, *Capsicum*, *Datura*, *Hyoscyamus*, *Lycopersion*, *Nicotiana*, *Solanum*, *Petunia*, *Digitalis*, *Majorana*, *Cichorium*, *Helianthus*, *Lactuca*, *Bromus*, *Asparagus*, *Antirrhinum*, *Hererocallis*, *Nemesia*, *Pelargonium*, *Panicum*, *Pennisetum*, *Ranunculus*, *Senecio*, *Salpiglossis*, *Cucumis*, *Browaalia*, *Glycine*, *Lolium*, *Zea*, *Triticum*, *Sorghum*, and *Datura*.

Means for regeneration vary from species to species of plants, but generally a suspension of transformed protoplasts
 25 containing copies of the heterologous gene is first provided. Callus tissue is formed and shoots may be induced from callus and subsequently rooted. Alternatively, embryo formation can be induced from the protoplast suspension. These embryos germinate as natural embryos to form plants. The culture media will generally contain various amino acids and hormones, such as auxin and cytokinins. It is also advantageous to add glutamic acid and proline to the medium, especially for such species as corn and alfalfa. Shoots and roots normally develop simultaneously. Efficient
 30 regeneration will depend on the medium, on the genotype, and on the history of the culture. If these three variables are controlled, then regeneration is fully reproducible and repeatable.

In some plant cell culture systems, the desired protein of the invention may be excreted or alternatively, the protein may be extracted from the whole plant. Where the desired protein of the invention is secreted into the medium, it may be collected. Alternatively, the embryos and embryoless-half seeds or other plant tissue may be mechanically
 35 disrupted to release any secreted protein between cells and tissues. The mixture may be suspended in a buffer solution to retrieve soluble proteins. Conventional protein isolation and purification methods will be then used to purify the recombinant protein. Parameters of time, temperature pH, oxygen, and volumes will be adjusted through routine methods to optimize expression and recovery of heterologous protein.

iv. Bacterial Systems

40 Bacterial expression techniques are known in the art. A bacterial promoter is any DNA sequence capable of binding bacterial RNA polymerase and initiating the downstream (3') transcription of a coding sequence (eg. structural gene)

into mRNA. A promoter will have a transcription initiation region which is usually placed proximal to the 5' end of the coding sequence. This transcription initiation region usually includes an RNA polymerase binding site and a transcription initiation site. A bacterial promoter may also have a second domain called an operator, that may overlap an adjacent RNA polymerase binding site at which RNA synthesis begins. The operator permits negative regulated (inducible) transcription, as a gene repressor protein may bind the operator and thereby inhibit transcription of a specific gene. Constitutive expression may occur in the absence of negative regulatory elements, such as the operator. In addition, positive regulation may be achieved by a gene activator protein binding sequence, which, if present is usually proximal (5') to the RNA polymerase binding sequence. An example of a gene activator protein is the catabolite activator protein (CAP), which helps initiate transcription of the lac operon in *Escherichia coli* (*E. coli*) [Raibaud *et al.* (1984) *Annu. Rev. Genet.* 18:173]. Regulated expression may therefore be either positive or negative, thereby either enhancing or reducing transcription.

Sequences encoding metabolic pathway enzymes provide particularly useful promoter sequences. Examples include promoter sequences derived from sugar metabolizing enzymes, such as galactose, lactose (*lac*) [Chang *et al.* (1977) *Nature* 198:1056], and maltose. Additional examples include promoter sequences derived from biosynthetic enzymes such as tryptophan (*trp*) [Goeddel *et al.* (1980) *Nuc. Acids Res.* 8:4057; Yelverton *et al.* (1981) *Nucl. Acids Res.* 9:731; US patent 4,738,921; EP-A-0036776 and EP-A-0121775]. The β -lactamase (*bla*) promoter system [Weissmann (1981) "The cloning of interferon and other mistakes." In *Interferon 3* (ed. I. Gresser)], bacteriophage lambda PL [Shimatake *et al.* (1981) *Nature* 292:128] and T5 [US patent 4,689,406] promoter systems also provide useful promoter sequences.

In addition, synthetic promoters which do not occur in nature also function as bacterial promoters. For example, transcription activation sequences of one bacterial or bacteriophage promoter may be joined with the operon sequences of another bacterial or bacteriophage promoter, creating a synthetic hybrid promoter [US patent 4,551,433]. For example, the *tac* promoter is a hybrid *trp-lac* promoter comprised of both *trp* promoter and *lac* operon sequences that is regulated by the *lac* repressor [Amann *et al.* (1983) *Gene* 25:167; de Boer *et al.* (1983) *Proc. Natl. Acad. Sci.* 80:21]. Furthermore, a bacterial promoter can include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. A naturally occurring promoter of non-bacterial origin can also be coupled with a compatible RNA polymerase to produce high levels of expression of some genes in prokaryotes. The bacteriophage T7 RNA polymerase/promoter system is an example of a coupled promoter system [Studier *et al.* (1986) *J. Mol. Biol.* 189:113; Tabor *et al.* (1985) *Proc Natl. Acad. Sci.* 82:1074]. In addition, a hybrid promoter can also be comprised of a bacteriophage promoter and an *E. coli* operator region (EPO-A-0 267 851).

In addition to a functioning promoter sequence, an efficient ribosome binding site is also useful for the expression of foreign genes in prokaryotes. In *E. coli*, the ribosome binding site is called the Shine-Dalgarno (SD) sequence and includes an initiation codon (ATG) and a sequence 3-9 nucleotides in length located 3-11 nucleotides upstream of the initiation codon [Shine *et al.* (1975) *Nature* 254:34]. The SD sequence is thought to promote binding of mRNA to the ribosome by the pairing of bases between the SD sequence and the 3' end of *E. coli* 16S rRNA [Steitz *et al.* (1979) "Genetic signals and nucleotide sequences in messenger RNA." In *Biological Regulation and Development: Gene Expression* (ed. R.F. Goldberg)]. To express eukaryotic genes and prokaryotic genes with weak ribosome-binding site [Sambrook *et al.* (1989) "Expression of cloned genes in *Escherichia coli*." In *Molecular Cloning: A Laboratory Manual*].

5 A DNA molecule may be expressed intracellularly. A promoter sequence may be directly linked with the DNA molecule, in which case the first amino acid at the N-terminus will always be a methionine, which is encoded by the ATG start codon. If desired, methionine at the N-terminus may be cleaved from the protein by *in vitro* incubation with cyanogen bromide or by either *in vivo* or *in vitro* incubation with a bacterial methionine N-terminal peptidase (EPO-A-0 219 237).

10 Fusion proteins provide an alternative to direct expression. Usually, a DNA sequence encoding the N-terminal portion of an endogenous bacterial protein, or other stable protein, is fused to the 5' end of heterologous coding sequences. Upon expression, this construct will provide a fusion of the two amino acid sequences. For example, the bacteriophage lambda cell gene can be linked at the 5' terminus of a foreign gene and expressed in bacteria. The
15 resulting fusion protein preferably retains a site for a processing enzyme (factor Xa) to cleave the bacteriophage protein from the foreign gene [Nagai *et al.* (1984) *Nature* 309:810]. Fusion proteins can also be made with sequences from the *lacZ* [Jia *et al.* (1987) *Gene* 60:197], *trpE* [Allen *et al.* (1987) *J. Biotechnol.* 5:93; Makoff *et al.* (1989) *J. Gen. Microbiol.* 135:11], and *Chey* [EP-A-0 324 647] genes. The DNA sequence at the junction of the two amino acid sequences may or may not encode a cleavable site. Another example is a ubiquitin fusion protein. Such a fusion
20 protein is made with the ubiquitin region that preferably retains a site for a processing enzyme (*eg.* ubiquitin specific processing-protease) to cleave the ubiquitin from the foreign protein. Through this method, native foreign protein can be isolated [Miller *et al.* (1989) *Bio/Technology* 7:698].

Alternatively, foreign proteins can also be secreted from the cell by creating chimeric DNA molecules that encode a fusion protein comprised of a signal peptide sequence fragment that provides for secretion of the foreign protein in
25 bacteria [US patent 4,336,336]. The signal sequence fragment usually encodes a signal peptide comprised of hydrophobic amino acids which direct the secretion of the protein from the cell. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). Preferably there are processing sites, which can be cleaved either *in vivo* or *in vitro* encoded between the signal peptide fragment and the foreign gene.

25 DNA encoding suitable signal sequences can be derived from genes for secreted bacterial proteins, such as the *E. coli* outer membrane protein gene (*ompA*) [Masui *et al.* (1983), in: *Experimental Manipulation of Gene Expression*; Ghayeb *et al.* (1984) *EMBO J.* 3:2437] and the *E. coli* alkaline phosphatase signal sequence (*phoA*) [Oka *et al.* (1985) *Proc. Natl. Acad. Sci.* 82:7212]. As an additional example, the signal sequence of the alpha-amylase gene from various *Bacillus* strains can be used to secrete heterologous proteins from *B. subtilis* [Palva *et al.* (1982) *Proc.*
30 *Natl. Acad. Sci. USA* 79:5582; EP-A-0 244 042].

Usually, transcription termination sequences recognized by bacteria are regulatory regions located 3' to the translation stop codon, and thus together with the promoter flank the coding sequence. These sequences direct the transcription of an mRNA which can be translated into the polypeptide encoded by the DNA. Transcription termination sequences frequently include DNA sequences of about 50 nucleotides capable of forming stem loop structures that aid in
35 terminating transcription. Examples include transcription termination sequences derived from genes with strong promoters, such as the *trp* gene in *E. coli* as well as other biosynthetic genes.

Usually, the above described components, comprising a promoter, signal sequence (if desired), coding sequence of interest, and transcription termination sequence, are put together into expression constructs. Expression constructs are often maintained in a replicon, such as an extrachromosomal element (*eg.* plasmids) capable of stable maintenance in
40 a host, such as bacteria. The replicon will have a replication system, thus allowing it to be maintained in a prokaryotic host either for expression or for cloning and amplification. In addition, a replicon may be either a high or low copy

number plasmid. A high copy number plasmid will generally have a copy number ranging from about 5 to about 200, and usually about 10 to about 150. A host containing a high copy number plasmid will preferably contain at least about 10, and more preferably at least about 20 plasmids. Either a high or low copy number vector may be selected, depending upon the effect of the vector and the foreign protein on the host.

5 Alternatively, the expression constructs can be integrated into the bacterial genome with an integrating vector. Integrating vectors usually contain at least one sequence homologous to the bacterial chromosome that allows the vector to integrate. Integrations appear to result from recombinations between homologous DNA in the vector and the bacterial chromosome. For example, integrating vectors constructed with DNA from various *Bacillus* strains integrate into the *Bacillus* chromosome (EP-A- 0 127 328). Integrating vectors may also be comprised of bacteriophage or
10 transposon sequences.

Usually, extrachromosomal and integrating expression constructs may contain selectable markers to allow for the selection of bacterial strains that have been transformed. Selectable markers can be expressed in the bacterial host and may include genes which render bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin (neomycin), and tetracycline [Davies *et al.* (1978) *Annu. Rev. Microbiol.* 32:469]. Selectable markers may
15 also include biosynthetic genes, such as those in the histidine, tryptophan, and leucine biosynthetic pathways.

Alternatively, some of the above described components can be put together in transformation vectors. Transformation vectors are usually comprised of a selectable market that is either maintained in a replicon or developed into an integrating vector, as described above.

Expression and transformation vectors, either extra-chromosomal replicons or integrating vectors, have been
20 developed for transformation into many bacteria. For example, expression vectors have been developed for, *inter alia*, the following bacteria: *Bacillus subtilis* [Palva *et al.* (1982) *Proc. Natl. Acad. Sci. USA* 79:5582; EP-A-0 036 259 and EP-A-0 063 953; WO 84/04541], *Escherichia coli* [Shimatake *et al.* (1981) *Nature* 292:128; Amann *et al.* (1985) *Gene* 40:183; Studier *et al.* (1986) *J. Mol. Biol.* 189:113; EP-A-0 036 776, EP-A-0 136 829 and EP-A-0 136 907], *Streptococcus cremoris* [Powell *et al.* (1988) *Appl. Environ. Microbiol.* 54:655]; *Streptococcus lividans* [Powell *et al.*
25 (1988) *Appl. Environ. Microbiol.* 54:655], *Streptomyces lividans* [US patent 4,745,056].

Methods of introducing exogenous DNA into bacterial hosts are well-known in the art, and usually include either the transformation of bacteria treated with CaCl_2 or other agents, such as divalent cations and DMSO. DNA can also be introduced into bacterial cells by electroporation. Transformation procedures usually vary with the bacterial species to be transformed. See *eg.* [Masson *et al.* (1989) *FEMS Microbiol. Lett.* 60:273; Palva *et al.* (1982) *Proc. Natl. Acad. Sci. USA* 79:5582; EP-A-0 036 259 and EP-A-0 063 953; WO 84/04541, *Bacillus*], [Miller *et al.* (1988) *Proc. Natl. Acad. Sci.* 85:856; Wang *et al.* (1990) *J. Bacteriol.* 172:949, *Campylobacter*], [Cohen *et al.* (1973) *Proc. Natl. Acad. Sci.* 69:2110; Dower *et al.* (1988) *Nucleic Acids Res.* 16:6127; Kushner (1978) "An improved method for transformation of *Escherichia coli* with ColE1-derived plasmids. In *Genetic Engineering: Proceedings of the International Symposium on Genetic Engineering* (eds. H.W. Boyer and S. Nicosia); Mandel *et al.* (1970) *J. Mol. Biol.* 53:159; Taketo (1988) *Biochim. Biophys. Acta* 949:318; *Escherichia*], [Chassy *et al.* (1987) *FEMS Microbiol. Lett.* 44:173 *Lactobacillus*]; [Fiedler *et al.* (1988) *Anal. Biochem* 170:38, *Pseudomonas*]; [Augustin *et al.* (1990) *FEMS Microbiol. Lett.* 66:203, *Staphylococcus*], [Barany *et al.* (1980) *J. Bacteriol.* 144:698; Harlander (1987) "Transformation of *Streptococcus lactis* by electroporation, in: *Streptococcal Genetics* (ed. J. Ferretti and R. Curtiss III); Perry *et al.* (1981) *Infect. Immun.* 32:1295; Powell *et al.* (1988) *Appl. Environ. Microbiol.* 54:655; Somkuti *et al.*
30 (1987) *Proc. 4th Evr. Cong. Biotechnology I*:412, *Streptococcus*].
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v. Yeast Expression

Yeast expression systems are also known to one of ordinary skill in the art. A yeast promoter is any DNA sequence capable of binding yeast RNA polymerase and initiating the downstream (3') transcription of a coding sequence (eg. structural gene) into mRNA. A promoter will have a transcription initiation region which is usually placed proximal to the 5' end of the coding sequence. This transcription initiation region usually includes an RNA polymerase binding site (the "TATA Box") and a transcription initiation site. A yeast promoter may also have a second domain called an upstream activator sequence (UAS), which, if present, is usually distal to the structural gene. The UAS permits regulated (inducible) expression. Constitutive expression occurs in the absence of a UAS. Regulated expression may be either positive or negative, thereby either enhancing or reducing transcription.

Yeast is a fermenting organism with an active metabolic pathway, therefore sequences encoding enzymes in the metabolic pathway provide particularly useful promoter sequences. Examples include alcohol dehydrogenase (ADH) (EP-A-0 284 044), enolase, glucokinase, glucose-6-phosphate isomerase, glyceraldehyde-3-phosphate-dehydrogenase (GAP or GAPDH), hexokinase, phosphofructokinase, 3-phosphoglycerate mutase, and pyruvate kinase (PyK) (EPO-A-0 329 203). The yeast *PHO5* gene, encoding acid phosphatase, also provides useful promoter sequences [Myanohara *et al.* (1983) *Proc. Natl. Acad. Sci. USA* 80:1].

In addition, synthetic promoters which do not occur in nature also function as yeast promoters. For example, UAS sequences of one yeast promoter may be joined with the transcription activation region of another yeast promoter, creating a synthetic hybrid promoter. Examples of such hybrid promoters include the ADH regulatory sequence linked to the GAP transcription activation region (US Patent Nos. 4,876,197 and 4,880,734). Other examples of hybrid promoters include promoters which consist of the regulatory sequences of either the *ADH2*, *GAL4*, *GAL10*, OR *PHO5* genes, combined with the transcriptional activation region of a glycolytic enzyme gene such as GAP or PyK (EP-A-0 164 556). Furthermore, a yeast promoter can include naturally occurring promoters of non-yeast origin that have the ability to bind yeast RNA polymerase and initiate transcription. Examples of such promoters include, *inter alia*, [Cohen *et al.* (1980) *Proc. Natl. Acad. Sci. USA* 77:1078; Henikoff *et al.* (1981) *Nature* 283:835; Hollenberg *et al.* (1981) *Curr. Topics Microbiol. Immunol.* 96:119; Hollenberg *et al.* (1979) "The Expression of Bacterial Antibiotic Resistance Genes in the Yeast *Saccharomyces cerevisiae*," in: *Plasmids of Medical, Environmental and Commercial Importance* (eds. K.N. Timmis and A. Puhler); Mercerau-Puigalon *et al.* (1980) *Gene* 11:163; Panthier *et al.* (1980) *Curr. Genet.* 2:109;].

A DNA molecule may be expressed intracellularly in yeast. A promoter sequence may be directly linked with the DNA molecule, in which case the first amino acid at the N-terminus of the recombinant protein will always be a methionine, which is encoded by the ATG start codon. If desired, methionine at the N-terminus may be cleaved from the protein by *in vitro* incubation with cyanogen bromide.

Fusion proteins provide an alternative for yeast expression systems, as well as in mammalian, baculovirus, and bacterial expression systems. Usually, a DNA sequence encoding the N-terminal portion of an endogenous yeast protein, or other stable protein, is fused to the 5' end of heterologous coding sequences. Upon expression, this construct will provide a fusion of the two amino acid sequences. For example, the yeast or human superoxide dismutase (SOD) gene, can be linked at the 5' terminus of a foreign gene and expressed in yeast. The DNA sequence at the junction of the two amino acid sequences may or may not encode a cleavable site. See eg. EP-A-0 196 056. Another example is a ubiquitin fusion protein. Such a fusion protein is made with the ubiquitin region that preferably retains a site for a processing enzyme (eg. ubiquitin-specific processing protease) to cleave the ubiquitin from the foreign protein. Through this method, therefore, native foreign protein can be isolated (eg. WO 88/024066).

Alternatively, foreign proteins can also be secreted from the cell into the growth media by creating chimeric DNA molecules that encode a fusion protein comprised of a leader sequence fragment that provide for secretion in yeast of the foreign protein. Preferably, there are processing sites encoded between the leader fragment and the foreign gene that can be cleaved either *in vivo* or *in vitro*. The leader sequence fragment usually encodes a signal peptide comprised of hydrophobic amino acids which direct the secretion of the protein from the cell.

DNA encoding suitable signal sequences can be derived from genes for secreted yeast proteins, such as the yeast invertase gene (EP-A-0 012 873; JPO. 62,096,086) and the A-factor gene (US patent 4,588,684). Alternatively, leaders of non-yeast origin, such as an interferon leader, exist that also provide for secretion in yeast (EP-A-0 060 057).

- 10 A preferred class of secretion leaders are those that employ a fragment of the yeast alpha-factor gene, which contains both a "pre" signal sequence, and a "pro" region. The types of alpha-factor fragments that can be employed include the full-length pre-pro alpha factor leader (about 83 amino acid residues) as well as truncated alpha-factor leaders (usually about 25 to about 50 amino acid residues) (US Patents 4,546,083 and 4,870,008; EP-A-0 324 274). Additional leaders employing an alpha-factor leader fragment that provides for secretion include hybrid alpha-factor leaders made with a presequence of a first yeast, but a pro-region from a second yeast alphafactor. (eg. see WO 89/02463.)

- Usually, transcription termination sequences recognized by yeast are regulatory regions located 3' to the translation stop codon, and thus together with the promoter flank the coding sequence. These sequences direct the transcription of an mRNA which can be translated into the polypeptide encoded by the DNA. Examples of transcription terminator sequence and other yeast-recognized termination sequences, such as those coding for glycolytic enzymes.

- Usually, the above described components, comprising a promoter, leader (if desired), coding sequence of interest, and transcription termination sequence, are put together into expression constructs. Expression constructs are often maintained in a replicon, such as an extrachromosomal element (eg. plasmids) capable of stable maintenance in a host, such as yeast or bacteria. The replicon may have two replication systems, thus allowing it to be maintained, for example, in yeast for expression and in a prokaryotic host for cloning and amplification. Examples of such yeast-bacteria shuttle vectors include YEp24 [Botstein *et al.* (1979) *Gene* 8:17-24], pC1/1 [Brake *et al.* (1984) *Proc. Natl. Acad. Sci USA* 81:4642-4646], and YRp17 [Stinchcomb *et al.* (1982) *J. Mol. Biol.* 158:157]. In addition, a replicon may be either a high or low copy number plasmid. A high copy number plasmid will generally have a copy number ranging from about 5 to about 200, and usually about 10 to about 150. A host containing a high copy number plasmid will preferably have at least about 10, and more preferably at least about 20. Enter a high or low copy number vector may be selected, depending upon the effect of the vector and the foreign protein on the host. See eg. Brake *et al.*, *supra*.

- Alternatively, the expression constructs can be integrated into the yeast genome with an integrating vector. Integrating vectors usually contain at least one sequence homologous to a yeast chromosome that allows the vector to integrate, and preferably contain two homologous sequences flanking the expression construct. Integrations appear to result from recombinations between homologous DNA in the vector and the yeast chromosome [Orr-Weaver *et al.* (1983) *Methods in Enzymol.* 101:228-245]. An integrating vector may be directed to a specific locus in yeast by selecting the appropriate homologous sequence for inclusion in the vector. See Orr-Weaver *et al.*, *supra*. One or more expression construct may integrate, possibly affecting levels of recombinant protein produced [Rine *et al.* (1983) *Proc. Natl. Acad. Sci. USA* 80:6750]. The chromosomal sequences included in the vector can occur either as a single segment in the vector, which results in the integration of the entire vector, or two segments homologous to adjacent

segments in the chromosome and flanking the expression construct in the vector, which can result in the stable integration of only the expression construct.

Usually, extrachromosomal and integrating expression constructs may contain selectable markers to allow for the selection of yeast strains that have been transformed. Selectable markers may include biosynthetic genes that can be expressed in the yeast host, such as *ADE2*, *HIS4*, *LEU2*, *TRP1*, and *ALG7*, and the G418 resistance gene, which confer resistance in yeast cells to tunicamycin and G418, respectively. In addition, a suitable selectable marker may also provide yeast with the ability to grow in the presence of toxic compounds, such as metal. For example, the presence of *CUP1* allows yeast to grow in the presence of copper ions [Butt *et al.* (1987) *Microbiol. Rev.* 51:351].

Alternatively, some of the above described components can be put together into transformation vectors. Transformation vectors are usually comprised of a selectable marker that is either maintained in a replicon or developed into an integrating vector, as described above.

Expression and transformation vectors, either extrachromosomal replicons or integrating vectors, have been developed for transformation into many yeasts. For example, expression vectors have been developed for, *inter alia*, the following yeasts: *Candida albicans* [Kurtz, *et al.* (1986) *Mol. Cell. Biol.* 6:142], *Candida maltosa* [Kunze, *et al.* (1985) *J. Basic Microbiol.* 25:141], *Hansenula polymorpha* [Gleeson, *et al.* (1986) *J. Gen. Microbiol.* 132:3459; Roggenkamp *et al.* (1986) *Mol. Gen. Genet.* 202:302], *Kluyveromyces fragilis* [Das, *et al.* (1984) *J. Bacteriol.* 158:1165], *Kluyveromyces lactis* [De Louvencourt *et al.* (1983) *J. Bacteriol.* 154:737; Van den Berg *et al.* (1990) *Bio/Technology* 8:135], *Pichia guilliermondii* [Kunze *et al.* (1985) *J. Basic Microbiol.* 25:141], *Pichia pastoris* [Cregg, *et al.* (1985) *Mol. Cell. Biol.* 5:3376; US Patent Nos. 4,837,148 and 4,929,555], *Saccharomyces cerevisiae* [Hinnen *et al.* (1978) *Proc. Natl. Acad. Sci. USA* 75:1929; Ito *et al.* (1983) *J. Bacteriol.* 153:163], *Schizosaccharomyces pombe* [Beach and Nurse (1981) *Nature* 300:706], and *Yarrowia lipolytica* [Davidow, *et al.* (1985) *Curr. Genet.* 10:380471 Gaillardin, *et al.* (1985) *Curr. Genet.* 10:49].

Methods of introducing exogenous DNA into yeast hosts are well-known in the art, and usually include either the transformation of spheroplasts or of intact yeast cells treated with alkali cations. Transformation procedures usually vary with the yeast species to be transformed. See *eg.* [Kurtz *et al.* (1986) *Mol. Cell. Biol.* 6:142; Kunze *et al.* (1985) *J. Basic Microbiol.* 25:141; *Candida*]; [Gleeson *et al.* (1986) *J. Gen. Microbiol.* 132:3459; Roggenkamp *et al.* (1986) *Mol. Gen. Genet.* 202:302; *Hansenula*]; [Das *et al.* (1984) *J. Bacteriol.* 158:1165; De Louvencourt *et al.* (1983) *J. Bacteriol.* 154:1165; Van den Berg *et al.* (1990) *Bio/Technology* 8:135; *Kluyveromyces*]; [Cregg *et al.* (1985) *Mol. Cell. Biol.* 5:3376; Kunze *et al.* (1985) *J. Basic Microbiol.* 25:141; US Patent Nos. 4,837,148 and 4,929,555; *Pichia*]; [Hinnen *et al.* (1978) *Proc. Natl. Acad. Sci. USA* 75:1929; Ito *et al.* (1983) *J. Bacteriol.* 153:163 *Saccharomyces*]; [Beach and Nurse (1981) *Nature* 300:706; *Schizosaccharomyces*]; [Davidow *et al.* (1985) *Curr. Genet.* 10:39; Gaillardin *et al.* (1985) *Curr. Genet.* 10:49; *Yarrowia*].

Antibodies

As used herein, the term "antibody" refers to a polypeptide or group of polypeptides composed of at least one antibody combining site. An "antibody combining site" is the three-dimensional binding space with an internal surface shape and charge distribution complementary to the features of an epitope of an antigen, which allows a binding of the antibody with the antigen. "Antibody" includes, for example, vertebrate antibodies, hybrid antibodies, chimeric antibodies, humanised antibodies, altered antibodies, univalent antibodies, Fab proteins, and single domain antibodies.

Antibodies against the proteins of the invention are useful for affinity chromatography, immunoassays, and distinguishing/identifying *Neisseria* proteins.

Antibodies to the proteins of the invention, both polyclonal and monoclonal, may be prepared by conventional methods. In general, the protein is first used to immunize a suitable animal, preferably a mouse, rat, rabbit or goat. Rabbits and goats are preferred for the preparation of polyclonal sera due to the volume of serum obtainable, and the availability of labeled anti-rabbit and anti-goat antibodies. Immunization is generally performed by mixing or emulsifying the protein in saline, preferably in an adjuvant such as Freund's complete adjuvant, and injecting the mixture or emulsion parenterally (generally subcutaneously or intramuscularly). A dose of 50-200 µg/injection is typically sufficient. Immunization is generally boosted 2-6 weeks later with one or more injections of the protein in saline, preferably using Freund's incomplete adjuvant. One may alternatively generate antibodies by *in vitro* immunization using methods known in the art, which for the purposes of this invention is considered equivalent to *in vivo* immunization. Polyclonal antisera is obtained by bleeding the immunized animal into a glass or plastic container, incubating the blood at 25°C for one hour, followed by incubating at 4°C for 2-18 hours. The serum is recovered by centrifugation (eg. 1,000g for 10 minutes). About 20-50 ml per bleed may be obtained from rabbits.

Monoclonal antibodies are prepared using the standard method of Kohler & Milstein [*Nature* (1975) 256:495-96], or a modification thereof. Typically, a mouse or rat is immunized as described above. However, rather than bleeding the animal to extract serum, the spleen (and optionally several large lymph nodes) is removed and dissociated into single cells. If desired, the spleen cells may be screened (after removal of nonspecifically adherent cells) by applying a cell suspension to a plate or well coated with the protein antigen. B-cells expressing membrane-bound immunoglobulin specific for the antigen bind to the plate, and are not rinsed away with the rest of the suspension. Resulting B-cells, or all dissociated spleen cells, are then induced to fuse with myeloma cells to form hybridomas, and are cultured in a selective medium (eg. hypoxanthine, aminopterin, thymidine medium, "HAT"). The resulting hybridomas are plated by limiting dilution, and are assayed for production of antibodies which bind specifically to the immunizing antigen (and which do not bind to unrelated antigens). The selected MAb-secreting hybridomas are then cultured either *in vitro* (eg. in tissue culture bottles or hollow fiber reactors), or *in vivo* (as ascites in mice).

If desired, the antibodies (whether polyclonal or monoclonal) may be labeled using conventional techniques. Suitable labels include fluorophores, chromophores, radioactive atoms (particularly ³²P and ¹²⁵I), electron-dense reagents, enzymes, and ligands having specific binding partners. Enzymes are typically detected by their activity. For example, horseradish peroxidase is usually detected by its ability to convert 3,3',5,5'-tetramethylbenzidine (TMB) to a blue pigment, quantifiable with a spectrophotometer. "Specific binding partner" refers to a protein capable of binding a ligand molecule with high specificity, as for example in the case of an antigen and a monoclonal antibody specific therefor. Other specific binding partners include biotin and avidin or streptavidin, IgG and protein A, and the numerous receptor-ligand couples known in the art. It should be understood that the above description is not meant to categorize the various labels into distinct classes, as the same label may serve in several different modes. For example, ¹²⁵I may serve as a radioactive label or as an electron-dense reagent. HRP may serve as enzyme or as antigen for a MAb. Further, one may combine various labels for desired effect. For example, MAbs and avidin also require labels in the practice of this invention: thus, one might label a MAb with biotin, and detect its presence with avidin labeled with ¹²⁵I, or with an anti-biotin MAb labeled with HRP. Other permutations and possibilities will be readily apparent to those of ordinary skill in the art, and are considered as equivalents within the scope of the instant invention.

Pharmaceutical Compositions

Pharmaceutical compositions can comprise either polypeptides, antibodies, or nucleic acid of the invention. The pharmaceutical compositions will comprise a therapeutically effective amount of either polypeptides, antibodies, or polynucleotides of the claimed invention.

- 5 The term "therapeutically effective amount" as used herein refers to an amount of a therapeutic agent to treat, ameliorate, or prevent a desired disease or condition, or to exhibit a detectable therapeutic or preventative effect. The effect can be detected by, for example, chemical markers or antigen levels. Therapeutic effects also include reduction in physical symptoms, such as decreased body temperature. The precise effective amount for a subject will depend upon the subject's size and health, the nature and extent of the condition, and the therapeutics or combination of therapeutics selected for administration. Thus, it is not useful to specify an exact effective amount in advance. However, the effective amount for a given situation can be determined by routine experimentation and is within the judgement of the clinician.

For purposes of the present invention, an effective dose will be from about 0.01 mg/kg to 50 mg/kg or 0.05 mg/kg to about 10 mg/kg of the DNA constructs in the individual to which it is administered.

- 15 A pharmaceutical composition can also contain a pharmaceutically acceptable carrier. The term "pharmaceutically acceptable carrier" refers to a carrier for administration of a therapeutic agent, such as antibodies or a polypeptide, genes, and other therapeutic agents. The term refers to any pharmaceutical carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition, and which may be administered without undue toxicity. Suitable carriers may be large, slowly metabolized macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers, and inactive virus particles. Such carriers are well known to those of ordinary skill in the art.

- 20 Pharmaceutically acceptable salts can be used therein, for example, mineral acid salts such as hydrochlorides, hydrobromides, phosphates, sulfates, and the like; and the salts of organic acids such as acetates, propionates, malonates, benzoates, and the like. A thorough discussion of pharmaceutically acceptable excipients is available in Remington's Pharmaceutical Sciences (Mack Pub. Co., N.J. 1991).

- 25 Pharmaceutically acceptable carriers in therapeutic compositions may contain liquids such as water, saline, glycerol and ethanol. Additionally, auxiliary substances, such as wetting or emulsifying agents, pH buffering substances, and the like, may be present in such vehicles. Typically, the therapeutic compositions are prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid vehicles prior to injection may also be prepared. Liposomes are included within the definition of a pharmaceutically acceptable carrier.

Delivery Methods

Once formulated, the compositions of the invention can be administered directly to the subject. The subjects to be treated can be animals; in particular, human subjects can be treated.

- 35 Direct delivery of the compositions will generally be accomplished by injection, either subcutaneously, intraperitoneally, intravenously or intramuscularly or delivered to the interstitial space of a tissue. The compositions can also be administered into a lesion. Other modes of administration include oral and pulmonary administration, suppositories, and transdermal or transcutaneous applications (eg. see WO98/20734), needles, and gene guns or hypodermic sprays. Dosage treatment may be a single dose schedule or a multiple dose schedule.

Vaccines

Vaccines according to the invention may either be prophylactic (*ie.* to prevent infection) or therapeutic (*ie.* to treat disease after infection).

Such vaccines comprise immunising antigen(s), immunogen(s), polypeptide(s), protein(s) or nucleic acid, usually in combination with "pharmaceutically acceptable carriers," which include any carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition. Suitable carriers are typically large, slowly metabolized macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers, lipid aggregates (such as oil droplets or liposomes), and inactive virus particles. Such carriers are well known to those of ordinary skill in the art. Additionally, these carriers may function as immunostimulating agents ("adjuvants"). Furthermore, the antigen or immunogen may be conjugated to a bacterial toxoid, such as a toxoid from diphtheria, tetanus, cholera, *H. pylori*, *etc.* pathogens.

Preferred adjuvants to enhance effectiveness of the composition include, but are not limited to: (1) aluminum salts (alum), such as aluminum hydroxide, aluminum phosphate, aluminum sulfate, *etc.*; (2) oil-in-water emulsion formulations (with or without other specific immunostimulating agents such as muramyl peptides (see below) or bacterial cell wall components), such as for example (a) MF59™ (WO 90/14837; Chapter 10 in *Vaccine design: the subunit and adjuvant approach*, eds. Powell & Newman, Plenum Press 1995), containing 5% Squalene, 0.5% Tween 80, and 0.5% Span 85 (optionally containing various amounts of MTP-PE (see below), although not required) formulated into submicron particles using a microfluidizer such as Model 110Y microfluidizer (Microfluidics, Newton, MA), (b) SAF, containing 10% Squalane, 0.4% Tween 80, 5% pluronic-blocked polymer L121, and thr-MDP (see below) either microfluidized into a submicron emulsion or vortexed to generate a larger particle size emulsion, and (c) Ribi™ adjuvant system (RAS), (Ribi Immunochem, Hamilton, MT) containing 2% Squalene, 0.2% Tween 80, and one or more bacterial cell wall components from the group consisting of monophosphorylipid A (MPL), trehalose dimycolate (TDM), and cell wall skeleton (CWS), preferably MPL + CWS (Detox™); (3) saponin adjuvants, such as Stimulon™ (Cambridge Bioscience, Worcester, MA) may be used or particles generated therefrom such as ISCOMs (immunostimulating complexes); (4) Complete Freund's Adjuvant (CFA) and Incomplete Freund's Adjuvant (IFA); (5) cytokines, such as interleukins (*eg.* IL-1, IL-2, IL-4, IL-5, IL-6, IL-7, IL-12, *etc.*), interferons (*eg.* gamma interferon), macrophage colony stimulating factor (M-CSF), tumor necrosis factor (TNF), *etc.*; and (6) other substances that act as immunostimulating agents to enhance the effectiveness of the composition. Alum and MF59™ are preferred.

As mentioned above, muramyl peptides include, but are not limited to, N-acetyl-muramyl-L-threonyl-D-isoglutamine (thr-MDP), N-acetyl-normuramyl-L-alanyl-D-isoglutamine (nor-MDP), N-acetylmuramyl-L-alanyl-D-isoglutaminyl-L-alanine-2-(1'-2'-dipalmitoyl-*sn*-glycero-3-hydroxyphosphoryloxy)-ethylamine (MTP-PE), *etc.*

The immunogenic compositions (*eg.* the immunising antigen/immunogen/polypeptide/protein/ nucleic acid, pharmaceutically acceptable carrier, and adjuvant) typically will contain diluents, such as water, saline, glycerol, ethanol, *etc.* Additionally, auxiliary substances, such as wetting or emulsifying agents, pH buffering substances, and the like, may be present in such vehicles.

Typically, the immunogenic compositions are prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid vehicles prior to injection may also be prepared. The preparation also may be emulsified or encapsulated in liposomes for enhanced adjuvant effect, as discussed above under pharmaceutically acceptable carriers.

Immunogenic compositions used as vaccines comprise an immunologically effective amount of the antigenic or immunogenic polypeptides, as well as any other of the above-mentioned components, as needed. By "immunologically effective amount", it is meant that the administration of that amount to an individual, either in a single dose or as part of a series, is effective for treatment or prevention. This amount varies depending upon the health and physical condition of the individual to be treated, the taxonomic group of individual to be treated (eg. nonhuman primate, primate, etc.), the capacity of the individual's immune system to synthesize antibodies, the degree of protection desired, the formulation of the vaccine, the treating doctor's assessment of the medical situation, and other relevant factors. It is expected that the amount will fall in a relatively broad range that can be determined through routine trials.

- 10 The immunogenic compositions are conventionally administered parenterally, eg. by injection, either subcutaneously, intramuscularly, or transdermally/transcutaneously (eg. WO98/20734). Additional formulations suitable for other modes of administration include oral and pulmonary formulations, suppositories, and transdermal applications. Dosage treatment may be a single dose schedule or a multiple dose schedule. The vaccine may be administered in conjunction with other immunoregulatory agents.
- 15 As an alternative to protein-based vaccines, DNA vaccination may be used [eg. Robinson & Torres (1997) *Seminars in Immunol* 9:271-283; Donnelly *et al.* (1997) *Annu Rev Immunol* 15:617-648; later herein].

Gene Delivery Vehicles

Gene therapy vehicles for delivery of constructs including a coding sequence of a therapeutic of the invention, to be delivered to the mammal for expression in the mammal, can be administered either locally or systemically. These constructs can utilize viral or non-viral vector approaches in *in vivo* or *ex vivo* modality. Expression of such coding sequence can be induced using endogenous mammalian or heterologous promoters. Expression of the coding sequence *in vivo* can be either constitutive or regulated.

The invention includes gene delivery vehicles capable of expressing the contemplated nucleic acid sequences. The gene delivery vehicle is preferably a viral vector and, more preferably, a retroviral, adenoviral, adeno-associated viral (AAV), herpes viral, or alphavirus vector. The viral vector can also be an astrovirus, coronavirus, orthomyxovirus, papovavirus, paramyxovirus, parvovirus, picornavirus, poxvirus, or togavirus viral vector. See generally, Jolly (1994) *Cancer Gene Therapy* 1:51-64; Kimura (1994) *Human Gene Therapy* 5:845-852; Connelly (1995) *Human Gene Therapy* 6:185-193; and Kaplitt (1994) *Nature Genetics* 6:148-153.

Retroviral vectors are well known in the art and we contemplate that any retroviral gene therapy vector is employable in the invention, including B, C and D type retroviruses, xenotropic retroviruses (for example, NZB-X1, NZB-X2 and NZB9-1 (see O'Neill (1985) *J. Virol.* 53:160) polytropic retroviruses eg. MCF and MCF-MLV (see Kelly (1983) *J. Virol.* 45:291), spumaviruses and lentiviruses. See RNA Tumor Viruses, Second Edition, Cold Spring Harbor Laboratory, 1985.

Portions of the retroviral gene therapy vector may be derived from different retroviruses. For example, retrovector LTRs may be derived from a Murine Sarcoma Virus, a tRNA binding site from a Rous Sarcoma Virus, a packaging signal from a Murine Leukemia Virus, and an origin of second strand synthesis from an Avian Leukosis Virus.

These recombinant retroviral vectors may be used to generate transduction competent retroviral vector particles by introducing them into appropriate packaging cell lines (see US patent 5,591,624). Retrovirus vectors can be constructed for site-specific integration into host cell DNA by incorporation of a chimeric integrase enzyme into the

retroviral particle (see WO96/37626). It is preferable that the recombinant viral vector is a replication defective recombinant virus.

Packaging cell lines suitable for use with the above-described retrovirus vectors are well known in the art, are readily prepared (see WO95/30763 and WO92/05266), and can be used to create producer cell lines (also termed vector cell lines or "VCLs") for the production of recombinant vector particles. Preferably, the packaging cell lines are made from human parent cells (eg. HT1080 cells) or mink parent cell lines, which eliminates inactivation in human serum.

Preferred retroviruses for the construction of retroviral gene therapy vectors include Avian Leukosis Virus, Bovine Leukemia Virus, Murine Leukemia Virus, Mink-Cell Focus-Inducing Virus, Murine Sarcoma Virus, Reticuloendotheliosis Virus and Rous Sarcoma Virus. Particularly preferred Murine Leukemia Viruses include 4070A and 1504A (Hartley and Rowe (1976) *J Virol* 19:19-25), Abelson (ATCC No. VR-999), Friend (ATCC No. VR-245), Graffi, Gross (ATCC No. VR-590), Kirsten, Harvey Sarcoma Virus and Rauscher (ATCC No. VR-998) and Moloney Murine Leukemia Virus (ATCC No. VR-190). Such retroviruses may be obtained from depositories or collections such as the American Type Culture Collection ("ATCC") in Rockville, Maryland or isolated from known sources using commonly available techniques.

Exemplary known retroviral gene therapy vectors employable in this invention include those described in patent applications GB2200651, EP0415731, EP0345242, EP0334301, WO89/02468; WO89/05349, WO89/09271, WO90/02806, WO90/07936, WO94/03622, WO93/25698, WO93/25234, WO93/11230, WO93/10218, WO91/02805, WO91/02825, WO95/07994, US 5,219,740, US 4,405,712, US 4,861,719, US 4,980,289, US 4,777,127, US 5,591,624. See also Vile (1993) *Cancer Res* 53:3860-3864; Vile (1993) *Cancer Res* 53:962-967; Ram (1993) *Cancer Res* 53 (1993) 83-88; Takamiya (1992) *J Neurosci Res* 33:493-503; Baba (1993) *J Neurosurg* 79:729-735; Mann (1983) *Cell* 33:153; Cane (1984) *Proc Natl Acad Sci* 81:6349; and Miller (1990) *Human Gene Therapy* 1.

Human adenoviral gene therapy vectors are also known in the art and employable in this invention. See, for example, Berkner (1988) *Biotechniques* 6:616 and Rosenfeld (1991) *Science* 252:431, and WO93/07283, WO93/06223, and WO93/07282. Exemplary known adenoviral gene therapy vectors employable in this invention include those described in the above referenced documents and in WO94/12649, WO93/03769, WO93/19191, WO94/28938, WO95/11984, WO95/00655, WO95/27071, WO95/29993, WO95/34671, WO96/05320, WO94/08026, WO94/11506, WO93/06223, WO94/24299, WO95/14102, WO95/24297, WO95/02697, WO94/28152, WO94/24299, WO95/09241, WO95/25807, WO95/05835, WO94/18922 and WO95/09654. Alternatively, administration of DNA linked to killed adenovirus as described in Curiel (1992) *Hum. Gene Ther.* 3:147-154 may be employed. The gene delivery vehicles of the invention also include adenovirus associated virus (AAV) vectors. Leading and preferred examples of such vectors for use in this invention are the AAV-2 based vectors disclosed in Srivastava, WO93/09239. Most preferred AAV vectors comprise the two AAV inverted terminal repeats in which the native D-sequences are modified by substitution of nucleotides, such that at least 5 native nucleotides and up to 18 native nucleotides, preferably at least 10 native nucleotides up to 18 native nucleotides, most preferably 10 native nucleotides are retained and the remaining nucleotides of the D-sequence are deleted or replaced with non-native nucleotides. The native D-sequences of the AAV inverted terminal repeats are sequences of 20 consecutive nucleotides in each AAV inverted terminal repeat (ie. there is one sequence at each end) which are not involved in HP formation. The non-native replacement nucleotide may be any nucleotide other than the nucleotide found in the native D-sequence in the same position. Other employable exemplary AAV vectors are pWP-19, pWN-1, both of which are disclosed in Nahreini (1993) *Gene* 124:257-262. Another example of such an AAV vector is psub201 (see Samulski (1987) *J. Virol.* 61:3096). Another exemplary AAV vector is the Double-D ITR vector. Construction of the Double-D ITR vector is disclosed in

US Patent 5,478,745. Still other vectors are those disclosed in Carter US Patent 4,797,368 and Muzyczka US Patent 5,139,941, Chartejee US Patent 5,474,935, and Kotin WO94/288157. Yet a further example of an AAV vector employable in this invention is SSV9AFABTKneo, which contains the AFP enhancer and albumin promoter and directs expression predominantly in the liver. Its structure and construction are disclosed in Su (1996) *Human Gene Therapy* 7:463-470. Additional AAV gene therapy vectors are described in US 5,354,678, US 5,173,414, US 5,139,941, and US 5,252,479.

The gene therapy vectors of the invention also include herpes vectors. Leading and preferred examples are herpes simplex virus vectors containing a sequence encoding a thymidine kinase polypeptide such as those disclosed in US 5,288,641 and EP0176170 (Roizman). Additional exemplary herpes simplex virus vectors include HFEM/ICP6-LacZ disclosed in WO95/04139 (Wistar Institute), pHSVlac described in Geller (1988) *Science* 241:1667-1669 and in WO90/09441 and WO92/07945, HSV Us3::pgC-lacZ described in Fink (1992) *Human Gene Therapy* 3:11-19 and HSV 7134, 2 RH 105 and GAL4 described in EP 0453242 (Breakefield), and those deposited with the ATCC with accession numbers VR-977 and VR-260.

Also contemplated are alpha virus gene therapy vectors that can be employed in this invention. Preferred alpha virus vectors are Sindbis viruses vectors. Togaviruses, Semliki Forest virus (ATCC VR-67; ATCC VR-1247), Middleberg virus (ATCC VR-370), Ross River virus (ATCC VR-373; ATCC VR-1246), Venezuelan equine encephalitis virus (ATCC VR923; ATCC VR-1250; ATCC VR-1249; ATCC VR-532), and those described in US patents 5,091,309, 5,217,879, and WO92/10578. More particularly, those alpha virus vectors described in US Serial No. 08/405,627, filed March 15, 1995, WO94/21792, WO92/10578, WO95/07994, US 5,091,309 and US 5,217,879 are employable. Such alpha viruses may be obtained from depositories or collections such as the ATCC in Rockville, Maryland or isolated from known sources using commonly available techniques. Preferably, alphavirus vectors with reduced cytotoxicity are used (see USSN 08/679640).

DNA vector systems such as eukaryotic layered expression systems are also useful for expressing the nucleic acids of the invention. See WO95/07994 for a detailed description of eukaryotic layered expression systems. Preferably, the eukaryotic layered expression systems of the invention are derived from alphavirus vectors and most preferably from Sindbis viral vectors.

Other viral vectors suitable for use in the present invention include those derived from poliovirus, for example ATCC VR-58 and those described in Evans, *Nature* 339 (1989) 385 and Sabin (1973) *J. Biol. Standardization* 1:115; rhinovirus, for example ATCC VR-1110 and those described in Arnold (1990) *J Cell Biochem* L401; pox viruses such as canary pox virus or vaccinia virus, for example ATCC VR-111 and ATCC VR-2010 and those described in Fisher-Hoch (1989) *Proc Natl Acad Sci* 86:317; Flexner (1989) *Ann NY Acad Sci* 569:86, Flexner (1990) *Vaccine* 8:17; in US 4,603,112 and US 4,769,330 and WO89/01973; SV40 virus, for example ATCC VR-305 and those described in Mulligan (1979) *Nature* 277:108 and Madzak (1992) *J Gen Virol* 73:1533; influenza virus, for example ATCC VR-797 and recombinant influenza viruses made employing reverse genetics techniques as described in US 5,166,057 and in Enami (1990) *Proc Natl Acad Sci* 87:3802-3805; Enami & Palese (1991) *J Virol* 65:2711-2713 and Luytjes (1989) *Cell* 59:110, (see also McMichael (1983) *NEJ Med* 309:13, and Yap (1978) *Nature* 273:238 and *Nature* (1979) 277:108); human immunodeficiency virus as described in EP-0386882 and in Buchschacher (1992) *J. Virol.* 66:2731; measles virus, for example ATCC VR-67 and VR-1247 and those described in EP-0440219; Aura virus, for example ATCC VR-368; Bebaru virus, for example ATCC VR-600 and ATCC VR-1240; Cabassou virus, for example ATCC VR-922; Chikungunya virus, for example ATCC VR-64 and ATCC VR-1241; Fort Morgan Virus, for example ATCC VR-924; Getah virus, for example ATCC VR-369 and ATCC VR-1243; Kyzylagach virus,

for example ATCC VR-927; Mayaro virus, for example ATCC VR-66; Mucambo virus, for example ATCC VR-580 and ATCC VR-1244; Ndumu virus, for example ATCC VR-371; Pixuna virus, for example ATCC VR-372 and ATCC VR-1245; Tonate virus, for example ATCC VR-925; Trinit virus, for example ATCC VR-469; Una virus, for example ATCC VR-374; Whataroa virus, for example ATCC VR-926; Y-62-33 virus, for example ATCC VR-375; O'Nyong virus, Eastern encephalitis virus, for example ATCC VR-65 and ATCC VR-1242; Western encephalitis virus, for example ATCC VR-70, ATCC VR-1251, ATCC VR-622 and ATCC VR-1252; and coronavirus, for example ATCC VR-740 and those described in Hamre (1966) *Proc Soc Exp Biol Med* 121:190.

Delivery of the compositions of this invention into cells is not limited to the above mentioned viral vectors. Other delivery methods and media may be employed such as, for example, nucleic acid expression vectors, polycationic condensed DNA linked or unlinked to killed adenovirus alone, for example see US Serial No. 08/366,787, filed December 30, 1994 and Curiel (1992) *Hum Gene Ther* 3:147-154 ligand linked DNA, for example see Wu (1989) *J Biol Chem* 264:16985-16987, eucaryotic cell delivery vehicles cells, for example see US Serial No.08/240,030, filed May 9, 1994, and US Serial No. 08/404,796, deposition of photopolymerized hydrogel materials, hand-held gene transfer particle gun, as described in US Patent 5,149,655, ionizing radiation as described in US5,206,152 and in WO92/11033, nucleic charge neutralization or fusion with cell membranes. Additional approaches are described in Philip (1994) *Mol Cell Biol* 14:2411-2418 and in Woffendin (1994) *Proc Natl Acad Sci* 91:1581-1585.

Particle mediated gene transfer may be employed, for example see US Serial No. 60/023,867. Briefly, the sequence can be inserted into conventional vectors that contain conventional control sequences for high level expression, and then incubated with synthetic gene transfer molecules such as polymeric DNA-binding cations like polylysine, protamine, and albumin, linked to cell targeting ligands such as asialoorosomucoid, as described in Wu & Wu (1987) *J. Biol. Chem.* 262:4429-4432, insulin as described in Hucked (1990) *Biochem Pharmacol* 40:253-263, galactose as described in Plank (1992) *Bioconjugate Chem* 3:533-539, lactose or transferrin.

Naked DNA may also be employed. Exemplary naked DNA introduction methods are described in WO 90/11092 and US 5,580,859. Uptake efficiency may be improved using biodegradable latex beads. DNA coated latex beads are efficiently transported into cells after endocytosis initiation by the beads. The method may be improved further by treatment of the beads to increase hydrophobicity and thereby facilitate disruption of the endosome and release of the DNA into the cytoplasm.

Liposomes that can act as gene delivery vehicles are described in US 5,422,120, WO95/13796, WO94/23697, WO91/14445 and EP-524,968. As described in USSN. 60/023,867, on non-viral delivery, the nucleic acid sequences encoding a polypeptide can be inserted into conventional vectors that contain conventional control sequences for high level expression, and then be incubated with synthetic gene transfer molecules such as polymeric DNA-binding cations like polylysine, protamine, and albumin, linked to cell targeting ligands such as asialoorosomucoid, insulin, galactose, lactose, or transferrin. Other delivery systems include the use of liposomes to encapsulate DNA comprising the gene under the control of a variety of tissue-specific or ubiquitously-active promoters. Further non-viral delivery suitable for use includes mechanical delivery systems such as the approach described in Woffendin *et al* (1994) *Proc. Natl. Acad. Sci. USA* 91(24):11581-11585. Moreover, the coding sequence and the product of expression of such can be delivered through deposition of photopolymerized hydrogel materials. Other conventional methods for gene delivery that can be used for delivery of the coding sequence include, for example, use of hand-held gene transfer particle gun, as described in US 5,149,655; use of ionizing radiation for activating transferred gene, as described in US 5,206,152 and WO92/11033

Exemplary liposome and polycationic gene delivery vehicles are those described in US 5,422,120 and 4,762,915; in WO 95/13796; WO94/23697; and WO91/14445; in EP-0524968; and in Stryer, Biochemistry, pages 236-240 (1975) W.H. Freeman, San Francisco; Szoka (1980) *Biochem Biophys Acta* 600:1; Bayer (1979) *Biochem Biophys Acta* 550:464; Rivnay (1987) *Meth Enzymol* 149:119; Wang (1987) *Proc Natl Acad Sci* 84:7851; Plant (1989) *Anal Biochem* 176:420.

A polynucleotide composition can comprises therapeutically effective amount of a gene therapy vehicle, as the term is defined above. For purposes of the present invention, an effective dose will be from about 0.01 mg/kg to 50 mg/kg or 0.05 mg/kg to about 10 mg/kg of the DNA constructs in the individual to which it is administered.

Delivery Methods

Once formulated, the polynucleotide compositions of the invention can be administered (1) directly to the subject; (2) delivered *ex vivo*, to cells derived from the subject; or (3) *in vitro* for expression of recombinant proteins. The subjects to be treated can be mammals or birds. Also, human subjects can be treated.

Direct delivery of the compositions will generally be accomplished by injection, either subcutaneously, intraperitoneally, intravenously or intramuscularly or delivered to the interstitial space of a tissue. The compositions can also be administered into a lesion. Other modes of administration include oral and pulmonary administration, suppositories, and transdermal or transcutaneous applications (eg. see WO98/20734), needles, and gene guns or hypodermic sprays. Dosage treatment may be a single dose schedule or a multiple dose schedule.

Methods for the *ex vivo* delivery and reimplantation of transformed cells into a subject are known in the art and described in eg. WO93/14778. Examples of cells useful in *ex vivo* applications include, for example, stem cells, particularly hematopoietic, lymph cells, macrophages, dendritic cells, or tumor cells.

Generally, delivery of nucleic acids for both *ex vivo* and *in vitro* applications can be accomplished by the following procedures, for example, dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei, all well known in the art.

Polynucleotide and polypeptide pharmaceutical compositions

In addition to the pharmaceutically acceptable carriers and salts described above, the following additional agents can be used with polynucleotide and/or polypeptide compositions.

A. Polypeptides

One example are polypeptides which include, without limitation: asialoglycoprotein (ASOR); transferrin; asialoglycoproteins; antibodies; antibody fragments; ferritin; interleukins; interferons, granulocyte, macrophage colony stimulating factor (GM-CSF), granulocyte colony stimulating factor (G-CSF), macrophage colony stimulating factor (M-CSF), stem cell factor and erythropoietin. Viral antigens, such as envelope proteins, can also be used. Also, proteins from other invasive organisms, such as the 17 amino acid peptide from the circumsporozoite protein of *Plasmodium falciparum* known as RII.

B. Hormones, Vitamins, etc.

Other groups that can be included are, for example: hormones, steroids, androgens, estrogens, thyroid hormone, or vitamins, folic acid.

C. Polyalkylenes, Polysaccharides, etc.

Also, polyalkylene glycol can be included with the desired polynucleotides/polypeptides. In a preferred embodiment, the polyalkylene glycol is polyethylene glycol. In addition, mono-, di-, or polysaccharides can be included. In a preferred embodiment of this aspect, the polysaccharide is dextran or DEAE-dextran. Also, chitosan and poly(lactide-co-glycolide)

D. Lipids, and Liposomes

The desired polynucleotide/polypeptide can also be encapsulated in lipids or packaged in liposomes prior to delivery to the subject or to cells derived therefrom.

Lipid encapsulation is generally accomplished using liposomes which are able to stably bind or entrap and retain nucleic acid. The ratio of condensed polynucleotide to lipid preparation can vary but will generally be around 1:1 (mg DNA:micromoles lipid), or more of lipid. For a review of the use of liposomes as carriers for delivery of nucleic acids, see, Hug and Sleight (1991) *Biochim. Biophys. Acta.* 1097:1-17; Straubinger (1983) *Meth. Enzymol.* 101:512-527.

Liposomal preparations for use in the present invention include cationic (positively charged), anionic (negatively charged) and neutral preparations. Cationic liposomes have been shown to mediate intracellular delivery of plasmid DNA (Felgner (1987) *Proc. Natl. Acad. Sci. USA* 84:7413-7416); mRNA (Malone (1989) *Proc. Natl. Acad. Sci. USA* 86:6077-6081); and purified transcription factors (Debs (1990) *J. Biol. Chem.* 265:10189-10192), in functional form.

Cationic liposomes are readily available. For example, N[1-2,3-dioleoyloxy)propyl]-N,N,N-triethylammonium (DOTMA) liposomes are available under the trademark Lipofectin, from GIBCO BRL, Grand Island, NY. (See, also, Felgner *supra*). Other commercially available liposomes include transfectace (DDAB/DOPE) and DOTAP/DOPE (Boehringer). Other cationic liposomes can be prepared from readily available materials using techniques well known in the art. See, *eg.* Szoka (1978) *Proc. Natl. Acad. Sci. USA* 75:4194-4198; WO90/11092 for a description of the synthesis of DOTAP (1,2-bis(oleoyloxy)-3-(trimethylammonio)propane) liposomes.

Similarly, anionic and neutral liposomes are readily available, such as from Avanti Polar Lipids (Birmingham, AL), or can be easily prepared using readily available materials. Such materials include phosphatidyl choline, cholesterol, phosphatidyl ethanolamine, dioleoylphosphatidyl choline (DOPC), dioleoylphosphatidyl glycerol (DOPG), dioleoylphosphatidyl ethanolamine (DOPE), among others. These materials can also be mixed with the DOTMA and DOTAP starting materials in appropriate ratios. Methods for making liposomes using these materials are well known in the art.

The liposomes can comprise multilamellar vesicles (MLVs), small unilamellar vesicles (SUVs), or large unilamellar vesicles (LUVs). The various liposome-nucleic acid complexes are prepared using methods known in the art. See *eg.* Straubinger (1983) *Meth. Immunol.* 101:512-527; Szoka (1978) *Proc. Natl. Acad. Sci. USA* 75:4194-4198; Papahadjopoulos (1975) *Biochim. Biophys. Acta* 394:483; Wilson (1979) *Cell* 17:77; Deamer & Bangham (1976) *Biochim. Biophys. Acta* 443:629; Ostro (1977) *Biochem. Biophys. Res. Commun.* 76:836; Fraley (1979) *Proc. Natl. Acad. Sci. USA* 76:3348; Enoch & Strittmatter (1979) *Proc. Natl. Acad. Sci. USA* 76:145; Fraley (1980) *J. Biol. Chem.* (1980) 255:10431; Szoka & Papahadjopoulos (1978) *Proc. Natl. Acad. Sci. USA* 75:145; and Schaefer-Ridder (1982) *Science* 215:166.

E. Lipoproteins

In addition, lipoproteins can be included with the polynucleotide/polypeptide to be delivered. Examples of lipoproteins to be utilized include: chylomicrons, HDL, IDL, LDL, and VLDL. Mutants, fragments, or fusions of

these proteins can also be used. Also, modifications of naturally occurring lipoproteins can be used, such as acetylated LDL. These lipoproteins can target the delivery of polynucleotides to cells expressing lipoprotein receptors. Preferably, if lipoproteins are including with the polynucleotide to be delivered, no other targeting ligand is included in the composition.

- 5 Naturally occurring lipoproteins comprise a lipid and a protein portion. The protein portion are known as apoproteins. At the present, apoproteins A, B, C, D, and E have been isolated and identified. At least two of these contain several proteins, designated by Roman numerals, AI, AII, AIV; CI, CII, CIII.

A lipoprotein can comprise more than one apoprotein. For example, naturally occurring chylomicrons comprises of A, B, C & E, over time these lipoproteins lose A and acquire C & E. VLDL comprises A, B, C & E apoproteins, LDL
10 comprises apoprotein B; and HDL comprises apoproteins A, C, & E.

The amino acid of these apoproteins are known and are described in, for example, Breslow (1985) *Annu Rev. Biochem* 54:699; Law (1986) *Adv. Exp Med. Biol.* 151:162; Chen (1986) *J Biol Chem* 261:12918; Kane (1980) *Proc Natl Acad Sci USA* 77:2465; and Utermann (1984) *Hum Genet* 65:232.

- 15 Lipoproteins contain a variety of lipids including, triglycerides, cholesterol (free and esters), and phospholipids. The composition of the lipids varies in naturally occurring lipoproteins. For example, chylomicrons comprise mainly triglycerides. A more detailed description of the lipid content of naturally occurring lipoproteins can be found, for example, in *Meth. Enzymol.* 128 (1986). The composition of the lipids are chosen to aid in conformation of the apoprotein for receptor binding activity. The composition of lipids can also be chosen to facilitate hydrophobic interaction and association with the polynucleotide binding molecule.

- 20 Naturally occurring lipoproteins can be isolated from serum by ultracentrifugation, for instance. Such methods are described in *Meth. Enzymol.* (*supra*); Pitas (1980) *J. Biochem.* 255:5454-5460 and Mahey (1979) *J Clin. Invest* 64:743-750. Lipoproteins can also be produced by *in vitro* or recombinant methods by expression of the apoprotein genes in a desired host cell. See, for example, Atkinson (1986) *Annu Rev Biophys Chem* 15:403 and Radding (1958) *Biochim Biophys Acta* 30: 443. Lipoproteins can also be purchased from commercial suppliers, such as Biomedical
25 Technologies, Inc., Stoughton, Massachusetts, USA. Further description of lipoproteins can be found in Zuckermann *et al.* PCT/US97/14465.

F. Polycationic Agents

Polycationic agents can be included, with or without lipoprotein, in a composition with the desired polynucleotide/polypeptide to be delivered.

- 30 Polycationic agents, typically, exhibit a net positive charge at physiological relevant pH and are capable of neutralizing the electrical charge of nucleic acids to facilitate delivery to a desired location. These agents have both *in vitro*, *ex vivo*, and *in vivo* applications. Polycationic agents can be used to deliver nucleic acids to a living subject either intramuscularly, subcutaneously, *etc.*

- The following are examples of useful polypeptides as polycationic agents: polylysine, polyarginine, polyornithine,
35 and protamine. Other examples include histones, protamines, human serum albumin, DNA binding proteins, non-histone chromosomal proteins, coat proteins from DNA viruses, such as (X174, transcriptional factors also contain domains that bind DNA and therefore may be useful as nucleic acid condensing agents. Briefly, transcriptional factors such as C/EBP, c-jun, c-fos, AP-1, AP-2, AP-3, CPF, Prot-1, Sp-1, Oct-1, Oct-2, CREP, and TFIID contain basic domains that bind DNA sequences.

- 40 Organic polycationic agents include: spermine, spermidine, and putrescine.

The dimensions and of the physical properties of a polycationic agent can be extrapolated from the list above, to construct other polypeptide polycationic agents or to produce synthetic polycationic agents.

Synthetic polycationic agents which are useful include, for example, DEAE-dextran, polybrene. Lipofectin™, and lipofectAMINE™ are monomers that form polycationic complexes when combined with
5 polynucleotides/polypeptides.

Immunodiagnostic Assays

Neisseria antigens of the invention can be used in immunoassays to detect antibody levels (or, conversely, anti-Neisseria antibodies can be used to detect antigen levels). Immunoassays based on well defined, recombinant antigens can be developed to replace invasive diagnostics methods. Antibodies to Neisseria proteins within biological samples,
10 including for example, blood or serum samples, can be detected. Design of the immunoassays is subject to a great deal of variation, and a variety of these are known in the art. Protocols for the immunoassay may be based, for example, upon competition, or direct reaction, or sandwich type assays. Protocols may also, for example, use solid supports, or may be by immunoprecipitation. Most assays involve the use of labeled antibody or polypeptide; the labels may be, for example, fluorescent, chemiluminescent, radioactive, or dye molecules. Assays which amplify the
15 signals from the probe are also known; examples of which are assays which utilize biotin and avidin, and enzyme-labeled and mediated immunoassays, such as ELISA assays.

Kits suitable for immunodiagnosis and containing the appropriate labeled reagents are constructed by packaging the appropriate materials, including the compositions of the invention, in suitable containers, along with the remaining reagents and materials (for example, suitable buffers, salt solutions, etc.) required for the conduct of the assay, as well
20 as suitable set of assay instructions.

Nucleic Acid Hybridisation

"Hybridization" refers to the association of two nucleic acid sequences to one another by hydrogen bonding. Typically, one sequence will be fixed to a solid support and the other will be free in solution. Then, the two sequences will be placed in contact with one another under conditions that favor hydrogen bonding. Factors that affect this
25 bonding include: the type and volume of solvent; reaction temperature; time of hybridization; agitation; agents to block the non-specific attachment of the liquid phase sequence to the solid support (Denhardt's reagent or BLOTTO); concentration of the sequences; use of compounds to increase the rate of association of sequences (dextran sulfate or polyethylene glycol); and the stringency of the washing conditions following hybridization. See Sambrook *et al.* [*supra*] Volume 2, chapter 9, pages 9.47 to 9.57.

"Stringency" refers to conditions in a hybridization reaction that favor association of very similar sequences over sequences that differ. For example, the combination of temperature and salt concentration should be chosen that is approximately 120 to 200°C below the calculated T_m of the hybrid under study. The temperature and salt conditions can often be determined empirically in preliminary experiments in which samples of genomic DNA immobilized on filters are hybridized to the sequence of interest and then washed under conditions of different stringencies. See
35 Sambrook *et al.* at page 9.50.

Variables to consider when performing, for example, a Southern blot are (1) the complexity of the DNA being blotted and (2) the homology between the probe and the sequences being detected. The total amount of the fragment(s) to be studied can vary a magnitude of 10, from 0.1 to 1µg for a plasmid or phage digest to 10⁻⁹ to 10⁻⁴ g for a single copy gene in a highly complex eukaryotic genome. For lower complexity polynucleotides, substantially shorter blotting,
40 hybridization, and exposure times, a smaller amount of starting polynucleotides, and lower specific activity of probes

can be used. For example, a single-copy yeast gene can be detected with an exposure time of only 1 hour starting with 1 µg of yeast DNA, blotting for two hours, and hybridizing for 4-8 hours with a probe of 10^8 cpm/µg. For a single-copy mammalian gene a conservative approach would start with 10 µg of DNA, blot overnight, and hybridize overnight in the presence of 10% dextran sulfate using a probe of greater than 10^8 cpm/µg, resulting in an exposure time of ~24 hours.

Several factors can affect the melting temperature (T_m) of a DNA-DNA hybrid between the probe and the fragment of interest, and consequently, the appropriate conditions for hybridization and washing. In many cases the probe is not 100% homologous to the fragment. Other commonly encountered variables include the length and total G+C content of the hybridizing sequences and the ionic strength and formamide content of the hybridization buffer. The effects of all of these factors can be approximated by a single equation:

$$T_m = 81 + 16.6(\log_{10} C_i) + 0.4[\%(G + C)] - 0.6(\% \text{ formamide}) - 600/n - 1.5(\% \text{ mismatch}).$$

where C_i is the salt concentration (monovalent ions) and n is the length of the hybrid in base pairs (slightly modified from Meinkoth & Wahl (1984) *Anal. Biochem.* 138: 267-284).

In designing a hybridization experiment, some factors affecting nucleic acid hybridization can be conveniently altered. The temperature of the hybridization and washes and the salt concentration during the washes are the simplest to adjust. As the temperature of the hybridization increases (*ie.* stringency), it becomes less likely for hybridization to occur between strands that are nonhomologous, and as a result, background decreases. If the radiolabeled probe is not completely homologous with the immobilized fragment (as is frequently the case in gene family and interspecies hybridization experiments), the hybridization temperature must be reduced, and background will increase. The temperature of the washes affects the intensity of the hybridizing band and the degree of background in a similar manner. The stringency of the washes is also increased with decreasing salt concentrations.

In general, convenient hybridization temperatures in the presence of 50% formamide are 42°C for a probe with is 95% to 100% homologous to the target fragment, 37°C for 90% to 95% homology, and 32°C for 85% to 90% homology. For lower homologies, formamide content should be lowered and temperature adjusted accordingly, using the equation above. If the homology between the probe and the target fragment are not known, the simplest approach is to start with both hybridization and wash conditions which are nonstringent. If non-specific bands or high background are observed after autoradiography, the filter can be washed at high stringency and reexposed. If the time required for exposure makes this approach impractical, several hybridization and/or washing stringencies should be tested in parallel.

30 Nucleic Acid Probe Assays

Methods such as PCR, branched DNA probe assays, or blotting techniques utilizing nucleic acid probes according to the invention can determine the presence of cDNA or mRNA. A probe is said to "hybridize" with a sequence of the invention if it can form a duplex or double stranded complex, which is stable enough to be detected.

The nucleic acid probes will hybridize to the *Neisseria* nucleotide sequences of the invention (including both sense and antisense strands). Though many different nucleotide sequences will encode the amino acid sequence, the native *Neisseria* sequence is preferred because it is the actual sequence present in cells. mRNA represents a coding sequence and so a probe should be complementary to the coding sequence; single-stranded cDNA is complementary to mRNA, and so a cDNA probe should be complementary to the non-coding sequence.

The probe sequence need not be identical to the *Neisseria* sequence (or its complement) — some variation in the sequence and length can lead to increased assay sensitivity if the nucleic acid probe can form a duplex with target

nucleotides, which can be detected. Also, the nucleic acid probe can include additional nucleotides to stabilize the formed duplex. Additional Neisseria sequence may also be helpful as a label to detect the formed duplex. For example, a non-complementary nucleotide sequence may be attached to the 5' end of the probe, with the remainder of the probe sequence being complementary to a Neisseria sequence. Alternatively, non-complementary bases or longer sequences can be interspersed into the probe, provided that the probe sequence has sufficient complementarity with the a Neisseria sequence in order to hybridize therewith and thereby form a duplex which can be detected.

The exact length and sequence of the probe will depend on the hybridization conditions (e.g. temperature, salt condition etc.). For example, for diagnostic applications, depending on the complexity of the analyte sequence, the nucleic acid probe typically contains at least 10-20 nucleotides, preferably 15-25, and more preferably at least 30 nucleotides, although it may be shorter than this. Short primers generally require cooler temperatures to form sufficiently stable hybrid complexes with the template.

Probes may be produced by synthetic procedures, such as the triester method of Matteucci *et al.* [*J. Am. Chem. Soc.* (1981) 103:3185], or according to Urdea *et al.* [*Proc. Natl. Acad. Sci. USA* (1983) 80: 7461], or using commercially available automated oligonucleotide synthesizers.

The chemical nature of the probe can be selected according to preference. For certain applications, DNA or RNA are appropriate. For other applications, modifications may be incorporated eg. backbone modifications, such as phosphorothioates or methylphosphonates, can be used to increase *in vivo* half-life, alter RNA affinity, increase nuclease resistance etc. [eg. see Agrawal & Iyer (1995) *Curr Opin Biotechnol* 6:12-19; Agrawal (1996) *TIBTECH* 14:376-387]; analogues such as peptide nucleic acids may also be used [eg. see Corey (1997) *TIBTECH* 15:224-229; Buchardt *et al.* (1993) *TIBTECH* 11:384-386].

Alternatively, the polymerase chain reaction (PCR) is another well-known means for detecting small amounts of target nucleic acid. The assay is described in Mullis *et al.* [*Meth. Enzymol.* (1987) 155:335-350] & US patents 4,683,195 & 4,683,202. Two "primer" nucleotides hybridize with the target nucleic acids and are used to prime the reaction. The primers can comprise sequence that does not hybridize to the sequence of the amplification target (or its complement) to aid with duplex stability or, for example, to incorporate a convenient restriction site. Typically, such sequence will flank the desired Neisseria sequence.

A thermostable polymerase creates copies of target nucleic acids from the primers using the original target nucleic acids as a template. After a threshold amount of target nucleic acids are generated by the polymerase, they can be detected by more traditional methods, such as Southern blots. When using the Southern blot method, the labelled probe will hybridize to the Neisseria sequence (or its complement).

Also, mRNA or cDNA can be detected by traditional blotting techniques described in Sambrook *et al* [*supra*]. mRNA, or cDNA generated from mRNA using a polymerase enzyme, can be purified and separated using gel electrophoresis. The nucleic acids on the gel are then blotted onto a solid support, such as nitrocellulose. The solid support is exposed to a labelled probe and then washed to remove any unhybridized probe. Next, the duplexes containing the labeled probe are detected. Typically, the probe is labelled with a radioactive moiety.

BRIEF DESCRIPTION OF DRAWINGS

There are no drawings.

MODES FOR CARRYING OUT THE INVENTION

The following examples describe nucleic acid sequences which have been identified in *N.gonorrhoeae*, along with their inferred translation products.

The examples are generally in the following format:

- 5 ◦ a nucleotide sequence which has been identified in *N.gonorrhoeae*. The strain used is FA1090 [Dempsey *et al.* (1991) *J. Bacteriol.* 173:5476-5486]
- the inferred translation product of this sequence
- a computer analysis (*e.g.* PSORT output) of the translation product, indicating antigenicity
- homologous sequences (where relevant)
- 10 ◦ results of expression and purification (where relevant)

15 These examples typically include details of sequence homology between species and strains. Proteins that are similar in sequence are generally similar in both structure and function, and the homology often indicates a common evolutionary origin. Comparison with sequences of proteins of known function is widely used as a guide for the assignment of putative protein function to a new sequence and has proved particularly useful in whole-genome analyses.

20 Open reading frames (ORFs) within nucleotide sequences were predicted using the GLIMMER program [Salzberg *et al.* (1998) *Nucleic Acids Res* 26:544-8]. All predicted open-reading frames longer than 60 aa were screened against the meningococcus serotype B ('MenB') ORFs (accession NC002183) using the BLASTP algorithm [Altschul *et al.* (1990) *J. Mol. Biol.* 215:403-410]. ORFs were considered to be gonococcus-specific if they showed sequence identity to a MenB ORF lower than 60% over the whole protein length, or matching the MenB ORF over less than 30% of the length.

25 Open reading frames are usually shown with a N-terminal methionine. Where this is not the case (*e.g.* SEQ IDs 12, 18, 20, 32, 54, 62, 66, 84, 98, 102, 104, 112, 116, 118, 126, 128, 130, 134, 136, 138, 146, 152, 162, 186, 228, 238, 240, 278, 280, 288, 290, 298, 300, 308, 314), a non-ATG start codon is present, but the N-terminus amino acid will be methionine when translated using this start codon. If an upstream start codon is used, however, the "native" amino acid will be translated (*e.g.* if the sequence is expressed with N-terminus fusion sequences). Even where the first amino acid is not shown as methionine, the invention encompasses sequences in which the first amino acid is methionine.

30 Various tests can be used to assess the *in vivo* immunogenicity of the proteins identified in the examples. For example, the proteins can be expressed recombinantly and used to screen patient sera by immunoblot. A positive reaction between the protein and patient serum indicates that the patient has previously mounted an immune response to the protein in question *i.e.* the protein is an immunogen. This method can also be used to identify immunodominant proteins.

35 The recombinant protein can also be conveniently used to prepare antibodies *e.g.* in a mouse. These can be used for direct confirmation that a protein is located on the cell-surface. Labelled antibody (*e.g.* fluorescent labelling for FACS) can be incubated with intact bacteria and the presence of label on the bacterial surface confirms the location of the protein.

For protein expression of 14 antigens, sequences were amplified using the following primers:

		Sequences	Restriction site
NGS5	Fwd	CGCGGATCCCATATG-TGGGCAGAACACCGGC	NdeI
	Rev	CCCGCTCGAG-GTTTTTCAGCAGGGGGATTG	XhoI
NGS7	Fwd	CGCGGATCCCATATG-GCCGGTAAAGAGCAATTTAC	NdeI
	Rev	CCCGCTCGAG-AGCCAAGAAGAACCCGTTAT	XhoI
NGS13	Fwd	CGCGGATCCGCTAGC-TGCGTTGCCGACCCCG	NheI
	Rev	CCCGCTCGAG-CATGTGCCGTGCGGCGT	XhoI
NGS36	Fwd	CGCGGATCCGCTAGC-GACACCCGAACAATACC	NheI
	Rev	CCCGCTCGAG-AAACCTGCCCTTGATGCC	XhoI
NGS37	Fwd	CGCGGATCCCATATG-GTAGAAGTTAAAGGCGGGG	NdeI
	Rev	CCCGCTCGAG-TTTTTTCGCGCCGCCGAA	XhoI
NGS38	Fwd	CGCGGATCCCATATG-GCCGACGAACGCCGCC	NdeI
	Rev	CCCGCTCGAG-AAACCGATATTTAAACCCAACAGCC	XhoI
NGS39	Fwd	CGCGGATCCGCTAGC-AACCAAGAAGGGATTACCG	NheI
	Rev	CCCGCTCGAG-TTTTTGAGCATAATGACTTTTGCCCT	XhoI
NGS67	Fwd	CGCGGATCCCATATG-CGTGCGCACGGACACG	NdeI
	Rev	CCCGCTCGAG-GGCGGCGAGTTTTTCGC	XhoI
NGS106	Fwd	CGCGGATCCCATATG-GCAAACAGCGGAACGATAG	NdeI
	Rev	CCCGCTCGAG-AAAATCCTGCGGGATCGGT	XhoI
NGS115	Fwd	CGCGGATCCCATATG-GGGGGCGGCTCCGGC	NdeI
	Rev	CCCGCTCGAG-TTCGGCCAACAATGCTTCC	XhoI
NGSΔG115	Fwd	CGCGGATCCCATATG-GATGCCCAATCTTCACAAAG	NdeI
	Rev	CCCGCTCGAG-TTCGGCCAACAATGCTTCC	XhoI
NGS118	Fwd	CGCGGATCCCATATG-ACCGCCCTTCCCTCTGA	NdeI
	Rev	CCCGCTCGAG-CGGCTGCCATTTCGCGTT	XhoI
NGS122	Fwd	CGCGGATCCCATATG-AACCCGAACGATGCGTTTT	NdeI
	Rev	CCCGCTCGAG-AGGGTAAAACTTATTCAAATCGGCAA	XhoI
NGS144	Fwd	CGCGGATCCCATATG-GCTTCTGAAAATTCTGTAGC	NdeI
	Rev	CCCGCTCGAG-GAACACGCTTTTCATTACACCCA	XhoI
NGS151	Fwd	CGCGGATCCCATATG-CACGGTATGCATAAGAGCA	NdeI
	Rev	CCCGCTCGAG-TTGCTGATGCGGCTTTATTCG	XhoI

Example 1

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1> which encodes amino acid sequence <SEQ ID 2; NGS1>. Analysis of this protein sequence reveals the following:

- 5 GvH: Examining signal sequence (von Heijne)
Signal Score (-7.5): -5.47
Possible cleavage site: 36
>>> Seems to have no N-terminal signal seq.
Amino Acid Composition of Predicted Mature Form:
10 calculated from 1
ALOM: Finding transmembrane regions (Klein et al.)
count: 0 value: 4.72 threshold: 0.0

-32-

PERIPHERAL Likelihood = 4.72
 modified ALOM score: -1.44
 Rule: cytoplasmic protein

5 *** Reasoning Step: 2

----- Final Results -----

10 bacterial cytoplasm --- Certainty= 0.326(Affirmative) < succ>
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

The protein has homology with the following sequences in the databases:

15 >sp|P45941|YQCF_BACSU HYPOTHETICAL 21.5 KD PROTEIN IN CWLA-CISA INTERGENIC REGION
 pir|E69949 hypothetical protein yqcF - Bacillus subtilis
 dbj|BAA06963.1| (D32216) ORF95 [Bacillus subtilis]
 dbj|BAA12427.1| (D84432) YqcF [Bacillus subtilis]
 emb|CAB14528.1| (Z99117) yqcF [Bacillus subtilis]
 20 Length = 192

Score = 35.5 bits (81), Expect = 0.45
 Identities = 36/162 (22%), Positives = 77/162 (47%), Gaps = 5/162 (3%)

25 Query: 19 DSGSQYKLNIAAIPSSPNRDLKTYITLGLSKHDLNYK---SRFEILFVCSLKYDENQIFP 75
 D ++I ++ P + +Y TLGLS H +NY+ + I V +++ +
 Sbjct: 29 DDKNSSSIDILSVSDQPQEGITSYSTLGLSDHSINYEYVNGTPLRIEIVAAMESASDIYAN 88

30 Query: 76 FLRWLAETIENKKILLRGQVVYLPRISVNS-TKMDALYVSAPFYFDDDFQVCYGEHYNI 134
 L A II + G + S + + T M + PF +++D ++ + N+
 Sbjct: 89 VLSTCAFNIINSNFTCAPGVIFKNVISMVYDQETDMKHIMFVPPFLWEEDLELLEFSNKNV 148

Query: 135 VFPLLVPYKQAEELVEKKGWNAFEQFLLDNEVGNLSDMNRK 176
 + + +P+ + E ++ EK G + + Q LL+++ ++ D+ R+
 35 Sbjct: 149 TWLMALPISEGELQVAEKHG--SDYLQDLLESKQIDIFDIKRE 189

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 2

40 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 3> which encodes amino acid sequence <SEQ ID 4; NGS2>. Analysis of this protein sequence reveals the following:

GvH: Examining signal sequence (von Heijne)
 Signal Score (-7.5): -7.2
 Possible cleavage site: 18

45 >>> Seems to have no N-terminal signal seq.

Amino Acid Composition of Predicted Mature Form:
 calculated from 1

ALOM: Finding transmembrane regions (Klein et al.)
 count: 0 value: 5.89 threshold: 0.0

50 PERIPHERAL Likelihood = 5.89
 modified ALOM score: -1.68

Rule: cytoplasmic protein

55 *** Reasoning Step: 2

----- Final Results -----

60 bacterial cytoplasm --- Certainty= 0.367(Affirmative) < succ>
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

The protein has homology with the following sequences in the databases:

```

5  >emb|CAC01359.1| (AL390975) hypothetical protein SCP8.21 [Streptomyces coelicolor A3(2)]
    Length = 198

    Score = 37.1 bits (85), Expect = 0.15
    Identities = 29/107 (27%), Positives = 51/107 (47%), Gaps = 3/107 (2%)

10  Query: 73  ETPEHIETLAMLASASMHYPDQFQLGKTVNIGRPWVEQSSFRHFLISLPYPYQGELEY-- 130
    +T + + LA+LA++          G ++++G P   + F  L++ P   ++LE
    Sbjct: 88  DTDKVLRLPLAVLAASPQVEGVIVAPGASLDVGEPLWPGAPFTSVLVAEPGGLVEDLELDA 147

    Query: 131 -MDNVRFFWLLPITQTERLFLNTHSVEELETKFDEAGIDYLDINRAS 176
    +D VRF LLP+T E + H   L+ ++   G D D +R S
15  Sbjct: 148 PLDPVRFLPLLPMTPNAAWKRVHGAPALQERWLNHGTDLRDPSRRS 194
  
```

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 3

20 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 5> which encodes amino acid sequence <SEQ ID 6; NGS3>. Analysis of this protein sequence reveals the following:

```

    GvH: Examining signal sequence (von Heijne)
          Signal Score (-7.5): -1.69
          Possible cleavage site: 32
25  >>> Seems to have a cleavable N-term signal seq.
    Amino Acid Composition of Predicted Mature Form:
          calculated from 33
    ALOM: Finding transmembrane regions (Klein et al.)
          count: 5   value: -10.56 threshold: 0.0
30  INTEGRAL    Likelihood = -10.56   Transmembrane 182 - 198 ( 171 - 201)
    INTEGRAL    Likelihood = -7.86    Transmembrane 251 - 267 ( 244 - 273)
    INTEGRAL    Likelihood = -7.48    Transmembrane 142 - 158 ( 136 - 167)
    INTEGRAL    Likelihood = -6.32    Transmembrane 55 - 71 ( 50 - 82)
    INTEGRAL    Likelihood = -2.97    Transmembrane 100 - 116 ( 99 - 117)
35  PERIPHERAL Likelihood = 4.72
    modified ALOM score: 2.61
    Rule: cytoplasmic membrane protein

    *** Reasoning Step: 2
40  ----- Final Results -----

          bacterial inner membrane --- Certainty= 0.522(Affirmative) < succ>
          bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
45  bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
          bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>
  
```

The protein has homology with the following sequences in the databases:

```

50  >sp|P19845|NOSY_PSEST MEMBRANE PROTEIN NOSY PRECURSOR
    pir|S13585 nosY protein precursor - Pseudomonas stutzeri
    emb|CAA37717.1| (X53676) nosY [Pseudomonas stutzeri]
    Length = 276

    Score = 163 bits (413), Expect = 2e-39
55  Identities = 117/275 (42%), Positives = 174/275 (62%), Gaps = 2/275 (0%)

    Query: 1  MNPVWIITGKEARDSLRNRWVLA AVLLLAALALSLGFLGSSPTGSVKVDPLTVTVVSLSS 60
    MN VW I KE D LRNRW+LA LL A LA+ + +LG++ +G + + T+ SL+S
    Sbjct: 1  MNQVWNIARKELSDGLRNRWLLAISLLFAVLAVGIAWLGAASGQLGFTSIPATIASLAS 60
60
  
```


Query: 61 LSIFLIPLIAMLLSYDALIGEIERGTALLLSYPIWRNQILAGKFVGHLLIILALATTAGY 120
 L+ FL+PLIA+LL+YDA++GE E GT+ LLL+YP+ R QIL GKFVGH +ILALA G+
 Sbjct: 61 LATFLMPLIALLLAYDAIVGEDEGDTMLLLTYPLGRGQILLGKFVGHLLIILALAVLIGF 120

5 Query: 121 GLAGITLQLANGGFDIAA-WKPFALLIAASVILGAAFLSMGYLISAKVKERGTAAGISIG 179
 G A + + L G ++ + F + +S +LG FL+ Y++S KV E+ +AAG+++G
 Sbjct: 121 GCAALALALLVEGVGLMFWAFGRFMISSTLLGWVFLAFAYVLSGKVNEKSSAAGLALG 180

10 Query: 180 VWLFFVVFIDMALLGILVADSKQVITAPVVETVLLFNPTDIYRLNLTYENTAMYAGMA 239
 VW F V+ +L L+ S+ ++ +LL NPTDIYRL+NL+G+E + G+
 Sbjct: 181 VW-FLFVLVFDLVLLALLVLVSEKGFNPELLPWLILLNPTDIYRLINLSGFEGSGSAMGVL 239

Query: 240 GLSGQIGLTVPVLLTAQVLWVIIPVLAAAGIFRRR 274
 L + + VL + W+ + L+LA IFR+R
 15 Sbjct: 240 SLGADLPVPAAVLWLCLLAWIGVSLLLAYAIRRR 274

A homolog (amino acids 226-276) was found in serogroup A *N.meningitidis* but not in serogroup B, so NGS3 protein and nucleic acid are useful for distinguishing between gonococcus and serogroup B *N.meningitidis*.

20 Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 4

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 7> which encodes amino acid sequence <SEQ ID 8; NGS4>. Analysis of this protein sequence reveals the following:

25 GvH: Examining signal sequence (von Heijne)
 Signal Score (-7.5): 1.53
 Possible cleavage site: 58
 >>> Seems to have no N-terminal signal seq.
 Amino Acid Composition of Predicted Mature Form:
 30 calculated from 1
 ALOM: Finding transmembrane regions (Klein et al.)
 count: 0 value: 0.63 threshold: 0.0
 PERIPHERAL Likelihood = 0.63
 modified ALOM score: -0.63
 35 Rule: cytoplasmic protein
 *** Reasoning Step: 2
 ----- Final Results -----
 40 bacterial cytoplasm --- Certainty= 0.103(Affirmative) < succ>
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

45 The protein has homology with the following sequences in the databases:

>sp|Q59746|NOSZ_RHIME NITROUS-OXIDE REDUCTASE PRECURSOR (N(2)OR) (N2O REDUCTASE)
 gb|AAC44023.1| (U47133) nitrous-oxide reductase [Sinorhizobium meliloti]
 prf||2209347B nitrous-oxide reductase [Rhizobium meliloti]
 50 Length = 639
 Score = 660 bits (1704), Expect = 0.0
 Identities = 344/536 (64%), Positives = 407/536 (75%), Gaps = 23/536 (4%)
 55 Query: 1 MSDEKLEQNGLSRRSFLGTAA--ASGAGIAGAGLLGLAGCSKDGEQAAANASGAAPVAKA 58
 MS+E+ + L+RR LGT A A+ + G L L+G G A A+A
 Sbjct: 1 MSNEETKMR-LNRRQMLGTTAFMAAAGAVGAGGALTLSG-----GTATPARA 46

-35-

Query: 59 QGESKPGQLSSEVGPGLDQYYGFLSGGQSGEMRLIGLPSMRELMRIPVFNMDSATGWGR 118
 Q S S EV PGELD+YY F S GQSGE+R++G PSMRE+MRIPVFN SATGWG+
 Sbjct: 47 QETSQS---SYEVKPGELDEYYVFFSSGQSGEIRIVGAPSMREMMRIPVFNRCSATGWGQ 103

5 Query: 119 TNESLKVNLGNITEETRKFLKDSGLRCYPNGDLHHPHLSFTDQTYDGRYAYANDKANNRV 178
 TNES KV+ + ET +FLKD G Y NGDLHHPH SFTD TYDGRY YANDK+N+RV
 Sbjct: 104 TNESRKVMTEGLLPETVEFLKDQG-GLYLNGLHHPHPSFTDGTYDGRYLYANDKNSNRV 162

10 Query: 179 CRVRLDVMKADKIIDIPNDSGIHGLRPQRYPKTGYVVFANGEHITPVSGVGK-LDDAKTWN 237
 .CR+RLDVMK DKII +PN +HGLR Q+YPKTGYVF NGE PV GK + D ++
 Sbjct: 163 CRIRLDVMKCDKIIQLPNQHTVHGLRVQYKPKTGYVFCNGEDAVFPVNDGKTMGDKNSYQ 222

15 Query: 238 AVYTAIDGETMEIAWQVLVDGNLDNGDADYQGYKSFATCYNSEALTVQGASSNEQDWCV 297
 A++TA+DGETME+AWQV+VDGNLDN DADYQGYK FATCYNSE T+ ++EQDW V
 Sbjct: 223 AIFTAVDGETMEVAWQVMVDGNLDNVDADYQGYKCFATCYNSEEGFTLADMMASEQDWVV 282

20 Query: 298 VFDLKAIEEGIKAGDFKEVNGVKMLDGRAEAKSKYTRYIPVPNSPHGCNASPDGKYIMPN 357
 +F+LK IEE + GD+KE+ GV +LDGR S YTRY+PVPNSPHG N +PDG +++ N
 Sbjct: 283 IFNLKRIEEAVAKGDYKEIGGVFVLDGR--KGSPTTRYVPVPNSPHGINTAPDGIHVVAN 340

25 Query: 358 GKLPTVTVLDVSKLDDLFAKIKERDVVVAEPQLGLGPLHTAFDGRGNAYTTLFIDSQM 417
 GKL PTVTV DV K DDLF KI+ RD VVAEP+LGLGPLHTA+DG+GNAYTTLFIDSQ+
 Sbjct: 341 GKLSPTVTVFDVRKFDLFDLDDKIQRDTTVVAEPELGLGPLHTAYDGKGNAYTTLFIDSQV 400

30 Query: 418 VKWNIDDAIKAYKGEKIDPIKQKLDVHYQPGHNHTTMTGETKEADGQWLVS LNKF SKDRFL 477
 KWN I+DA +AY GEK+DPI+ KLDVHYQPGHNHT+MG+TKEADG+WL+SLNKF SKDR+L
 Sbjct: 401 CKWNIEDAKRAYAGEKVDPIRHKLDVHYQPGHNHTSMGQTKEADGKWLISLNKF SKDRYL 460

Query: 478 NAGPLKPECQQLIGISGDEMRLVHDNPTFAEPHDLCLVAASKLNPGKTWDRKDPWF 533
 N GPLKPE DQLI ISGDEM LVHDNPTFAEPHD +V ASK+NP W+R DP+F
 Sbjct: 461 NVGPLKPENQQLIDISGDEMVLVDNPTFAEPHDATIVHASKINPVHVWNRDDPFF 516

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

35 Example 5

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 9> which encodes amino acid sequence <SEQ ID 10; NGS5>. Analysis of this protein sequence reveals the following:

GvH: Examining signal sequence (von Heijne)
 Signal Score (-7.5): 1.09
 Possible cleavage site: 19
 >>> Seems to have a cleavable N-term signal seq.
 Amino Acid Composition of Predicted Mature Form:
 calculated from 20
 ALOM: Finding transmembrane regions (Klein et al.)
 count: 0 value: 7.43 threshold: 0.0
 PERIPHERAL Likelihood = 7.43
 modified ALOM score: -1.99
 Score for OM-PP discrimination: 4.97
 Rule: outer membrane or periplasmic protein
 Score for OM-PP discrimination: 4.97
 Rule: outer membrane or periplasmic protein
 *** Reasoning Step: 2
 Outer membrane? Score: 0.496525
 ----- Final Results -----
 bacterial outer membrane --- Certainty= 0.781(Affirmative) < succ>
 bacterial periplasmic space --- Certainty= 0.138(Affirmative) < succ>
 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>
 bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

The protein has no homology with sequences in the databases.

The protein was expressed in *E.coli* as an insoluble 43.56kDa His-fusion product and then purified.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be
5 useful antigens for vaccines or diagnostics.

Example 6

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 11> which encodes amino acid sequence
<SEQ ID 12; NGS6>. Analysis of this protein sequence reveals the following:

```

10  GvH: Examining signal sequence (von Heijne)
      Signal Score (-7.5): -3.93
      Possible cleavage site: 36
      >>> Seems to have no N-terminal signal seq.
      Amino Acid Composition of Predicted Mature Form:
      calculated from 1
15  ALOM: Finding transmembrane regions (Klein et al.)
      count: 0 value: 6.42 threshold: 0.0
      PERIPHERAL Likelihood = 6.42
      modified ALOM score: -1.78
20  Rule: cytoplasmic protein

      *** Reasoning Step: 2

      ----- Final Results -----

25      bacterial cytoplasm --- Certainty= 0.447(Affirmative) < succ>
      bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
      bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
      bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

30  The protein has homology with the following sequences in the databases:

      >pir||F83173 outer membrane protein OprC PA3790 [imported] - Pseudomonas
      aeruginosa (strain PAO1)
      dbj|BAA05664.1| (D28119) outer membrane protein C [Pseudomonas aeruginosa]
      gb|AAG07177.1|AE004797_12 (AE004797) outer membrane protein OprC [Pseudomonas
35  aeruginosa]
      Length = 723

      Score = 77.9 bits (191), Expect = 1e-13
      Identities = 58/188 (30%), Positives = 89/188 (46%), Gaps = 13/188 (6%)

40  Query: 49 VKDLIIFDRAHGQSGTASKDGGIITRNVDARLFTAQAYARYNFNPHWAAGIKAAYNYGHN 108
      V+D I+F G G++++ NVDAR+ + A Y +W AY +G N
      Sbjct: 546 VQDFILFSYREGMMGSSTQ-----ATNVDARIMGGELGASYQLTGNWKT DASLAYAWGKN 600

45  Query: 109 ETDGRPPYQIRPFEEAAVQADYKNYFAHGSYNIGAATRFVAKQTRGDFDMASGLGIDKREA 168
      +D R QI P EA Y+ G ++ G+ R VA Q R D + +G D ++
      Sbjct: 601 SSDDRALPQIPPLEARFGLTYE----EGDWSAGSLWRVVAPQNRIARDQGNVVGKDFDKS 656

      Query: 169 AKGFTVADVYAGVNIKDKYGLRLGVNNVFNKKYVEYI--SGDHVLALSPS-VVYAPGRTY 225
      A GF V + + L GV+N+F+K Y E++ +GD S + V PGRT+
50  Sbjct: 657 A-GFGVFSLNGAYRVTRNVKLSAGVDNLFDKDYTEHLNKAGDAGFGFSANETVPEPGRTF 715

      Query: 226 WLSLHAAF 233
      W + +F
55  Sbjct: 716 WTKVDFSF 723

```


Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 7

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 13> which encodes amino acid sequence

5 <SEQ ID 14; NGS7>. Analysis of this protein sequence reveals the following:

GvH: Examining signal sequence (von Heijne)
 Signal Score (-7.5): 4.94
 Possible cleavage site: 26
 >>> Seems to have a cleavable N-term signal seq.
 10 Amino Acid Composition of Predicted Mature Form:
 calculated from 27
 ALOM: Finding transmembrane regions (Klein et al.)
 count: 0 value: 0.79 threshold: 0.0
 PERIPHERAL Likelihood = 0.79
 15 modified ALOM score: -0.66
 Score for OM-PP discrimination: -18.85
 Rule: outer membrane or periplasmic protein
 Score for OM-PP discrimination: -18.85
 Rule: outer membrane or periplasmic protein
 20 *** Reasoning Step: 2
 Periplasmic space? Score: 1.8846
 25 ----- Final Results -----
 bacterial periplasmic space --- Certainty= 0.929(Affirmative) < succ>
 bacterial outer membrane --- Certainty= 0.211(Affirmative) < succ>
 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>
 30 bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

The protein has homology with the following sequences in the databases:

>pir|D72405 hypothetical protein - Thermotoga maritima (strain MSB8)
 gb|AAD35294.1|AE001705_5 (AE001705) hypothetical protein [Thermotoga maritima]
 35 Length = 300
 Score = 81.8 bits (201), Expect = 1e-14
 Identities = 72/289 (24%), Positives = 124/289 (41%), Gaps = 17/289 (5%)
 40 Query: 38 PAMPSVTIAVAALQGKLAQADVSLKIWRSPDQLRAGVASGQFKVMMSPSNVGNLRNQG 97
 P P++ V + GK+ DV ++IW++P++ A + S + + P VG NL +G
 Sbjct: 24 PLGPALIPVVPIMDGKIP--TDVKIEIWKNPEEAVAKIVSKEVDFAVLPTVVGANLYGKG 81
 45 Query: 98 QKVGVMNILTNGITQLVCKGSAIASP-QDLVGKKILVPP-KNDMPDIVLQALLKKLKIDA 155
 ++ +V + + LV A + L G+++ P + D++++ L K +
 Sbjct: 82 VRIKLVGVHEWKVLYLVASDDATFDGWESLRGQEVYTPHGRGQTVDVLRYFLSKAGLTL 141
 Query: 156 HK-VSITYAATPPEAVGLFPSKGYHAVILPEPMATASLLKGKTIGINVVHGFDLVKAWGQ 214
 + V I YA P E V L F S LPEP + L +GK + D K WG+
 50 Sbjct: 142 DRDVKILYAP-PQEIVLAFKSGVKYAAALPEPFVSMCLDRGKVV-----LDFQKEWGK 193
 Query: 215 AFDTKPLIPMAGIIANEEYFHAHKAQFDIFHQDLKNALNWILANRQNAKIGKNYLPAP 274
 IP+AG+ E K + + L +++ W+ N ++ L P
 Sbjct: 194 ELGVPGRIPRIAGLFVRE---GVDKETVEKVEKALIDSIRWMKENLDETQVLSSEKLGIPA 250
 55 Query: 275 PALVMGLDGARLTVSKGSEVKNEILKFYEILMQFNPELLGGKLPDNGFF 323
 L L+ + + E+ F + L + PE K+PD GF+
 Sbjct: 251 KILKSSLERIEFEYVPVEKCREEVETFLKKLNELYPEGF-EKIPDEGFF 298

60 The protein was expressed in *E.coli* as an insoluble 32.89kDa His-fusion product and then purified.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 8

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 15> which encodes amino acid sequence

5 <SEQ ID 16; NGS8>. Analysis of this protein sequence reveals the following:

```

GvH: Examining signal sequence (von Heijne)
      Signal Score (-7.5): 2.39
      Possible cleavage site: 15
>>> Seems to have a cleavable N-term signal seq.
10 Amino Acid Composition of Predicted Mature Form:
    calculated from 16
ALOM: Finding transmembrane regions (Klein et al.)
      count: 4 value: -8.23 threshold: 0.0
15 INTEGRAL    Likelihood = -8.23    Transmembrane 49 - 65 ( 41 - 73)
    INTEGRAL    Likelihood = -7.38    Transmembrane 83 - 99 ( 75 - 106)
    INTEGRAL    Likelihood = -7.06    Transmembrane 110 - 126 ( 100 - 133)
    INTEGRAL    Likelihood = -4.41    Transmembrane 164 - 180 ( 163 - 187)
    PERIPHERAL  Likelihood = 5.89
      modified ALOM score: 2.15
20 Rule: cytoplasmic membrane protein

*** Reasoning Step: 2

----- Final Results -----
25 bacterial inner membrane --- Certainty= 0.429(Affirmative) < succ>
    bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
    bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
    bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>
30

The protein has homology with the following sequences in the databases:

>sp|P38044|NRTB_SYNPF NITRATE TRANSPORT PERMEASE PROTEIN NRTB
  pir||S30892 nitrate transport protein nrtB - Synechococcus sp. (strain PCC
    7942)
35 emb|CAA43810.1| (X61625) nitrate transporter [Synechococcus sp.]
  prf||1908370A nitrate transporter [Synechococcus sp.]
    Length = 279

Score = 67.5 bits (164), Expect = 1e-10
40 Identities = 54/202 (26%), Positives = 96/202 (46%), Gaps = 7/202 (3%)

Query: 4 VALWAWGSAVFGEFMLPAPVEVFQKSL--DLLKHFQEN-----EIGISLWRSVVGISVAL 56
      +A+W SA+ G+ LP P+ V + +++ F +N +G+ + S+ +++
Sbjct: 36 LAIWQVISAILGQDRLPGPINVVANTWMPYIIVEPFFDNGGTSKGLGLQILISLQ RVAIGY 95

45 Query: 57 IAGLAAGLVAGLVAGSFKTAMALLKPVITILLAMPPIIWVVMALFWFGFNGPSVLFTIIV 116
      + G++ G V G K L PVI +L +PP+ W ++L F N S +F I +
Sbjct: 96 LLAAGTGLVGGVLGMSKFLGKGLDPVIQVLRTPPLAWFPISLMVFQDANTS AIFVIFI 155

50 Query: 117 LVAPLTFASAAGMASVNKQHEELFDAYKLGRLKKIRYLYIPHLTG YVISSVGVAVAMGV 176
      + AVG+ + + + KL + I + IP YV + + +AV +
Sbjct: 156 TAIWPIIINTAVGINQIPDDYNNVARVLKLSKKDYILNIPSTVPYVFPAGLR IAVGLAW 215

55 Query: 177 KAVIMAELLGASKGVGARIADA 198
      A++ AE+L A G+G I DA
Sbjct: 216 LAIVAAEMLKADGGIGYFIWDA 237

```

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 9

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 17> which encodes amino acid sequence <SEQ ID 18; NGS9>. Analysis of this protein sequence reveals the following:

```

5   GvH: Examining signal sequence (von Heijne)
      Signal Score (-7.5): -5.07
      Possible cleavage site: 29
      >>> Seems to have no N-terminal signal seq.
      Amino Acid Composition of Predicted Mature Form:
      calculated from 1
10  ALOM: Finding transmembrane regions (Klein et al.)
      count: 1 value: -1.81 threshold: 0.0
      INTEGRAL Likelihood = -1.81 Transmembrane 97 - 113 ( 96 - 113)
      PERIPHERAL Likelihood = 4.24
      modified ALOM score: 0.86
15  Rule: cytoplasmic membrane protein

```

*** Reasoning Step: 2

```

20  ----- Final Results -----
      bacterial inner membrane --- Certainty= 0.172(Affirmative) < succ>
      bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
      bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
      bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>
25

```

The protein has homology with the following sequences in the databases:

```

>sp|P97027|SSUB_BACSU PUTATIVE ALIPHATIC SULFONATES TRANSPORT ATP-BINDING PROTEIN
SSUB
30  pir|G69816 nitrate ABC transporter (binding protein) homolog ygaL - B.subtilis
     emb|CAB07520.1| (Z93102) hypothetical 30.6 kd protein [Bacillus subtilis]
     emb|CAB12711.1| (Z99108) similar to nitrate ABC transporter (binding protein)
       [Bacillus subtilis]
       Length = 274

35  Score = 99.5 bits (247), Expect = 3e-20
     Identities = 68/181 (37%), Positives = 102/181 (55%), Gaps = 9/181 (4%)

Query: 4  LFGPSGCGKTTVLRLLIAGLETTPKSGTIRNTFH-----KTGFLFQENRLPENLTAMQNI 56
          L GPSGCGK+T+L++IAGL++ G++ + GF+QOE+RL LT QNI
40  Sbjct: 56  LIGPSGCGKSTLLKIIAGLDSEYDGSVEINGRSVTAPGIQQGFIFQEHRLFPWLTVEQNI 115

Query: 57  A--IFMDNPDEGEIVALAAKVGLTAGDLNKYPTELSSGGMARVAFRLRLLCGCDLALLDE 114
          A ++ +P + V ++ G YP ELSSGM++RVA R LL ++ LLDE
45  Sbjct: 116  AADLNLKDPKVQKQVDLEIIVRLKGSEKAYPRELSSGMSQRVAITRALLREPEVILLDE 175

Query: 115  PFVGLDRDLRDILVAMLVKIERQGMACILVTHDRFEAARLSHEIMLLSAKGMNVQNVIT 174
          PF LD R L +L++ ++ ILVTHD E+ L +E+ +L AK + ++
50  Sbjct: 176  PFGALDAFTRKHLQDVLLDIWRKKKTTMILVTHDIDESVYLGNELAILKAKPGKIHLMP 235

Query: 175 L 175
          +
55  Sbjct: 236 I 236

```

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 10

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 19> which encodes amino acid sequence <SEQ ID 20; NGS10>. Analysis of this protein sequence reveals the following:

-40-

GvH: Examining signal sequence (von Heijne)
 Signal Score (-7.5): 2.27
 Possible cleavage site: 26
 >>> Seems to have no N-terminal signal seq.
 5 Amino Acid Composition of Predicted Mature Form:
 calculated from 1
 ALOM: Finding transmembrane regions (Klein et al.)
 count: 0 value: 5.14 threshold: 0.0
 10 PERIPHERAL Likelihood = 5.14
 modified ALOM score: -1.53

*** Reasoning Step: 2

imb2 HYPID: 2 CFP: 0.1

15 ----- Final Results -----

bacterial inner membrane --- Certainty= 0.100(Affirmative) < succ>
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
 20 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
 bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

The protein has homology with the following sequences in the databases:

25 >pir||A82615 surface protein XF1981 [imported] - Xylella fastidiosa (strain
 9a5c)
 gb|AAF84783.1|AE004017_6 (AE004017) surface protein [Xylella fastidiosa]
 Length = 1190

Score = 50.2 bits (119), Expect = 2e-05
 30 Identities = 59/210 (28%), Positives = 92/210 (43%), Gaps = 5/210 (2%)

Query: 17 SIGTSAEANAPGALALGGSSEASKKFSIABGYLASSDGYGALIGAIAIGSAAKI-KQLEKGTIN 75
 ++G A+A GA A+G + AS K S A G A + G++A+G AK + +
 35 Sbjct: 876 AVGVGTLASAEAGATAVGSAAASGKGSTAIGRNAVASADGSVALGDGAKDGARGAESYTG 935

Query: 76 HIVGNDNKGLYVDADGNVTKITVRTESEKDILSRYGQTYGAVALGFRSSSHNLFA----S 131
 G N + + G+ +K RT S L + N +
 35 Sbjct: 936 KYSGLQNNVTGTVSVGDASKGETRTVSNVADAKEATDAVNLRQLDRVAQDANRYVDNKIE 995

Query: 132 SFGAFSTATAIESLAVGDSSQSTGYRSATFGSHSRALAEESLALGYETRANAYGSVALGA 191
 S T + SL + + G + G + A +S+A+G + A+A +VA+G
 40 Sbjct: 996 SLSEGQTFVKVNSLNN SATPIAAGVDATAIGVGATASGADSIAMGNKASASADNAVAIGN 1055

Query: 192 ESVANEENTVSVSSDTLKRKIVNVADGTED 221
 45 SVA+ NTVSV S +R++ NVA GT D
 Sbjct: 1056 HSVADRANTVSVGSAGSERQVTNVAAGTAD 1085

>sp|P10858|YADA_YERPS INVASIN PRECURSOR (OUTER MEMBRANE ADHESIN)
 pir||S04534 invasin precursor - Yersinia pseudotuberculosis plasmid pIBI
 50 emb|CAA32088.1| (X13883) YopI preprotein (AA 1 - 434) [Yersinia
 pseudotuberculosis]
 prf||1411295A invasin [Yersinia pseudotuberculosis]
 Length = 434

Score = 42.1 bits (98), Expect = 0.006
 Identities = 35/134 (26%), Positives = 68/134 (50%), Gaps = 28/134 (20%)

Query: 116 AVALGFRSSSHNLFASSFGAFSTATAIESLAVGDSSQSTGYRSATFGSHSRA----- 167
 ++A+G + + A + G+ S AT + S+A+G S++ G + T+G+ S A
 60 Sbjct: 107 SIAIGATAEAAKPAAVAVGSGSIATGVNSVAIGPLSKALGDSAVTYGASSTAQKDGVAIG 166

Query: 168 -----LAEESLALGYETRANAYGSVALGA-----ESVANEENTVSVSSDT 207
 ++ +A+G+ ++ +A SVA+G S + EN+VS+ ++
 65 Sbjct: 167 ARASASDTGVAVGFNSKVDAQNSVAIGHSSHVAADHGYSIAIGDHSKTDRENSVSIGHS 226

Query: 208 LKRKIVNVADGTED 221
 L R++ ++A GTED

Sbjct: 227 LNRQLTHLAAGTED 240

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

5 Example 11

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 21> which encodes amino acid sequence <SEQ ID 22; NGS11>. Analysis of this protein sequence reveals the following:

```

10  GvH: Examining signal sequence (von Heijne)
      Signal Score (-7.5): -0.16
      Possible cleavage site: 60
      >>> Seems to have no N-terminal signal seq.
      Amino Acid Composition of Predicted Mature Form:
      calculated from 1
15  ALOM: Finding transmembrane regions (Klein et al.)
      count: 0 value: 4.67 threshold: 0.0
      PERIPHERAL Likelihood = 4.67
      modified ALOM score: -1.43
      Rule: cytoplasmic protein

20  *** Reasoning Step: 2

      ----- Final Results -----

      bacterial cytoplasm --- Certainty= 0.297(Affirmative) < succ>
25  bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
      bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
      bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

```

The protein has homology with the following sequences in the databases:

```

30  >sp|P10858|YADA_YERPS INVASIN PRECURSOR (OUTER MEMBRANE ADHESIN)
      pir|S04534|invasin precursor - Yersinia pseudotuberculosis plasmid pIBI
      emb|CAA32088.1|(X13883) Yop1 preprotein (AA 1 - 434) [Yersinia
      pseudotuberculosis]
      prf||1411295A|invasin [Yersinia pseudotuberculosis]
      Length = 434

35  Score = 41.3 bits (96), Expect = 0.007
      Identities = 27/71 (38%), Positives = 48/71 (67%), Gaps = 4/71 (5%)

40  Query: 16 QLNRLSKRTNVRVGASAAALASL-KPAQLGKNDKFAFSLGFGSYKNAQAVAMGAVFKPAEN 74
      +L++L KR ++ AS+AAL SL +P +GK + F+ G G Y+++QA+A+G+ ++ E+
      Sbjct: 353 RLDKLDKRVDKGLASSAALNSLFQPYGVGVKNV---FTAGVGGYRSSQALAIGSGYRVNES 409

      Query: 75 VLLNVAGSFAG 85
      V L ++AG
45  Sbjct: 410 VALKAGVAYAG 420

```

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 12

50 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 23> which encodes amino acid sequence <SEQ ID 24; NGS12>. Analysis of this protein sequence reveals the following:

```

      GvH: Examining signal sequence (von Heijne)
      Signal Score (-7.5): -1.29
      Possible cleavage site: 61
55  >>> Seems to have a cleavable N-term signal seq.

```


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Amino Acid Composition of Predicted Mature Form:
calculated from 62

ALOM: Finding transmembrane regions (Klein et al.)
count: 0 value: 6.36 threshold: 0.0

5 PERIPHERAL Likelihood = 6.36
modified ALOM score: -1.77

Score for OM-PP discrimination: 6.03

Rule: outer membrane or periplasmic protein

10 Score for OM-PP discrimination: 6.03

Rule: outer membrane or periplasmic protein

*** Reasoning Step: 2

Outer membrane? Score: 0.602784

15

----- Final Results -----

20 bacterial outer membrane --- Certainty= 0.867(Affirmative) < succ>
bacterial periplasmic space --- Certainty= 0.158(Affirmative) < succ>
bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>
bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

The protein has no homology with sequences in the databases.

25 Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be
useful antigens for vaccines or diagnostics.

Example 13

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 25> which encodes amino acid sequence
<SEQ ID 26; NGS13>. Analysis of this protein sequence reveals the following:

30 GvH: Examining signal sequence (von Heijne)
Signal Score (-7.5): -3.64
Possible cleavage site: 51

>>> May be a lipoprotein

Amino Acid Composition of Predicted Mature Form:
calculated from 21

35 ALOM: Finding transmembrane regions (Klein et al.)
count: 1 value: -1.01 threshold: 0.0

INTEGRAL Likelihood = -1.01 Transmembrane 36 - 52 (36 - 52)

PERIPHERAL Likelihood = 5.14

modified ALOM score: 0.70

40 Rule: inner or outer membrane protein

Rule: inner or outer membrane protein

Rule: cytoplasmic membrane protein

45 *** Reasoning Step: 2

Lipoprotein?

Inner membrane?

50 ----- Final Results -----

55 bacterial outer membrane --- Certainty= 0.790(Affirmative) < succ>
bacterial inner membrane --- Certainty= 0.742(Affirmative) < succ>
bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

The protein has homology with the following sequences in the databases:

>gb|AAC33455.1| (AF067083) outer membrane protein homolog [Vitreoscilla sp.]
Length = 217

60 Score = 236 bits (602), Expect = 2e-61

Identities = 134/217 (61%), Positives = 166/217 (75%)

```

5  Query: 1  MTFFKPSTVVLTAASALALSGCVADPVTGQQSPNKSAMYGLGGAAVCGIVGALTHSGKGAR 60
    M +K +++ T +A+ALS C DP+TGQ N + + LGGAA CGIVGALTH KGAR
    Sbjct: 1  MKAWKKFSLMATVAVALSACATDPMTGQVDRNNTVLGALGGAATCGIVGALTHSGKGAR 60

10 Query: 61  NSALACGAIGAGVGGYMDYQEQRLRQNLQAGTQIEIQRQGNQIRLVMPESVTFATGSAALG 120
    NSALACGAIGAGVG YMD+QE++LRQ+LA TQ+E+ R G++IRLVMPES+TFATGS L
    Sbjct: 61  NSALACGAIGAGVGAYMDHQERQLRQSLANTQVEVNRVGDIEIRLVMPESITFATGSYQLN 120

15 Query: 121  GSAQYALNTAAQTLVQYPTDTTLTINGHTDNTGSDAVNNPLSQHRAQAVAYYLQTRGVAAS 180
    SA +LN+ + L QY DTT+ I GHTD+TGSDA+N PLS++RA AVA YL +R VA++
    Sbjct: 121  SSASTSLNSVSSVLAQYTTDTTINIVGHTDSTGSDAINEPLSRNRASAVANYLVSERNVASN 180

20 Query: 181  RITVYGYGSHMPVASNATVEGRAQNRRVEILINPDQR 217
    R+T G G PVASN TV GRA+NRRVEI +NP QR
    Sbjct: 181  RITTVGAGCRQFVASNNTVAGRAENRRVEITVNPIQR 217

    >gb|AAD40344.1|U88088_22 (U88088) OmpA [Pseudomonas alcaligenes]
    Length = 220

    Score = 130 bits (328), Expect = 1e-29
    Identities = 90/219 (41%), Positives = 127/219 (57%), Gaps = 6/219 (2%)

25 Query: 7  STVVLTAASALALSGCVA---DPVTGQQSPNKSAMYGLGGAAVCGIVGALTHSGKGARN 63
    S + + L+GC + + T + + A L GA ++G + +GA A
    Sbjct: 3  SVIAASLVIFTLTGCASIQNEDGTTKNTALYGAGGALAGAVAGALIGK-ENRAQGALIGA 61

30 Query: 64  LACGAIGAGVGGYMDYQEQRLRQNLQAGTQIEIQRQGNQIRLVMPESVTFATGSAALGSA 123
    G++GAG G Y D QE LR+ + G+ ++++RQG++I +VMP ++TFATG A + +
    Sbjct: 62  AVAGSLGAGYGYADKQEAELEQMKSGVQVERQGDIEIVIMPGAITFATGKAEIQPNF 121

35 Query: 124  QYALNTAAQTLVQYPTDTTLTINGHTDNTGSDAVNNPLSQHRAQAVAYYLQTRGVAASRLT 183
    LN A + YPD+ L + GHTD+ GS N LSQ RAQ+VA +L+ GV R+
    Sbjct: 122  ANTNLQLAGSFRNYPDSRLIVTGHTDSVGSYEANELLSQRRASQAQFLRGNGVQTDRIE 181

40 Query: 184  VYGYGSHMPVASNATVEGRAQNRRVEILINPDQRAVNAA 222
    V G G + PVASNAT EGRAQNRRVEI + P RAV A
    Sbjct: 182  VIGAGPNQFVASNATAEGRAQNRRVEIKLAP--RAVQQA 218

```

The protein was expressed in *E.coli* as a soluble 22.55kDa His-fusion product and then purified.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 14

45 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 27> which encodes amino acid sequence <SEQ ID 28; NGS14>. Analysis of this protein sequence reveals the following:

```

50 GvH: Examining signal sequence (von Heijne)
    Signal Score (-7.5): -5.32
    Possible cleavage site: 40
    >>> Seems to have no N-terminal signal seq.
    Amino Acid Composition of Predicted Mature Form:
        calculated from 1
    ALOM: Finding transmembrane regions (Klein et al.)
        count: 0 value: 3.39 threshold: 0.0
55 PERIPHERAL Likelihood = 3.39
    modified ALOM score: -1.18
    Rule: cytoplasmic protein

60 *** Reasoning Step: 2
    ----- Final Results -----

```


5 bacterial cytoplasm --- Certainty= 0.254(Affirmative) < succ>
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

The protein has no homology with sequences in the databases.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

10 Example 15

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 29> which encodes amino acid sequence <SEQ ID 30; NGS15>. Analysis of this protein sequence reveals the following:

15 GvH: Examining signal sequence (von Heijne)
 Signal Score (-7.5): -1.75
 Possible cleavage site: 45
 >>> Seems to have no N-terminal signal seq.
 Amino Acid Composition of Predicted Mature Form:
 calculated from 1
 20 ALOM: Finding transmembrane regions (Klein et al.)
 count: 0 value: 5.89 threshold: 0.0
 PERIPHERAL Likelihood = 5.89
 modified ALOM score: -1.68
 Rule: cytoplasmic protein
 25 *** Reasoning Step: 2
 ----- Final Results -----
 30 bacterial cytoplasm --- Certainty= 0.232(Affirmative) < succ>
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

The protein has homology with the following sequences in the databases:

35 >sp|P10487|RCI1_ECOLI SHUFFLON-SPECIFIC DNA RECOMBINASE
 pir||S03815 probable integrase - Escherichia coli
 dbj|BAA77989.1| (AB027308) shufflon-specific DNA recombinase [Plasmid R64]
 Length = 384
 40 Score = 67.1 bits (163), Expect = 3e-10
 Identities = 75/301 (24%), Positives = 125/301 (40%), Gaps = 34/301 (11%)
 Query: 68 KVKMMTLSEAMRKYLNETLGAGRSKKMGL---RFLMEFPPIGGIGIDKLKRSDFAEHVMQR 124
 +++ M+LS A+ KYL + + +PI +D++ D A + R
 45 Sbjct: 5 RIRKMSLSRALDKYLKTVSVHKKGHQQEFYRSNVIKRYPIALRNMDIITVDIATYRDVR 64
 Query: 125 RRGIPELDIAPIAASTALQELQYIRSVLKHAFYVWGLEIGWQELDFAANGLKRSNMVAKS 184
 I PI +T EL + S+ A WG N ++ S
 50 Sbjct: 65 LAEINPRTGKPITGNTVRLELALLSSLFNIARVEWG-----TCRTNPVELVRKPKVS 116
 Query: 185 AIRDRLPTTEELQTLTYFLRQWQSRKSSIPMHLIMWLAIYTSRRQDEICRLLFDDWHKN 244
 + RDR T+ E + L+ YF R+ ++ +++I LA+ T+ RQ EI L W
 Sbjct: 117 SGRDRRLTSSEERRLSRYF-----REKNLMLYVIFHLALETAMRQGEILAL---RWEHI 167
 55 Query: 245 DCTRPVRDLKNPNGSTGNNKEFDILEPMALPVIDELPEESVRKRMLANKGIADSLVPCNGK 304
 D V L P G++++ + A +P + ++
 Sbjct: 168 DLRHGVAHL--PETKNHGSRDVPLSRRARNFLQMP-----VNLHGNVFDYTAS 214
 60 Query: 305 SVSAAWTRACKVLGIKDLRFHDLRHEAATRMABDG-FTIPQMQRVTLHDGWNLSLQRYVSVR 364
 AW A + L I+DL FHLRHEA +R E G + ++ ++ H N L+RY +R

Sbjct: 215 GFKNAWRIATQRLRIEDLHFHDLRHEAISRFELGSLNVMEIAAISGHRSMNMLKRYTHLR 275

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

5 Example 16

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 31> which encodes amino acid sequence <SEQ ID 32; NGS16>. Analysis of this protein sequence reveals the following:

```

10  GvH: Examining signal sequence (von Heijne)
      signal Score (-7.5): -3.64
      Possible cleavage site: 20
      >>> Seems to have no N-terminal signal seq.
      Amino Acid Composition of Predicted Mature Form:
          calculated from 1
15  ALOM: Finding transmembrane regions (Klein et al.)
      count: 0 value: 4.67 threshold: 0.0
      PERIPHERAL Likelihood = 4.67
      modified ALOM score: -1.43
      Rule: cytoplasmic protein
      *** Reasoning Step: 2
20  ----- Final Results -----
          bacterial cytoplasm --- Certainty= 0.262(Affirmative) < succ>
          bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
          bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
25  bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

```

The protein has homology with the following sequences in the databases:

```

30  >sp|P10484|T1M1_ECOLI TYPE I RESTRICTION ENZYME ECOR124II M PROTEIN (M.ECOR124II)
      pir||S02166 type I site-specific deoxyribonuclease (EC 3.1.21.3) EcoR124/3
          chain hsdM - Escherichia coli plasmid R124/3
      emb|CAA31541.1| (X13145) hsdM protein (AA 1-520) [Escherichia coli]
          Length = 520
      Score = 44.4 bits (104), Expect = 0.002
      Identities = 65/235 (27%), Positives = 99/235 (41%), Gaps = 55/235 (23%)
35  Query: 107 NRKKAGGYAEYITGGSRLRLVAAKVRRCYGEHPGVFDGAAGSG-----QLEQYIEPS 158
          N K+GG E+ T + +L+A ++D AAGSG Q + +I
      Sbjct: 191 NAGKSGG--EFFTPQHVSKLIAQLAMHGQTHVKNKIYDPAAGSGSLLLQAKKQFDNHIIEE 248
40  Query: 159 DFRAVEIQAEACKALLQNYPAKVYNTSLFL-----YTDGEPQDC 198
          F EI N+ + ++FL + D +P D
      Sbjct: 249 GFFGQEI-----NHTTYNLARMNMFLEHNINYDKFDIKLGNTLTTEPHFRDEKPFDA 298
45  Query: 199 TVMNPPFSIKLKDLSEDEKSRIAQEPWKKSGV-----ADEIFVLKGLE--NARRFGFF 250
          V NPP+S+K + D+ + I E + +GV AD FVL L +A+
      Sbjct: 299 IVSNPPYSVKW--IGSDDPTLINDER-FAPAGVLAPKSKADFAFVLHALNYLSAKGRAAI 355
      Query: 251 ILFPGIAYR-KSEQRPRE-IIGNRLAE--LNRIQNAFEDTFIEVLLLVIDKDKTD 301
          + FPGI YR +EQ+ R+ ++ N E ++ N F T I V +LV+ K KTD
50  Sbjct: 356 VCFPGIFYRGGAEQKIRQYLVDNNYVETVISLAPNLFFGTTIAVNILLVLSKHKTD 410

```

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 17

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 33> which encodes amino acid sequence <SEQ ID 34; NGS17>. Analysis of this protein sequence reveals the following:

```

5   GvH: Examining signal sequence (von Heijne)
      Signal Score (-7.5): -5.29
      Possible cleavage site: 16
      >>> Seems to have no N-terminal signal seq.
      Amino Acid Composition of Predicted Mature Form:
      calculated from 1
10  ALOM: Finding transmembrane regions (Klein et al.)
      count: 0 value: 2.60 threshold: 0.0
      PERIPHERAL Likelihood = 2.60
      modified ALOM score: -1.02
15  Rule: cytoplasmic protein

      *** Reasoning Step: 2

      ----- Final Results -----

20      bacterial cytoplasm --- Certainty= 0.284(Affirmative) < succ>
      bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
      bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
      bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

25  The protein has homology with the following sequences in the databases:

      >ref|NP_052389.1| translocator YopD [Yersinia enterocolitica]
      sp|P37132|YOPD_YEREN YOPD PROTEIN
      gb|AAD16812.1| (AF102990) translocator YopD [Yersinia enterocolitica]
      Length = 306

30      Score = 32.1 bits (72), Expect = 8.2
      Identities = 29/93 (31%), Positives = 43/93 (46%), Gaps = 17/93 (18%)

35  Query: 13  MLAAKRAAKESTRQERAVKRAGTVRNVDNRNLSARSKAQKENIARMLSGAKVSEDEALTC 72
      +L  R A+E  Q+R ++  T+          AQKE +A M+SGAK+  A+
      Sbjct: 89  LLELARKAREMGLQORDIENKATI-----SAQKEQVAEMVSGAKLMIAMAVVS 136

      Query: 73  GIMMRLSLQDMRYACNQELINFAEHIVKQVQRL 105
      GIM  S  ++  +E+  IVKQ Q L
40  Sbjct: 137  GIMAATSTVASAFSIAKEV-----KIVKQEQIL 164

```

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 18

45 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 35> which encodes amino acid sequence <SEQ ID 36; NGS18>. Analysis of this protein sequence reveals the following:

```

50  GvH: Examining signal sequence (von Heijne)
      Signal Score (-7.5): -2.56
      Possible cleavage site: 38
      >>> Seems to have no N-terminal signal seq.
      Amino Acid Composition of Predicted Mature Form:
      calculated from 1
      ALOM: Finding transmembrane regions (Klein et al.)
      count: 0 value: 4.56 threshold: 0.0
55  PERIPHERAL Likelihood = 4.56
      modified ALOM score: -1.41
      Rule: cytoplasmic protein

```


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*** Reasoning Step: 2

----- Final Results -----

5 bacterial cytoplasm --- Certainty= 0.397(Affirmative) < succ>
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

10 The protein has no homology with sequences in the databases.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 19

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 37> which encodes amino acid sequence
 15 <SEQ ID 38; NGS19>. Analysis of this protein sequence reveals the following:

GvH: Examining signal sequence (von Heijne)
 Signal Score (-7.5): -4.12
 Possible cleavage site: 43
 >>> Seems to have no N-terminal signal seq.
 20 Amino Acid Composition of Predicted Mature Form:
 calculated from 1
 ALOM: Finding transmembrane regions (Klein et al.)
 count: 0 value: 8.49 threshold: 0.0
 PERIPHERAL Likelihood = 8.49
 25 modified ALOM score: -2.20
 Rule: cytoplasmic protein

*** Reasoning Step: 2

----- Final Results -----

30 bacterial cytoplasm --- Certainty= 0.250(Affirmative) < succ>
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
 35 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

The protein has homology with the following sequences in the databases:

>ref|NP_043483.1| orf14 [Bacteriophage HP1]
 40 sp|P51716|YO14_BPHP1 HYPOTHETICAL 14.9 KD PROTEIN IN REP-HOL INTERGENIC REGION
 (ORF14)
 pir||S69520 hypothetical protein 14 - phage HP1
 gb|AAB09199.1| (U24159) orf14 [Bacteriophage HP1]
 Length = 133
 45 Score = 73.3 bits (179), Expect = 1e-12
 Identities = 44/129 (34%), Positives = 74/129 (57%), Gaps = 6/129 (4%)
 Query: 1 MFIPALHKDEHSAYGVITPDLPGCFSCGDTVEEAVANARSAAYMHIDGMIEDGGFKNLA 60
 M P + K + Y V++PD+PGCFS GDT+ EA+ NA+ A HI+GM+ED + L
 50 Sbjct: 1 MLYPICIEK-VNDGYVVSVPDVPDVGCFSGAGDTLSEAMLNKAEAISFHIEGMLLEDD--EELP 57
 Query: 61 VSS-IADLSQEPDYHGATWVMIEIDPAKISRQQIRFNVSWFQYLLDRVDEY--TSANHET 117
 S+ I +P+Y ++++D + + + N++ P LL R+D++ T ++
 Sbjct: 58 KSNPIEQYINQPEYKDFIVTVVDVLDLTHLMGKAEKINITVPAALLHHRIDQFIATHPEYKN 117
 55 Query: 118 RSGFLAKAA 126
 RS FL++ A
 Sbjct: 118 RSNFLSQLA 126

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 20

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 39> which encodes amino acid sequence <SEQ ID 40; NGS20>. Analysis of this protein sequence reveals the following:

```

5  GvH: Examining signal sequence (von Heijne)
    Signal Score (-7.5): -0.1
    Possible cleavage site: 19
10 >>> Seems to have no N-terminal signal seq.
    Amino Acid Composition of Predicted Mature Form:
        calculated from 1
    ALOM: Finding transmembrane regions (Klein et al.)
        count: 0 value: 7.58 threshold: 0.0
        PERIPHERAL Likelihood = 7.58
15 modified ALOM score: -2.02
    Rule: cytoplasmic protein

    *** Reasoning Step: 2

20 ----- Final Results -----

        bacterial cytoplasm --- Certainty= 0.057(Affirmative) < succ>
        bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
        bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
25        bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

```

The protein has no homology with sequences in the databases.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

30 Example 21

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 41> which encodes amino acid sequence <SEQ ID 42; NGS21>. Analysis of this protein sequence reveals the following:

```

35 GvH: Examining signal sequence (von Heijne)
    Signal Score (-7.5): -3.52
    Possible cleavage site: 52
    >>> Seems to have no N-terminal signal seq.
    Amino Acid Composition of Predicted Mature Form:
        calculated from 1
    ALOM: Finding transmembrane regions (Klein et al.)
40 count: 0 value: 5.83 threshold: 0.0
        PERIPHERAL Likelihood = 5.83
        modified ALOM score: -1.67
    Rule: cytoplasmic protein

45 *** Reasoning Step: 2

    ----- Final Results -----

        bacterial cytoplasm --- Certainty= 0.311(Affirmative) < succ>
50        bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
        bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
        bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

```

The protein has homology with the following sequences in the databases:


```

>ref|NP_040628.1| cI (repressor;237) [bacteriophage lambda]
ref|NP_061378.1| phage lambda repressor protein CI [Escherichia coli]
sp|P03034|RPC1_LAMB REPRESSOR PROTEIN CI
pir||RBPPL repressor protein cI - phage lambda
5 emb|CAA24991.1| (X00166) coding sequence cI gene [bacteriophage lambda]
gb|AAA96581.1| (J02459) cI (repressor;237) [bacteriophage lambda]
emb|CAB96428.1| (AJ277653) phage lambda repressor protein CI [Escherichia coli]
    Length = 237

10 Score = 62.5 bits (151), Expect = 5e-09
    Identities = 36/85 (42%), Positives = 51/85 (59%)

Query: 2 KKRELNEIETAECAELKRIFNSKKEELKLTQYKLAEAVGVTSQSAVNHYLNGTNALNASTA 61
      KK+ L + + + LK I+ KK EL L+Q +A+ +G+ QS V NG NALNA A
15 Sbjct: 4 KKKPLTQEQLEDARRLKAIEYKKKKNELGLSQESVADKMGMGQSGVGALFNGINALNAYNA 63

Query: 62 SQFAKILQIPVSDPSLRLAEIISM 86
      + AKIL++ V +FS +A EI M
20 Sbjct: 64 ALLAKILKVSVEEFSPSIARBIYEM 88

```

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 22

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 43> which encodes amino acid sequence
 25 <SEQ ID 44; NGS22>. Analysis of this protein sequence reveals the following:

```

GvH: Examining signal sequence (von Heijne)
      Signal Score (-7.5): -2.6
      Possible cleavage site: 43
>>> Seems to have no N-terminal signal seq.
30 Amino Acid Composition of Predicted Mature Form:
    calculated from 1
ALOM: Finding transmembrane regions (Klein et al.)
      count: 0 value: 7.74 threshold: 0.0
      PERIPHERAL Likelihood = 7.74
35 modified ALOM score: -2.05
Rule: cytoplasmic protein

*** Reasoning Step: 2

40 ----- Final Results -----

      bacterial cytoplasm --- Certainty= 0.072(Affirmative) < succ>
      bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
      bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
45      bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

```

The protein has homology with the following sequences in the databases:

```

>pir||S30432 hypothetical protein - Streptomyces clavuligerus plasmid pSCL
      Length = 307

50 Score = 43.6 bits (102), Expect = 0.002
    Identities = 25/86 (29%), Positives = 49/86 (56%), Gaps = 2/86 (2%)

Query: 6 MGMAFKT-GIPRGQRFVLVKLCDNCANDDGLCYPSQETLAEDTGFAETA VRQH IKWLKDNN 64
      MGM F G+ ++ +L+ + + G C+PS++ L +D G + + V++ + L N
55 Sbjct: 1 MGMVFAAEGLDGSEKLLLLGYTNWTD P YG C W P S E D R L V D D C G T S R S T V Q R T K R K L V K K N 60

Query: 65 FIKSARRQGR-ERKSDIYRIN VALL 89
      ++S RR+ + E S++ R+N+ LL
60 Sbjct: 61 LLRSVRRKNSKGEFISNLSRVNLP LL 86

```


Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 23

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 45> which encodes amino acid sequence
5 <SEQ ID 46; NGS23>. Analysis of this protein sequence reveals the following:

GvH: Examining signal sequence (von Heijne)
Signal Score (-7.5): -2.8
Possible cleavage site: 59
>>> Seems to have no N-terminal signal seq.
10 Amino Acid Composition of Predicted Mature Form:
calculated from 1
ALOM: Finding transmembrane regions (Klein et al.)
count: 0 value: 0.05 threshold: 0.0
PERIPHERAL Likelihood = 0.05
15 modified ALOM score: -0.51
Rule: cytoplasmic protein
*** Reasoning Step: 2
20 ----- Final Results -----
bacterial cytoplasm --- Certainty= 0.195(Affirmative) < succ>
bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
25 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

The protein has homology with the following sequences in the databases:

>sp|P07905|DNAC_ECOLI DNA REPLICATION PROTEIN DNAC
30 pir||XMECNC DNA replication protein dnaC - Escherichia coli (strain K-12)
Length = 245
Score = 110 bits (275), Expect = 2e-23
Identities = 75/224 (33%), Positives = 116/224 (51%), Gaps = 23/224 (10%)
35 Query: 50 EAADEMAAYAETLRRGAMRDA-----LEKRIGRSGIAPRFRNCRIENYAV--SDS 97
+ +E+ A+ + +GA+R A +++ RSGI P +NC ENY V
Sbjct: 24 KTGEELLAWQK--EQGAIRSAALERENRAMKMQRTFNRSIGIRPLHQNCSEFENYRVECEGQ 81
40 Query: 98 IPGMARAKAAAAEYAAANFADVLQGRSMIFSGRRGTGKNHLACGIAREVIAAGKSALVIT 157
+ +++A+ E+ N A S IFSG+ GTGKNHLA I E++ GKS L+IT
Sbjct: 82 MNALSKARQYVEEFDGNIA-----SFIFSGKPGTGKNHLAAICNELLRLGRKSVLIIT 134
Query: 158 VGDMLRTVKDSF--GGGGEAGAVGIFVKPDLLVLDEFGAGSLSETDGRILFSVNVNARYER 215
V D++ +KD+F G E + DLLV+DE G + S+ + I+ +V+ R
45 Sbjct: 135 VADIMSAMKDTFRNSGTSEEQLNDLSNVDLLVIDEIGVQTESKYEKVIINQIVDRRSSS 194
Query: 216 LMPMLVLTLNLTAEAFRENTDARIRDRLRDGGGKLIPFDWESYRA 259
P +LTN E + R+ DR+R G + F+W+SYR+
50 Sbjct: 195 KRPTGMLTNSNMEEMTKLLGERVMDRMLGNSLWVIFNWDYSYS 238

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 24

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 47> which encodes amino acid sequence
55 <SEQ ID 48; NGS24>. Analysis of this protein sequence reveals the following:

-51-

GvH: Examining signal sequence (von Heijne)
 Signal Score (-7.5): -5.76
 Possible cleavage site: 26
 >>> Seems to have no N-terminal signal seq.
 5 Amino Acid Composition of Predicted Mature Form:
 calculated from 1
 ALOM: Finding transmembrane regions (Klein et al.)
 count: 0 value: 1.43 threshold: 0.0
 10 PERIPHERAL Likelihood = 1.43
 modified ALOM score: -0.79
 Rule: cytoplasmic protein
 *** Reasoning Step: 2
 15 ----- Final Results -----
 bacterial cytoplasm --- Certainty= 0.112(Affirmative) < succ>
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
 20 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

The protein has homology with the following sequences in the databases:

>ref|NP_053228.1| pXO2-73 [Bacillus anthracis]
 gb|AAF13678.1|AF188935_76 (AF188935) pXO2-73 [Bacillus anthracis]
 25 Length = 541
 Score = 125 bits (315), Expect = 9e-28
 Identities = 139/535 (25%), Positives = 254/535 (46%), Gaps = 70/535 (13%)
 30 Query: 14 PVLFIGTGMSLRYL DNSYTW DGLLSKIAIDLFGDDREYLN IKSRYCEDGRFQYEEIAEEL 73
 P LFIG+G S RYL N W GL+ K + +L + EY Y + E+AE +
 Sbjct: 19 PFLFIGSGFSKRYL-NLEDWAGLMKKFS-NLMPYEFY-----YSSTANKDWAELM 70
 35 Query: 74 QSKFDKVL---ENDPDGRFKEINDKFFENMRAGNTLSRFKIYISTLLSQLNYK----DNSN 127
 F + E + KE D R + S K+ ++ L+ + YK + ++
 Sbjct: 71 AKDFHPIWKEQQFENNRKEFKD-----RISSKQSPLKVEVAKYLN SIEYKYGLDEKND 124
 40 Query: 128 TELSELKKARKNVGSIITTN YDKLAQDIFEFNPL---IGN-DILLSNPFY--GSVYKIHGC 181
 E++ LKK + IITTN+D L + IFB + IG ++L S+P +YKIHGC
 Sbjct: 125 KEIAALKKIV--IDGIITTNWDL L BQIFEEQEMQVYIGQKELLF SHPLEINEIYKIHGC 182
 45 Query: 182 VDDPSKIIITKDYEFKEKYELIRAQLLSLFIHNPIIFLGYNVGDENIKEILKTIFTYV 241
 P +++T DY+ + EK + A+LL++FI +P+IFLGY++ D+NI++ILK I +
 Sbjct: 183 SSIPDSLVLTTSDYKGYNEKNAYLA AKLLTVFIEHPVIFLGYSISDDNIQQILKAITRCL 242
 50 Query: 242 EQNSPSANKIRNFFLLVEYEPESNNEDIVEHDIDIT-GFSTIRINKIKTDNFSQIYKALA 300
 +Q++ K R L+ E ED E++ +T G T+ I ++KT+++ +IY ALA
 Sbjct: 243 DQDNIHKLKDR-----LIFVERAGQEEDSFENNSSLTIGKITVPITRVKTNDEYKIYNALA 298
 55 Query: 301 ELTLPISAMDVRKFQSI AKIETTGNIKVSF---TEDMDNLNNSDKVVAIGSTKTISYNF 357
 + S +R+ +S E+ + + + D+ + + V+ +G K +
 Sbjct: 299 QNKRKFSMKMMRQMSQIYELVKTNDPEEKIYVVDGEYDDTQDIEFVIGLG-VKNVVEEM 357
 Query: 358 QTTSEMMSN-----YFKIIEENS-----QLLKLIDKHSIASTQYFPI-- 395
 Q+ E+ ++ + +++ +E ++K+ + S QY P+
 Sbjct: 358 QSNHEISASKELSEHG YGGISDIELFNELLSDEPKYDYDSIVKISLPQILRSNQYVPLFR 417
 60 Query: 396 YGFSRICSDIHKEAVLKRQKEKLDHFIEBINRCKNNHSSIQSILDDENISDTYKND AI 455
 Y D ++ +K + K + F+ E ++ N S + + + + +
 Sbjct: 418 YVLESSVEDELLDSKIKNKLKMYTDFLTETQKKNIKNLSWDWQFKNLDEV LKGFPPDIKV 477
 65 Query: 456 AWG-----IWNQNQLSEDEVENYL---KNFVNKKN-----THYKRLLCMFDYKKYADT 499
 A + L+ D++++L FV +KN T +RL ++D+ KY +
 Sbjct: 478 AIEQIPLL GQKNLNCDDLKDFLIKNSKFVKEKNTPERTGIRRLFRIYDWLKYGQS 532

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 25

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 49> which encodes amino acid sequence
5 <SEQ ID 50; NGS25>. Analysis of this protein sequence reveals the following:

```

GvH: Examining signal sequence (von Heijne)
      Signal Score (-7.5): 4.76837e-07
      Possible cleavage site: 56
>>> May be a lipoprotein
10 Amino Acid Composition of Predicted Mature Form:
      calculated from 21
ALOM: Finding transmembrane regions (Klein et al.)
      count: 0 value: 6.68 threshold: 0.0
      PERIPHERAL Likelihood = 6.68
15 modified ALOM score: -1.84
Rule: inner or outer membrane protein
Rule: inner or outer membrane protein

*** Reasoning Step: 2

20 Lipoprotein?
Inner membrane?

----- Final Results -----
25
      bacterial outer membrane --- Certainty= 0.790(Affirmative) < succ>
      bacterial inner membrane --- Certainty= 0.700(Affirmative) < succ>
      bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
30      bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

```

The protein has homology with the following sequences in the databases:

```

>gi|7433005|pir|B70313 cytochrome-c peroxidase (EC 1.11.1.5) - Aquifex aeolicus
gi|2982865|gb|AAC06485.1| (AE000675) cytochrome c peroxidase [Aquifex aeolicus]
35      Length = 355

Score = 345 bits (885), Expect = 7e-94
Identities = 180/336 (53%), Positives = 237/336 (69%), Gaps = 12/336 (3%)

40 Query: 59 EDQDLLKRAQGVFQPLPTVEEMQKIRPFTEEQVKLGHLWYEPRLSKGNTVSCNSCHNLA 118
      +D++LLK A+ F+PLP V E + P T E+VKLG L+Y+PRLSK +SCN+CHNLA
Sbjct: 22 DDKELLKMARQYFKPLPKVAENPQ-NPVTPEKVKLGKMLYYDPRLSKSGLISCNTCHNLA 80

Query: 119 SAGVDNMPTSQGHKGQFGGRNSPTALNAAALLGSQFWDGRAADVEEQAGGPLVNPVEMAND 178
      GVDN+PTS GH+ G RN+PT NAA+ +QFWDGRA DVEEQA GP+VNP+EMAN
45 Sbjct: 81 RYGVDNLPTSIGHRWAIGPRNAPTIVYNAIHLAQFWDGRAKDVEEQALGPVNPPIEMAN- 139

Query: 179 SQEAAAIAKAVPEYQEMFKAFP-EDGAVSFKNITTLGAFERTLLTPTKWDEYLKGNV 237
      ++E A + +PEY E+FKKAFP E V ++NI A+GAFERTL+TP+++DE+LKGN
50 Sbjct: 140 TEENAVKTLKSIPEYVELFKKAFPNEKDPVKYENIGKAIGAFERTLMTPSRFDEFLKGNT 199

Query: 238 NALSEQERKGVRAFMDNGCIACHNGVNLGGTTTFQKFGLVQGPYWK-----FIEDP--KR 289
      AL+EQE++G++ F++ GC+ACHNG +GG F KFG++ YWK + P K
Sbjct: 200 KALTEQEKRLKTFIEVGCVACHNGPGVGGNMFAKFGMIT-EYWKVTYPYVLVGKPAIKV 258

55 Query: 290 DKGRADVTKKTEDEFFFRVPLGRNVAKTYPYFHNGSVWELDKAVTIMKAQLGKDIPKED 349
      D GR VTKK ED F F+VP LRN+ TYPYFH+GSVW L+ AV IM K QLKG++ +
Sbjct: 259 DFGRFGVTKEEDMFVFKVPSLRNIEHTYPYFHDGSVWSLEDAVRIMAKTQLGKELTDQQ 318

Query: 350 VDNIVVFLNALSGNVSESARTMPPLTAPMESKPD 385
      V +IV FL AL+G + + A +PELP + KP+
60 Sbjct: 319 VKDIVAFLKALTGKIPKHALEVPPELPSTDKTPKPE 354

```


Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 26

- 5 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 51> which encodes amino acid sequence <SEQ ID 52; NGS26>. Analysis of this protein sequence reveals the following:

```

GvH: Examining signal sequence (von Heijne)
Signal Score (-7.5): 0.610001
Possible cleavage site: 15
10 >>> Seems to have no N-terminal signal seq.
Amino Acid Composition of Predicted Mature Form:
calculated from 1
ALOM: Finding transmembrane regions (Klein et al.)
count: 0 value: 5.04 threshold: 0.0
15 PERIPHERAL Likelihood = 5.04
modified ALOM score: -1.51
Rule: cytoplasmic protein

*** Reasoning Step: 2

20 ----- Final Results -----

bacterial cytoplasm --- Certainty= 0.127 (Affirmative) < succ>
bacterial periplasmic space --- Certainty= 0.000 (Not Clear) < succ>
25 bacterial outer membrane --- Certainty= 0.000 (Not Clear) < succ>
bacterial inner membrane --- Certainty= 0.000 (Not Clear) < succ>

```

The protein has homology with the following sequences in the databases:

```

30 >pir|T13296 hypothetical protein 8 - Streptococcus phage phi-01205
gb|AAC79524.1| (U88974) ORF8 [Streptococcus thermophilus temperate bacteriophage
01205]
Length = 157

Score = 62.5 bits (151), Expect = 2e-09
35 Identities = 53/161 (32%), Positives = 86/161 (52%), Gaps = 8/161 (4%)

Query: 5 TLYRCAADVQAALDYYFDSETEREDTLEAV--IGQFEVKAQSVIAYIKNQEITEKMLEGH 62
TLY + + D ET + DTLEA+ +E K + + IK+ E + +
Sbjct: 3 TLYELTDQLLEIYNMDVDDDET-KLDTLEAIDWTTDYENKVEGYVKVKSLEADIEARKNE 61

40 Query: 63 IRQMTGKLKAAKARNQSLKDYLRNMQAAGITEIKADDGTFKASFRKSEAVVILDEAQIP 122
+++ G K+ +++ LK LA +M G T + D FK FRKSEAVV+ +E ++P
Sbjct: 62 KKRLDGLNKSQSKIDKLKTALAVSMAETGQTRV--DTTLFKVGFRKSEAVVV-NEEKLP 118

45 Query: 123 AEFMREAVKTEPDKTAIRKAIESGRQVAGAKIEGRKNLQIR 163
E+ K PDK +++ ++SG+ + GA +E R+NL IR
Sbjct: 119 KEYQIATYK--PDKKTLKELLKSGKHIEGATLEERRNLNIR 157

```

- 50 Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 27

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 53> which encodes amino acid sequence <SEQ ID 54; NGS27>. Analysis of this protein sequence reveals the following:

```

55 GvH: Examining signal sequence (von Heijne)
Signal Score (-7.5): -5.45

```


-54-

Possible cleavage site: 49
 >>> Seems to have no N-terminal signal seq.
 Amino Acid Composition of Predicted Mature Form:
 calculated from 1
 5 ALOM: Finding transmembrane regions (Klein et al.)
 count: 0 value: 1.80 threshold: 0.0
 PERIPHERAL Likelihood = 1.80
 modified ALOM score: -0.86
 Rule: cytoplasmic protein
 10 *** Reasoning Step: 2
 ----- Final Results -----
 15 bacterial cytoplasm --- Certainty= 0.559 (Affirmative) < succ>
 motifs:
 Subtilase_Asp (S,T,A,I,V)x(L,I,V,M,F) (L,I,V,M)D(D,S,T,A)G(L,I,V,M,F,C)x
 (A)x(L)(I)D(D)G(I)x(2)(D)
 20 79: DDDFL AALIDDGIVFD V

A homolog was found in serogroup A *N.meningitidis* but not in serogroup B, so NGS27 protein and nucleic acid are useful for distinguishing between gonococcus and serogroup B *N.meningitidis*.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be
 25 useful antigens for vaccines or diagnostics.

Example 28

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 55> which encodes amino acid sequence <SEQ ID 56; NGS28>. Analysis of this protein sequence reveals the following:

30 GvH: Examining signal sequence (von Heijne)
 Signal Score (-7.5): -0.19
 Possible cleavage site: 61
 >>> Seems to have a cleavable N-term signal seq.
 Amino Acid Composition of Predicted Mature Form:
 calculated from 62
 35 ALOM: Finding transmembrane regions (Klein et al.)
 count: 0 value: 0.69 threshold: 0.0
 PERIPHERAL Likelihood = 0.69
 modified ALOM score: -0.64
 Score for OM-PP discrimination: -24.78
 40 Rule: outer membrane or periplasmic protein
 Score for OM-PP discrimination: -24.78
 Rule: outer membrane or periplasmic protein
 *** Reasoning Step: 2
 45 Periplasmic space? Score: 2.47798
 Periplasmic space? Score: 2.47798
 ----- Final Results -----
 50 bacterial periplasmic space --- Certainty= 0.916 (Affirmative) < succ>

The protein has homology with the following sequences in the databases:

55 >prf||1306286A mobilization protein B [Escherichia coli]
 Length = 529
 Score = 34.7 bits (78), Expect = 2.4
 Identities = 24/69 (34%), Positives = 31/69 (44%), Gaps = 12/69 (17%)

-55-

Query: 344 QLRARQQEIPVDYARTAVCGRIPFRRHSRPTLRSRTLGAQRRRIVPNVGQAGGIRAD--- 400
 +LRA Q++P D+ +T V P R R + GA GQ G IR D
 Sbjct: 440 RLRAAGQDLPAFVKTTVLDTNTPIRWFYRAASQESRSGA-----GQTGEIRVDVER 490

5 Query: 401 RTPNTQRGT 409
 R P +RGT
 Sbjct: 491 RGPAGRRGT 499

10 A homolog was found in serogroup A *N.meningitidis* but not in serogroup B, so NGS28 protein and nucleic acid are useful for distinguishing between gonococcus and serogroup B *N.meningitidis*.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 29

15 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 57> which encodes amino acid sequence <SEQ ID 58; NGS29>. Analysis of this protein sequence reveals the following:

GvH: Examining signal sequence (von Heijne)
 Signal Score (-7.5): -3.61
 Possible cleavage site: 31
 >>> Seems to have no N-terminal signal seq.
 20 Amino Acid Composition of Predicted Mature Form:
 calculated from 1
 ALOM: Finding transmembrane regions (Klein et al.)
 count: 0 value: 4.03 threshold: 0.0
 PERIPHERAL Likelihood = 4.03
 25 modified ALOM score: -1.31
 Rule: cytoplasmic protein
 *** Reasoning Step: 2
 30 ----- Final Results -----
 bacterial cytoplasm --- Certainty= 0.106(Affirmative) < succ>

The protein has homology with the following sequences in the databases:

35 emb|CAB83930.1| (AL162753) hypothetical protein NMA0640 [Neisseria meningitidis
 Z2491]
 Length = 387
 Score = 653 bits (1685), Expect = 0.0
 40 Identities = 324/388 (83%), Positives = 351/388 (89%), Gaps = 1/388 (0%)
 Query: 1 MNITIAAPYCSLPSEPHFNRFWYLAELLSQSHDVLLITSNFKHYDKSFRRPEDAKAASQG 60
 MNITI APYCSLPSEP+FNRFWYLAELLSQSHDVLLITS F+HYDKSFRR EDA A S G
 Sbjct: 1 MNITIVAPYCSLPSEPFYFNRFWYLAERLSQSHDVLLITSRFRHYDKSFRRHEDAAATSNG 60
 45 Query: 61 RLKVMLLEESGYSKNVSLGRVTSHHRFVKHFKEWLENCRPGEQDVVYSAYPLIATNLLLG 120
 RL+V LL+E GY KNVSL RV SH FV++ +WL + + EQD+VYSAYPL+ATNLLLG
 Sbjct: 61 RLRVKLLDEPGYRKNVSLARVASHRVFVRNLARWLHSPQAAEQDIVYSAYPLMATNLLLG 120
 50 Query: 121 KHKARLGYKLIVDVQDVWPESFSSVVPFLKKIPHNLLPFASRANRAYRYADALVAVSQTY 180
 KHKARLGYKLIVDVQDVWPESFSSVVPFLKK+PH LLPFASRANRAYR ADAL+AVSQTY
 Sbjct: 121 KHKARLGYKLIVDVQDVWPESFSSVVPFLKKVPHKLLPFASRANRAYRCADALIAVSQTY 180
 55 Query: 181 LDRAKEANPNVPGEVVYIGADFAAIAPPPFRSKTVRFFYLGTLSSYNDVETVCKGVRKL 240
 LDRAKEANPNVPG E VYIG DFAAIA PPRFRSKTVR FYLGTLSSY+YDVETVCKGVRKL
 Sbjct: 181 LDRAKEANPNVGETVYIGTDFAAIA-PPFRSKTVRLFYLGTLSSYNDVETVCKGVRKL 239
 Query: 241 LDDGENVELHIMGGGPDLDRLKQYACDGKIFYGYIPYAEMMSVAKGCDIAVNATHSYAMQ 300
 LDDGENVELHIMGGGPD++LKQY IKFYGY+PY+EMMS+AK CDIAVNATHS+AMQ

-56-

Sbjct: 240 LDDGENVELHIMGGPDLEKFKQYENRAIKFYGYLPYSEMMSIKACDIAVNAIHSAMQ 299

Query: 301 SITNKLSDYMALQKPILNSQVHDEVAEVLTLPHENYRSGDVGDFVQAAKDILKRKNDPV 360
S+TNKLSDYMALQKPILNSQ + EV ++L LLPHENYRSGDVD FVQAAK+ILKRK+DPV

5 Sbjct: 300 SVTNKLSDYMALQKPILNSQNNAEVLDLLNLLPHENYRSGDVDSFVQAAKNILKRKDDPV 359

Query: 361 QSDEIVRRFRHDISYRKIVNLIERLANE 388
QSDEIVRRFR DISYRKIVNLIERLA+E

10 Sbjct: 360 QSDEIVRRFRDISYRKIVNLIERLAHE 387

>emb|CAB58324.1| (AL121855) hypothetical protein SCF62.09 [Streptomyces
coelicolor
A3(2)]
Length = 407

15 Score = 54.7 bits (130), Expect = 2e-06
Identities = 57/243 (23%), Positives = 105/243 (42%), Gaps = 24/243 (9%)

Query: 99 RPGEQDVVYSAYP---LIATNLLLGKHKARLGYKLIVDVQDVWPESFSSVVPFLKKIPHN 155
R G DVV++ P L L L R G ++ D D+ PE + S K ++

20 Sbjct: 81 RVGFPVDVHACNPPDLLFLPALWL---KRRGARFVFDQHDLIPELYLSRFRGKDLLYR 136

Query: 156 LLPFASRANRAYRYADALVAVSQTYLDRAKEANPNVPGEVVYIGA-----DFAAIAPPPR 210
+ R YR AD ++A ++Y D A P +V + + F + P P

25 Sbjct: 137 AVCALERWT--YRAADVVLATNESYKDVAIRRGRRPDDVFVRSAPATDRFQFVPPEPE 194

Query: 211 F-RSKTVRFFYLGTLSYNYDVETVCKGVRKLLDDGENVELH--IMGGPDLDRLKQYA-- 265
R K YLG + V+ + + KL D+ + H +G G D + + +

30 Sbjct: 195 LKRKPHLLCYLGVMGPQDGVYALRALAKLRDEVGRTDWHAVFVGSQDAFDAMVELSRS 254

Query: 266 ---CDGIKFGYIPIYAEMMSVAKGCDIAVNAIHSYAMQSIT--NKLSDYMALQKPILNSQ 320
+ ++F G IP A+++ D+ ++ + ++ NK+ +YMA+ +PI++

35 Sbjct: 255 LGLDEQVRFTGRIPDADLVRHLSTADVCLSPDPRNPLNDVSTMNKVLEYMAMGRPIVSFD 314

Query: 321 VHD 323
+ +

Sbjct: 315 LRE 317

As a homolog was found in serogroup A *N.meningitidis* but not in serogroup B, NGS29 protein and
40 nucleic acid are useful for distinguishing between gonococcus and serogroup B *N.meningitidis*.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be
useful antigens for vaccines or diagnostics.

Example 30

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 59> which encodes amino acid sequence
45 <SEQ ID 60; NGS30>. Analysis of this protein sequence reveals the following:

Signal Score (-7.5): -4.8
Possible cleavage site: 46
>>> Seems to have no N-terminal signal seq.
Amino Acid Composition of Predicted Mature Form:
50 calculated from 1
ALOM: Finding transmembrane regions (Klein et al.)
count: 0 value: 1.54 threshold: 0.0
PERIPHERAL Likelihood = 1.54
modified ALOM score: -0.81
55 Rule: cytoplasmic protein

*** Reasoning Step: 2

----- Final Results -----

60

bacterial cytoplasm --- Certainty= 0.113(Affirmative) < succ>

The protein has homology with the following sequences in the databases:

```

5   fastidiosa (strain 9a5c)
    gb|AAF84279.1|AE003977_2 (AE003977) conserved hypothetical protein [Xylella
    fastidiosa]
      Length = 376

    Score = 73.6 bits (179), Expect = 3e-12
10   Identities = 82/354 (23%), Positives = 143/354 (40%), Gaps = 35/354 (9%)

    Query: 1   MKIILTTSMSGGGTETATVRLGRLLKRHGHDIILASSDG-PFVGEAQASGIRWQPVDFY 59
           MKI+ T + +G GG E   R   ++ GH + L   G P   A+ +G+   ++ +
    Sbjct: 1   MKILHTEAATGCGGEETIYIRHMLSMQAQGHMALLCQPGAPLSTMARNAGLPVYHINMH 60

15   Query: 60  RGGLAGYLKSTFAYARMLRREQPDIIQCMARVVPACALAAKIVSPKTKIICHSHGLDAA 119
           G   L           +L+RE D+++           A AA++ +T++I S L A
    Sbjct: 61  --GPWRVLNGIHTVQHLLQRETDFDVNNTTSHVDTLIAAAAAARLT--RTRLIVRSRHLMAP 116

20   Query: 120 TYPKTAKLFDKLGAYIIGNCKHEREKLIRHGFPPAGRIAYA-----YNTPEFHFHRK 170
           K+   + L   +I   +H R+ LI+ G   RI           +T PE   +++
    Sbjct: 117 I--KSQLTYTYLPHRVITVSQHVRLDLIKQGIQPTRIGIVPPITAQPPWMDTDPEHAWQR 174

25   Query: 171 TEK-----ECAVLGTLRLDTRAVHMLDLILKMKVGRNIPVRLNMAGIGEE 217
           ++           ++G ++ L   +   +LD +   +   N   + L +AG GE
    Sbjct: 175 LQQTRHVVRTELGFNDNDIIVGCVAVLREAKGHRELLDALAPLCQANPRHLVIAGDGEP 234

    Query: 218 -MDNLKAQAKRLGIEDKVTFLGGVRDLTGIFYKEVDILVNTPHCVGDHAGVGNINLEAGL 276
           M +L A K L +E ++ LG   D           DI           +   G   LEA
30   Sbjct: 235 VMQHLLAHRKTLTLETQIHLLGYRHDAPRLMSGFDIFA-----LATQKEAAGTVFLBAAQ 289

    Query: 277 YDTPVVVTYNMAGISEMVTGQTYGCIFFGDDEAFIEAVDTLIKHPELRSQMGKA 330
           P++   + G+ EM+ G           + G+ A   A+ TL+ + + R MG+A
35   Sbjct: 290 AGIPIIATRVGGVPEMLQEGTNAILVTPGNQTALTNALHTLVNTNNQQRHSMGRA 343

```

A homolog was found in serogroup A *N.meningitidis* but not in serogroup B, so NGS30 protein and nucleic acid are useful for distinguishing between gonococcus and serogroup B *N.meningitidis*.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

40 Example 31

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 61> which encodes amino acid sequence <SEQ ID 62; NGS31>. Analysis of this protein sequence reveals the following:

```

    GvH: Examining signal sequence (von Heijne)           Signal Score (-7.5): -5.36
    Possible cleavage site: 16
45   >>> Seems to have no N-terminal signal seq.
    Amino Acid Composition of Predicted Mature Form:
        calculated from 1
    ALOM: Finding transmembrane regions (Klein et al.)
        count: 0 value: 3.50 threshold: 0.0
50   PERIPHERAL Likelihood = 3.50
        modified ALOM score: -1.20
    Rule: cytoplasmic protein

    *** Reasoning Step: 2
55   ----- Final Results -----

```

bacterial cytoplasm --- Certainty= 0.299(Affirmative) < succ>

The protein has homology with the following sequences in the databases:

gb|AAB49297.1| (U84350) hypothetical hydroxylase a [Amycolatopsis orientalis]
Length = 491

5 Score = 111 bits (278), Expect = 1e-23
 Identities = 87/269 (32%), Positives = 123/269 (45%), Gaps = 15/269 (5%)

Query: 1 LKNGAAPSWGSRYTEFD-----TDKFSGPGTVYQVRRVFDKILIEBAKQGVEVRFGH 56
 +K G F WG+R + F + K + YQV RA FD IL++ A +GV VR G

10 Sbjct: 73 IKRGGTFRWGARPEPWTFFHGISAAMAGSTSHAYQVERAKFDDILLKNAKSKGVVREGC 132

Query: 57 GVTAFDNSGDFARLNIEITD--GESYELTAKFVLDASGY--GRVLPRLNLETSPHLPPTQT 114
 V G+ TD G ++E++A+FV+DASG R+ ++ S

15 Sbjct: 133 SVNDVVEDGERVTGARVTDADGNAHEVSARFVIDASGNKSRLYTKVNGSRNYSEFFRSLA 192

Query: 115 HFTHIDDNITHPKFDRNKILITTHPQHRDVWIWLIFFGDNRCSVGVV---GTPDKLAGES 171
 F + + P+ IL W W IP D SVG V DK+ G+

20 Sbjct: 193 LFGYFEGGKRLPEPVSGNLSVAFDSG---WFWYIPLSDTLTSVGAVVRREDADKIQDR 249

Query: 172 ETVLKKFVYECPLSEILDKAVWENDFPFRSIQ---GYSANVKSLHGRHFALLGNAAEFL 228
 E L + ECP++SE L A + ++ YS S L+G+AA F+

25 Sbjct: 250 EKALNTLIAECPLISEYLSNATRVTTGRYGELRVKDYDYSYQQDSYWRPGMVLVGDAACFV 309

Query: 229 DPVFSSGVTTIALHSARLAADLLTKQLKGE 257
 DPVFSSGV +A +SA LAA + L G+

25 Sbjct: 310 DPVFSSGVHLATYSALLAARSINSVLAD 338

30 A homolog (amino acids 280-341) was found in serogroup A *N.meningitidis* but not in serogroup B, so
 NGS31 protein and nucleic acid are useful for distinguishing between gonococcus and serogroup B
 N.meningitidis.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be
useful antigens for vaccines or diagnostics.

Example 32

35 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 63> which encodes amino acid sequence
 <SEQ ID 64; NGS32>. Analysis of this protein sequence reveals the following:

Signal Score (-7.5): -3.49
Possible cleavage site: 38
>>> Seems to have no N-terminal signal seq.
Amino Acid Composition of Predicted Mature Form:
40 calculated from 1
ALOM: Finding transmembrane regions (Klein et al.)
 count: 0 value: 7.80 threshold: 0.0
 PERIPHERAL Likelihood = 7.80
45 modified ALOM score: -2.06
Rule: cytoplasmic protein

*** Reasoning Step: 2

50 ----- Final Results -----
 bacterial cytoplasm --- Certainty= 0.278(Affirmative) < succ>

The protein has homology with the following sequences in the databases:

55 fastidiosa (strain 9a5c)
 gb|AAF83310.1|AE003899_2 (AE003899) phage-related repressor protein [Xylella
 fastidiosa]
 Length = 143

-59-

Score = 87.0 bits (214), Expect = 2e-16
 Identities = 40/71 (56%), Positives = 54/71 (75%)

5 Query: 1 MFSGEQLGQAISEAIKRNVSQKEVADHFGVKQPSVSGWIKNGRIDKKHLDKLIDYFSDV 60
 M +GEQLG+AI +A++ K V+ ++A+HFGVK PSV GWIK GRI K+ L L YFSDV
 Sbjct: 1 MLTGEQLGRAIKQAMQLKGVTPTKMAEHFGVKAPSVYGWIKGRIKELPSLWSYFSDV 60

10 Query: 61 VTPSHFGIETF 71
 V P+H+G+E +
 Sbjct: 61 VGPTHWGLEAW 71

>sp|P18680|RPC1_BPHK0 26 KD REPRESSOR PROTEIN (REGULATORY PROTEIN CI)
 emb|CAA34222.1| (X16093) cI gene product (AA 1-208) [Bacteriophage HK022]
 15 Length = 235

Score = 80.5 bits (197), Expect = 2e-14
 Identities = 60/200 (30%), Positives = 99/200 (49%), Gaps = 15/200 (7%)

20 Query: 22 QKEVADHFGVKQPSVSGWIKNGRIDKKHLDKLIDYFSDVVTPSHF-----GIETFRV 73
 Q ++A V ++S W I +K DK+ S + T + + GI +
 Sbjct: 29 QADLAVRLKVTTPKAISKWFNGESIPRK--DKMESLASVLGTTAAYLHGYADDDGITVNL 86

25 Query: 74 LKSNEQSSIRFPRLNAEATCGAGT-INDHYIEVVDYVTVAAWAREKLGGNLNK-IQVIT 131
 +SN+ R L+ +A+ G GT +++ +IE + + AR G + ++VIT
 Sbjct: 87 SRSNDY--YRVDVLDVQASAGPGTMVSNEFIEKIRALEYTTTEQARILFNGRPQESVKVIT 144

Query: 132 ARGDSMEPTIENGDMFVDTAVEAFDGDGLYLLWYIDGLKAKRLQSTVGGGLMIISDNSS 191
 RGDSME TI GD +FVD ++ FDGDG+Y+ Y + KRLQ L +ISDN++
 30 Sbjct: 145 VRGDSMEGTINPGDEIFVDVSITCFDGDGIYVFVYGKTMHVKRLQMQ-KNRLAVISDNAA 203

Query: 192 YRTETVRGEDLNAVRIIGRI 211
 Y + + + I+ ++
 35 Sbjct: 204 YDRWYIEEGEEQLHILAKV 223

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 33

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 65> which encodes amino acid sequence <SEQ ID 66; NGS33>. Analysis of this protein sequence reveals the following:

40 GvH: Examining signal sequence (von Heijne)
 Signal Score (-7.5): -4.87
 Possible cleavage site: 31
 >>> Seems to have no N-terminal signal seq.

45 Amino Acid Composition of Predicted Mature Form:
 calculated from 1
 ALOM: Finding transmembrane regions (Klein et al.)
 count: 0 value: 4.88 threshold: 0.0
 PERIPHERAL Likelihood = 4.88
 50 modified ALOM score: -1.48
 Rule: cytoplasmic protein

*** Reasoning Step: 2

55 ----- Final Results -----
 bacterial cytoplasm --- Certainty= 0.313(Affirmative) < succ>

The protein has homology with the following sequences in the databases:

60 gb|AAF31132.1| (AF069529) Gp54 [Bacteriophage HK97]
 Length = 273

-60-

Score = 47.4 bits (111), Expect = 3e-04
 Identities = 33/123 (26%), Positives = 52/123 (41%), Gaps = 20/123 (16%)

5 Query: 221 NGGLSGKPKNANVPRRRKTHGVPLQEIADLYNEVLGGRLPSVQVLNDRKRAIANRWCEM 280
 NGG G+ K P RRK + + + YN +G RLP +N+ RKR + +
 Sbjct: 160 NGGGDGQVK----PERRKAERIDYESFLNAYNTEVGDRLPHAVAVNEKRKRRL-KKIIPQ 214

10 Query: 281 LGTAAPNGKVRFGDKETGLAWFAGFFRKVA--MNPFFWMGENQTGFAVGFDWIFKAGNFVK 338
 L T +G F + R PF+ G+N TG+ FD++ + +
 Sbjct: 215 LKTPNVDG-----FRAYVRAFVHQAKPFYFGDNDTGWTADFDYLLREDSLTG 261

Query: 339 ILE 341
 + E
 15 Sbjct: 262 VRE 264

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 34

20 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 67> which encodes amino acid sequence <SEQ ID 68; NGS34>. Analysis of this protein sequence reveals the following:

GvH: Examining signal sequence (von Heijne)
 Signal Score (-7.5): -5.65
 Possible cleavage site: 50
 25 >>> Seems to have no N-terminal signal seq.
 Amino Acid Composition of Predicted Mature Form:
 calculated from 1
 ALOM: Finding transmembrane regions (Klein et al.)
 count: 0 value: 3.76 threshold: 0.0
 30 PERIPHERAL Likelihood = 3.76
 modified ALOM score: -1.25
 Rule: cytoplasmic protein

*** Reasoning Step: 2
 35 ----- Final Results -----

bacterial cytoplasm --- Certainty= 0.310(Affirmative) < succ>
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
 40 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

The protein has homology with the following sequences in the databases:

45 >pir|H82649 hypothetical protein XF1674 XF1569 [imported] - Xylella fastidiosa
 (strain 9a5c)
 gb|AAF84378.1|AE003986_8 (AE003986) hypothetical protein [Xylella fastidiosa]
 gb|AAF84483.1|AE003993_2 (AE003993) hypothetical protein [Xylella fastidiosa]
 Length = 316

50 Score = 167 bits (424), Expect = 2e-40
 Identities = 108/308 (35%), Positives = 152/308 (49%), Gaps = 30/308 (9%)

Query: 10 ETSVIRSLSSASLYMFTTRRMFYQRRGYVWQRANHHAPICNALERVFNGETKRLLIINIPPR 69
 E +VI++ A FTR F QR+ ++ HH I ++ V G K ++IN+PP
 55 Sbjct: 10 EQAVIKARCEADHLFFTRYFFKQROQLRFRVNWHHVVIAGVVDDVIAGRRKDVVINVPPG 69

Query: 70 YSKTEIAVVNFIAWAMGRVPDCEFIHASYSAA LAVNNSVQIRNLVQHEEYRAIFP-DLAL 128
 SKTE+ +N +A + P F+H SYS LA+ NS R +VQ +EYRA++P ++A
 Sbjct: 70 SSKTELVAINV MARGLALNPFARFLHISYSDDLALLNSETAREIVQSDEYRALWPLEIAD 129

60 Query: 129 AGESGHHWKT-----AGGVMYXXXXXXXXXXXXXXXXXRHREGFGGCIIDDPHKADEARSE 183

-61-

```

      +S   W       AGGV Y               G+ G I I I D D P K ++A S+
Sbjct: 130 DAKSKKRWNVVVDGKKAGGV-YAVSLGGQVTGFRAGHMAPGWQGAI I I D D P L K V E D A Y S K 188

5  Query: 184 VRRQNVIDWFQNTVESRKNSPDTPFIILIMQRLHEKDLAGWLLDGGNGEWEHLCLPAIQE 243
      R       +TV+SRK SPDTPII+IMQRL + D G++ GG   WE + +PA+ +
Sbjct: 189 TGRSKANRKLVS TVKSRKASPDTPFIIVIMQRLAQDDPTGFIQSGGFPGAWECEIIPALID 248

Query: 244 DG-----TALWPEKHDIETLRRMEQAAPYVFAGQYLQKPAPP 280
      D               + WP K + L +E   YVF+GQY Q+P+P
10 Sbjct: 249 DAYVSRLPEHVQGVVRDAQDQDGRYSYWFYKEPLAELLALEATDRYVFSGQYQQRPSPL 308

Query: 281 DGGTFKPD 288
      GG K D
Sbjct: 309 GGGIIGD 316

```

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 35

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 69> which encodes amino acid sequence <SEQ ID 70; NGS35>. Analysis of this protein sequence reveals the following:

```

20  GvH: Examining signal sequence (von Heijne)
      Signal Score (-7.5): -1.07
      Possible cleavage site: 40
      >>> Seems to have no N-terminal signal seq.
25  Amino Acid Composition of Predicted Mature Form:
      calculated from 1
      ALOM: Finding transmembrane regions (Klein et al.)
      count: 0 value: 1.64 threshold: 0.0
      PERIPHERAL Likelihood = 1.64
30  modified ALOM score: -0.83
      Rule: cytoplasmic protein

      *** Reasoning Step: 2

35  ----- Final Results -----

      bacterial cytoplasm --- Certainty= 0.020(Affirmative) < succ>

```

The protein has homology with the following sequences in the databases:

```

40  >ref|NP_047925.1| gp34 [Bacteriophage phi-C31]
      emb|CAA07104.1| (AJ006589) gp34 [Bacteriophage phi-C31]
      Length = 457

      Score = 59.7 bits (143), Expect = 1e-07
45  Identities = 68/272 (25%), Positives = 117/272 (43%), Gaps = 49/272 (18%)

Query: 226 GYSPVEQIIMTVNIALKRQVHALEYTAGSVPDALVGVPETWSADDIRRFQYEWDL L L S G 285
      G SP+   ++ +AL Q +   +++ G++P A+V VP T S + + R +E W   SG
50 Sbjct: 192 GCSPISYARESIGLALAAQKYGSKFFANGAMPGAVVEVPGTMSEGLARAREAWRAANS G 251

Query: 286 -----ETAQRRKMRFPVGELSRNFRETKQPLKDVYDEWLARVVCFAFSVEPTP 334
      E A+ K+   P E   F +T+Q + ++   AR+   F V P
Sbjct: 252 VDNAHRVALLTEGAKFSKVAMSPDEAQ--FLQTRQFQVPEI-----ARI-----FGVPPH- 299

55 Query: 335 FVAQVNRSAETS--REQLSDGMGSLKNWVKALIDDLARYMDMAA--YEFVWKGESL 390
      ++   S + S   EQ+++ M SL+ W++ +   A + FV   + +
Sbjct: 300 LISDATNSTSWGSLAEQNI AFTMFSLRPWLERIEAGFNRL LFAETADRF R FVKNLDEI 359

Query: 391 N---PREQAEIYAIYKNAGILTADEIRAE L GKEPLP-GQG-----QPEPDK 432
      PKE+ E++++ GI + DE+RA   PLP G G   +PEP+
60 Sbjct: 360 KRGAPKERMELWSLGLQNGIYSIDEVRAEDMTPLPDGLGEKYRVPLNLGEVGEEPEPEP 419

```


Query: 433 QDG----RKPEPPNQGAERLKGSESPMSDE 460
 P E P++ E GK + + +E
 Sbjct: 420 APAPPAIEPPAREPDKEPEPEGKPDDEGATEE 451

A homolog (amino acids 641-700) was found in serogroup A *N.meningitidis* but not in serogroup B, so NGS35 protein and nucleic acid are useful for distinguishing between gonococcus and serogroup B *N.meningitidis*.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 36

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 71> which encodes amino acid sequence <SEQ ID 72; NGS36>. Analysis of this protein sequence reveals the following:

15 GvH: Examining signal sequence (von Heijne)
 Signal Score (-7.5): 4.3
 Possible cleavage site: 26
 >>> Seems to have a cleavable N-term signal seq.
 Amino Acid Composition of Predicted Mature Form:
 calculated from 27
 20 ALOM: Finding transmembrane regions (Klein et al.)
 count: 0 value: 1.70 threshold: 0.0
 PERIPHERAL Likelihood = 1.70
 modified ALOM score: -0.84
 Score for OM-PP discrimination: 0.02
 25 Rule: outer membrane or periplasmic protein
 Score for OM-PP discrimination: 0.02
 Rule: outer membrane or periplasmic protein
 *** Reasoning Step: 2
 30 Outer membrane? Score: 0.00213559
 Outer membrane? Score: 0.00213559
 ----- Final Results -----
 35 bacterial outer membrane --- Certainty= 0.232(Affirmative) < succ>

The protein has homology with the following sequences in the databases:

40 >pir||D82437 TonB receptor-related protein VCA0625 [imported] - *Vibrio cholerae*
 (group O1 strain N16961)
 gb|AAF96526.1| (AE004392) TonB receptor-related protein [*Vibrio cholerae*]
 Length = 784
 Score = 103 bits (256), Expect = 2e-20
 45 Identities = 104/427 (24%), Positives = 162/427 (37%), Gaps = 100/427 (23%)
 Query: 31 NTEQQKELNTIVVHGKRS-ADQKGADVVYKVNVSAYVGKEYLERYRVQSAGDVLKGLNG 89
 NTEQ + T+ VHG+ DQ+ D L++ R + D+ G+
 Sbjct: 57 NTEQAVD-ETVTVHGQSILTDQTRSD-----LDKVRGIANADIFSGITS 100
 50 Query: 90 VYNNMTRTAGGAITPNIRGITGKGRIPVTIDGTEQTIDVMMNNYGVGDRNYLDPALFRSI 149
 V + N GA+ IRG+ G+GR+P+ IDG+ Q+ GV DR Y+D L S+
 Sbjct: 101 VQSNMHNHEAGALDIGIRGVQGEGRVPIFIDGSLQSTHTSRGYQGVSDRTYIDTDLSSL 160
 55 Query: 150 AVEKSPALTRG--VKSGVGGAMSIRTIPEPSDIIPEGRNWGIEVKTEFSGNTVAQKNDLRQ 207
 V K + VGG ++ T+ DII + + +G+ +K
 Sbjct: 161 TVNKGATIESSPYASGAVGGVVNATILGIKDIKDDQAFGVVLK----- 204

Query: 208 FLGRDYRTLSPIGATADGVSGMPDVLTYGTGKPSPTALLLDEGIADTKFSGGKSHTNFKD 267
 A A+ + PDV Y+ + LDE + F G
 Sbjct: 205 -----ARANNHNRTPDVSGDYSEQGQ---YALDERGEHSAFKHG----- 240

5 Query: 268 DRQLMLSAAFKTDITDGLAAYSHRQKGNYYAGKRGYQSYLNNPI--YGADACYDQYPKS 325
 LML ++ + + + AYS R KGN++AGK+GY+ Y P+ G + + S
 Sbjct: 241 --SLMLGLGYQAESFNTVLAYSRSKGNHFAKKGYEY--QEPVVGGQGEVVNTSFSRSDS 297

10 Query: 326 WREKDILCKSSASLVPNMAVLFPRGEEIMNSHTDTKILLKNNWYLPDNQKISLQYMDNK 385
 W K S N +R H +L WY Y D K
 Sbjct: 298 WLFK---LASDTGTAHNADFNYR-----HHAQKAGEVLMAWYKSSSEDWEGNPFYDPGK 347

15 Query: 386 IGFGEINPLITAWILGFABEQSLNBFVQAPGIGTKIDSKTYKIGYEWKPNKKNWIDLQAD 445
 + W LG A+ + TY Y ++P ++ W++L A+
 Sbjct: 348 -----DRMPQWGLGTAKVN-----TYSANYYYQP-DHPWLNLAN 381

20 Query: 446 MWRVKTD 452
 W + D
 Sbjct: 382 FWYTRAD 388

Score = 94.7 bits (234), Expect = 5e-18
 Identities = 80/290 (27%), Positives = 126/290 (42%), Gaps = 37/290 (12%)

25 Query: 929 SYDLADNHLRFARYARMSRFPSPLYELTAATGSGGLYGSETVAEYS-----LKPEKSTNWEV 984
 +Y L + +LF + +R R PSLYE T S V Y+ +KPE++ N EV
 Sbjct: 514 TYALTPTQLFLKSSRTYRMPSLYETTL-----SNEVFSYNPYNPIKPEQAWNNEV 564

30 Query: 985 GYNFNFAPHFAKLKQGLRLTYYSNKIKNQIDTSN--EDGGMIQ-----YDKAVSK 1033
 G F + + +L ++Y+ N IK+ I + GM + YDK
 Sbjct: 565 GVQFMASNSVLQDDRLNLSVSYFRNSIKDFISGRLAKTPGMSEWQANFTFTNYDKLQLS 624

35 Query: 1034 GVELQSRLDSGRFFASPGGTYYRLKHMVCDKGIAFKFDYYLQRVPECLEGGFGLSRFFQSL 1093
 G EL + + F T + +C A C GF +
 Sbjct: 625 GWELGAHYQYAWLYTHFAATLYSETKICSVQQA-----QYAESDTCNSLGFAGLTPTRI 679

40 Query: 1094 QPKYSLTLDVGTTRFFNEKLELGMRAIHHSKARRNYDKLIADGAGQVYARNGKPYGWHA 1153
 PK +L L+VGT+FFN+ L+ G++ +HS + N +A A Y
 Sbjct: 680 PPKQNLVNLVGTGKFFNDTLDGSKVSVYHSG--KSNPSDWLAGTAANPILEIPSDY----- 732

Query: 1154 TLDDAYARYRIGKHIDLNFSVTNLANRYLDPMSSTFVPGPGRTITFGIK 1203
 +D Y++Y + + L F++ N+ +RY + P S +P PGRTIT G +
 Sbjct: 733 -TIDLYSQYELNANTQLFFAINNVTDRYQVRPGSVVSMPPDGRITITLGF 781

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be
 45 useful antigens for vaccines or diagnostics.

Example 37

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 73> which encodes amino acid sequence
 <SEQ ID 74; NGS37>. Analysis of this protein sequence reveals the following:

50 GvH: Examining signal sequence (von Heijne)
 Signal Score (-7.5): 4.47
 Possible cleavage site: 21
 >>> Seems to have a cleavable N-term signal seq.
 Amino Acid Composition of Predicted Mature Form:
 calculated from 22

55 ALOM: Finding transmembrane regions (Klein et al.)
 count: 0 value: 7.21 threshold: 0.0
 PERIPHERAL Likelihood = 7.21
 modified ALOM score: -1.94

60 Score for OM-PP discrimination: 16.42
 Rule: outer membrane or periplasmic protein
 Score for OM-PP discrimination: 16.42
 Rule: outer membrane or periplasmic protein

*** Reasoning Step: 2

Outer membrane? Score: 1.64214
Outer membrane? Score: 1.64214

----- Final Results -----

bacterial outer membrane --- Certainty= 0.938(Affirmative) < succ>

The protein has homology with the following sequences in the databases:

```
>sp|Q03155|AIDA_ECOLI ADHESIN AIDA-I. PRECURSOR
pir|S28634 adhesin AIDA-I precursor - Escherichia coli plasmid pIB6
emb|CAA46156.1| (X65022) AIDA-I [Escherichia coli]
Length = 1286

Score = 35.8 bits (81), Expect = 0.67
Identities = 34/138 (24%), Positives = 62/138 (44%), Gaps = 16/138 (11%)

Query: 3  ASQLTLAVLLAAAFGSAYAVEVKGDDSSKGQLIQAESDFLPFGSGAADIKVSTGNGLSK 62
          A   L + + +  G+A+AV + G  SS G  + +  E+  +  G G ++  V++G  ++
Sbjct: 31  AKNTLLVLAVVSTIGNAFAVNISGTVSS-GGTVSSGETQIVYSGRGNSNATVNSGG--TQ 87

Query: 63  SINLEAGPAQRIRNKYGNAPINGGNQNTNVNGAANSRYLPQGDINPIA--GWFSKTRLA- 119
          +N              N          + G+QN  +GA S  +  G I  ++  G S T L+
Sbjct: 88  IVNNGGKTTATTVN-----SSGSQNVGTSGATISTIVNSGGIQRVSSGGVASATNLSG 140

Query: 120 ---QVWYEKRANNTVEVFS 134
          ++      A+NT +FS
Sbjct: 141 GAQNIYNLGHASNTVIFS 158
```

The protein was expressed in *E.coli* as an insoluble 32.45kDa His-fusion product and then purified.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 38

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 75> which encodes amino acid sequence <SEQ ID 76; NGS38>. Analysis of this protein sequence reveals the following:

```
GvH: Examining signal sequence (von Heijne)
Signal Score (-7.5): 0.34
Possible cleavage site: 24
>>> Seems to have a cleavable N-term signal seq.
Amino Acid Composition of Predicted Mature Form:
calculated from 25
ALOM: Finding transmembrane regions (Klein et al.)
count: 0 value: 3.98 threshold: 0.0
PERIPHERAL Likelihood = 3.98
modified ALOM score: -1.30
Score for OM-PP discrimination: 2.87
Rule: outer membrane or periplasmic protein
Score for OM-PP discrimination: 2.87
Rule: outer membrane or periplasmic protein
```

*** Reasoning Step: 2

Outer membrane? Score: 0.287446
Outer membrane? Score: 0.287446

----- Final Results -----

bacterial outer membrane --- Certainty= 0.607(Affirmative) < succ>

The protein has homology with the following sequences in the databases:

```

5  >sp|Q03155|AIDA_ECOLI ADHESIN AIDA-I PRECURSOR
   pir||S28634 adhesin AIDA-I precursor - Escherichia coli plasmid pIB6
   emb|CAA46156.1| (X65022) AIDA-I [Escherichia coli]
      Length = 1286

   Score = 35.8 bits (81), Expect = 0.67
   Identities = 34/138 (24%), Positives = 62/138 (44%), Gaps = 16/138 (11%)
10 Query: 3  ASQLTLAVLLAAAFGSAYAVEVKGDDSSKQQLIQAAESDFLPFGSGAADIKVSTGNGLSK 62
      A   L + + + G+A+AV + G SS G + + E+ + G G ++ V++G ++
   Sbjct: 31 AKNTLLVLAVVSTIGNAFVNISGTVSS-GGTVSSGETQIVYSGRGNSNATVNSGG--TQ 87

15 Query: 63 SINLEAGPAQRIRNKYGNAPINGGNQNTNVNGAANSRYLQPGDINPIA--GWFSKTRLA- 119
      +N      N      + G+QN +GA S + G I ++ G S T L+
   Sbjct: 88 IVNNGGKTTATTVN-----SSGSQNVGTSGATISTIVNSGGIQRVSSGGVASATNLSG 140

20 Query: 120 ---QVWYEKRANNTTEVFS 134
      ++      A+NT +FS
   Sbjct: 141 GAQNIYNLGHASNTVIFS 158

25 >pir||G81213 conserved hypothetical protein NMB0313 [imported] - Neisseria
      meningitidis (group B strain MD58)
   gb|AAF40758.1| (AE002388) conserved hypothetical protein [Neisseria meningitidis
      MC58]
      Length = 488

   Score = 84.3 bits (207), Expect = 3e-15
   Identities = 111/498 (22%), Positives = 185/498 (36%), Gaps = 35/498 (7%)
30 Query: 7  LLFLPLCTVCLAAPSNDAADERRRLLEDEGSRQTQQYRESGW--LDTEQARGEVEENDGYI 64
      +L LPL      S  A+E R D SR + E+ +D E+ G+V E +
   Sbjct: 19 MLLLPLLA-----SAAYAEETPREPDLRSRPEFRLHEAEVKPIDREKVPGQVREKGV 72

35 Query: 65 SIGGEIYQVGDTAEELESATYHALNARQWHKVRQFAARYAKLPRHKPALIHLADALQKRD 124
      I GE      E L A+Y A+ + +R Y + + L A + +
   Sbjct: 73 QIDGETLL--KNPELLSRAMYSAVVSNNIAGIRVILPIYLQQAQDDKMLALYAQGILAAQA 130

40 Query: 125 EGDFAAGNSPQTALAEAPDNPRLLLEAGRFYAEDNQNKESAAAFEKVLKTDIPAEIRPI 184
      +G + A + ++ + A+PD P + + E+ QN+ +A F+++ ++P +
   Sbjct: 131 DGRVKEAISHYRELIAAQPDAPAVRMRLAAALFENRQNEAADQFDRLEAENLPPQIMEQ 190

45 Query: 185 VENYLSELGKRRRWGQISLGYGYNNSNVNQNGINQCVWEIAGMCLMERTLPAPTDSTFS 244
      VE Y L +R W      N+NQ Q      + T P D T
   Sbjct: 191 VELYRKALRERDAWKVNGGFSVTREHNINQAPKRQ-----YGKWTFPKQVDGTAV 241

   Query: 245 SYSATAEKTIVPLKGNHGVQVRGVLYGNRYTEKDKDSAAMPDYGYRNGSLYAGYAYADARS 304
      +Y AEK LK      G + G Y K      +      + G +AD R
50 Sbjct: 242 NYRLGAEEKWSLKNGWYTTAGGDVSGRVYPGNKK-----FNDMTAGVSGGIGFADRRK 294

   Query: 305 SFSLLPYFEYDFRNRHHTYRAWGADADWSRTLSPHWRINSHAGAKKTGYGGQSKTYFADF 364
      L + E      + GA ++R +P W+ S A + G ++ +D
55 Sbjct: 295 DAGLAVFHERRTYGNDAYSYTNGARLYFNRWQTPKWQTLSSA---EWGRLEKNTRRARSND 351

   Query: 365 KQVELGAGAEFSITLKSGLLVNFDAARKAYP-EKSSSSKEYTARLGAYRLFSGGTYLNAV 423
      ++      F + + D R+ P ++ + Y R A+ GG+ L+++
   Sbjct: 352 THLQISNSLVFYRNARQYWMGGLDFYRERNPADRGDNFNRYGLRF-AWGQEWGSGSLSSL 410

60 Query: 424 LLY--RRSLYDAASFVSDNK--RRRDKQYIMAAAGFPQWNIGVYPELRFRTIAHSNA 479
      L + Y+ F S K RRRDK+      +      + KG+ P L SN
   Sbjct: 411 LRLGAARKHYEKPGFSSGFGERRRDKELNTSLSLWHRALHFKGITPRLTLSHRETRSDN 470

   Query: 480 VYYRYRQNEWLLGFKYRF 497
      V+ Y +N + F F
65 Sbjct: 471 VFNEYEKNRAFVEFNKTF 488

```


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```

>pir|[C81790 conserved hypothetical protein NMA2174 [imported] - Neisseria
      meningitidis (group A strain Z2491)
emb|CAB85386.1| (AL162758) conserved hypothetical protein [Neisseria
meningitidis
5      Z2491]
      Length = 490

Score = 84.0 bits (206), Expect = 4e-15
Identities = 111/498 (22%), Positives = 185/498 (36%), Gaps = 35/498 (7%)

10 Query: 7  LLFLPLCTVCLAAPSNDAADERRRLLEDEGSRQTQQYRESGW--LDTEQARGEVEENDGYI 64
      +L LPL      S  A+E R D SR  + E+  +D E+  G+V E  +
Sbjct: 21  MLLLPLLA-----SAAYAETPREPDLRSRPEFRLHEAEVKPIDREKVPQGVRKGV 74

15 Query: 65  SIGGEIYQVGDTAEELSAIYHALNARQWHKVRQFAARYAKLPRHKPALIHLADALQKRD 124
      I GE      E L  A+Y A+  +  +R  Y  +  +  L  A  +  +
Sbjct: 75  QIDGETLL--KNPELLSRAMYSAVVSNNIAGIRVILPIYLQQAQODKMLALYAQGILAQ 132

20 Query: 125  EGDFAAGNSFQTALEAEFPDNPRLLEAGRFYAEDNQNKESAAAFKVLKTDIPAE TRPI 184
      +G  + A  +  ++  + A+PD P  +  +  E+ QN+  +A  F+++  ++P  +
Sbjct: 133  DGRVKEAISHYRELIVAQPDAPAVRMRLAAALFENRQNEAAADQFDRLKAENLPPQIMEQ 192

25 Query: 185  VENYLSELGKRRRWHGQISLGYGYNVNVNQNGINQCVWEIAGMCLMERTLPAPT DSTFS 244
      VE Y  L  +R  W      N+NQ  Q      + T P  D T
Sbjct: 193  VELYRKALRERDAWKVNGGFSVTREHNINQAPKRQ-----YGKWTFPKQVDGTAV 243

30 Query: 245  SYSATAEKTVP LKGNHGVQVRGVLYGNRYTEKDKDSAAMPDYGYRNGSLYAGYAYADARS 304
      +Y  AEK  LK      G  + G  Y  K      +      + G  +AD R
Sbjct: 244  NYRLGAEEKWSLKNGWYTTAGGDVSGRVYPGNKK-----FNDMTAGVSGGIGFADRRK 296

35 Query: 305  SFSLLPYFEYDFRNRHETHYRAWGADADWSRTLSPHWRINSHAGAKRTGYGGQSKTYFADF 364
      L  + E      +  GA  ++R  +P W+  S A  + G  ++  +D
Sbjct: 297  DAGLAVFHERRTYGNDAYSYTNGARLYFNRWQTPKWQTLSSA---EWGRLKNTRRARSND 353

40 Query: 365  KQYELGAGARFSITLKSGLLVNFDAARKAYP-EKSSSSKEYTARLGAYRLFSGGTYLNAV 423
      ++  F  +  +  D R+  P ++  +  Y R A+  GG+  L+++
Sbjct: 354  THLQISNSLVFYRNARQYWMGGDLFYRERNPADRGDNFNRYGLRF-AWGQEWGGSGLSSL 412

45 Query: 424  LLY--RRSLYDAASFVSDNK--RRRDKQYIMAAAGFPQWNIGVYPELRFRTIAHSNA 479
      L  +  Y+  F S  K  RRRDK+  +  +  KG+  P L      SN
Sbjct: 413  LRLGAAKRHYEKPGFFSGFGKERRRDKELNTSLSLWHRALHFKGITPRLTSLSHRETRSDN 472

Query: 480  VYRYRQNEWLLGFKYRF 497
      V+  Y +N  + F  F
Sbjct: 473  VFNEYEKNRAFVEFNKTF 490

```

The protein was expressed in *E.coli* as an insoluble 52.03kDa His-fusion product and then purified.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

50 Example 39

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 77> which encodes amino acid sequence <SEQ ID 78; NGS39>. Analysis of this protein sequence reveals the following:

```

GvH: Examining signal sequence (von Heijne)
Signal Score (-7.5): -5.38
Possible cleavage site: 18
>>> Seems to have no N-terminal signal seq.
Amino Acid Composition of Predicted Mature Form:
      calculated from 1
ALOM: Finding transmembrane regions (Klein et al.)
count: 0 value: 7.16 threshold: 0.0
PERIPHERAL Likelihood = 7.16

```


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modified ALOM score: -1.93
Rule: cytoplasmic protein

*** Reasoning Step: 2

5

----- Final Results -----

bacterial cytoplasm --- Certainty= 0.325(Affirmative) < succ>

10 The protein has homology with the following sequences in the databases:

>ref|NP_052685.1| serine protease EspP [Escherichia coli]
pir|T00317 probable serine proteinase espP, extracellular - Escherichia coli
plasmid pO157
pir|T42120 probable serine proteinase espP, extracellular - Escherichia coli
plasmid pO157
15 emb|CAA66144.1| (X97542) putative exoprotein-precursor [Escherichia coli]
dbj|BAA31836.1| (AB011549) serine protease EspP [Escherichia coli]
gb|AAC70088.1| (AF074613) putative exoprotein-precursor [Escherichia coli
0157:H7]
20 Length = 1300

Score = 58.9 bits (141), Expect = 2e-07
Identities = 153/687 (22%), Positives = 248/687 (35%), Gaps = 106/687 (15%)

25 Query: 194 DLTVENKNTLSDA---EFGVYALNTSMVNLSSKDNNEVKSTQVGLYSQDGGSSINVDR--- 247
D +NT +DA Y N ++ +LS D E + + G + +V R
Sbjct: 595 DYVAGMQNTEADAVKQNGNAYKTNNNAVSDLSPDW-ETGTFRFGTLHLENSDFSVGRNAN 653

30 Query: 248 -----KDNIEGDAVALVGKGGSQNIRAS-----RTNLISSKSLGIHAEQAAKIAITG 295
K NI GD A + +NI R N++ S G E IT
Sbjct: 654 VIGDIQASKSNITIGDTTAYIDLHAGKNITGDFGFRQNIVRGNSQG---ETLFTGGITA 710

35 Query: 296 ASNTIHASNAAIRSLDKSEVKIDQITIDSNVANLARQDGSIH---LNYKDDTRITGATV 352
+TI + A ++ + TI+ N A++ Q G ++ + +TG
Sbjct: 711 EDSTIVIKDKAKALFSNYYVLLNTKATIE-NGADVTTQSGMFSTSDISISGNLSMTGNPD 769

40 Query: 353 SDKGLVAIKPLNNTNIVADTIHYKGDVLAVNKGKVELDF----TPNILLAGRLDNFSGLT 408
D LN+ + + + ++A NK V D + +I+ + S L+
Sbjct: 770 KDNKFEPSTYLNDAASYLLTDDSAR--LVAKNKASVVDIHSKTSASIMFGHDESLSQLS 827

45 Query: 409 DSKHKNLFENYVANLDSKSAGEINFNLAKDAL----WTMTGQSWLDKLEGQGTIDFNDA 464
D K L + D G +N A + W +TG S L L+ ++ + D+
Sbjct: 828 DRTSKGLALGLLGGFDVSYRGSVNAPSASATMNTTWQLTGDSALKTLKSTNSMVFYFTDS 887

50 Query: 465 KTSGR--ALHIGELAGANK-FLMHLNKDGIHSDMLYVKKGTSTPQEVVVKNLSEVLDSMN 521
+ + L + ELA +N + M N SD L VKK S ++ L + L
Sbjct: 888 ANKKFHTLTVDLATSNSAYAMRTNLS--ESDKLEVKKHLSGENNIL---LVDPLQKPT 942

55 Query: 522 YGERLRFATVTNSKNEFVNGKKYIDDTLHLMEDALTVEYSAHNGXXXXXXXXXXSFNGSEM 581
++L V+ K+ N K T D V
Sbjct: 943 PEKQLNIELVSAPKDTNENVFKASKQTIGFSDVTFV----- 978

60 Query: 582 TAEKAGDDYVNKTYTDNRQNVYLKQATGNPSRVKNINDMFDSTAHYAFT--LDTYAKR 639
+ DD + T++ N K+AT N + S + AF ++ KR
Sbjct: 979 ITTRETDDKI--TWSLTGYNTVANKEATRMAA-----LPSVDYKAFLNEVNNLNKR 1028

65 Query: 640 EGERAFSTLDKKEGDWIRLTHTRVIQSNAPFRHNNDFEIGYDRFSLNEQEKRRKWGISLD 699
G+ ++ + G W R+ S F + ++G D+ K G+ L
Sbjct: 1029 MGD--LRDINGEAGAWARIMSGTGSASGGFSDNYTHVQVGVDR-----KHLDGLDLF 1079

70 Query: 700 YGHGRTSLWNTFGKD----KIRKYELALYNTTQYIDKEGDETYIDNVLRIGKLRNRVIA 755
G T ++ D K + LY + + D YID + K N A
Sbjct: 1080 TGFTVTHTDSSASADVFSGKTKSVGAGLYASAMF-----DSGAYIDLIGKYVHHDNEYTA 1134

75 Query: 756 RNHMQQLWGKGKYSNTLFSISTEYGRRKFLDDDKLWRITPQVQLQYSYLRTGYRI-DNG 814
G G YS + E G R + +D W I PQ +L Y + G + D G
Sbjct: 1135 -TFAGL--GTRDYSTHSWYAGAEAGYRYHVTEA-W-IEPQAEVLVYGSVSGKQFAWKDQG 1189

Query: 815 INVNLSHA--NSLIGRLGLDVVRKFDG 839
 +++++ N LIGR G+DV + F G
 Sbjct: 1190 MHL SMKDKDYNPLIGRTGVDVGKSFSG 1216

Score = 36.6 bits (83), Expect = 1.2
 Identities = 97/412 (23%), Positives = 164/412 (39%), Gaps = 83/412 (20%)

Query: 63 DNIVTMKSGDADADYVNNKVLTTETPYYSKRGSGNGIFAYGDKSLVKLIGENNIVK--SE 120
 D V G + ++ SK Y + +G + A+ S V + +N + +E
 Sbjct: 163 DKFVVETRGATEGADISLSKQQALERYGVNYRGEKKLIAFRAGSGVVSVKKNRITPFNE 222

Query: 121 ISEKSKALNGGFRHIGIYS-W---QNAKVE---LSAKSDN-----IVQGG 158
 +S K + LNG F HI +S W N + + +++++ D+ +V G
 Sbjct: 223 VSYKPEMLNGSFVHIDDWSGWLILTNQFDEFNNIASQGDGSGSALFVYDNQKKRWVAGT 282

Query: 159 IWGLYS---NNSSISLKGKNNVISNPKNVFAKKAQVDLTVENKNTLSDAEFGVYALN 214
 +WG+Y+ N + K I N K N ++Y VD++ T+ + + +
 Sbjct: 283 VWGIYNYANGKNHAAYSKWNQTTIDNLK-NKYSY---NVDMSGAQVATIENGR--LTGTG 336

Query: 215 TSMVNLSSKDNNEVKSTQVGLYSQ----DGGSINVDKDNIEGDAVALVGKG----GS 265
 + ++ +KD + L S GG + D+K + GD G G GS
 Sbjct: 337 SDTTDIKNKDLIFTGGGDILLKSSFDNGAGGLVFNDRKTYRVNGDDFTFKGAGVDTRNGS 396

Query: 266 Q---NIR-ASRTNL--ISSKSLGIHAEQAQAK-----IAITGASNTIHASNAAIRSLDKS 313
 NIR ++ NL I +L + Q + I GA T +N I S D
 Sbjct: 397 TVEWNIRYDNKDNLHKIGDGLTDRKTKTQNTNLKTGEGLVILGAETKTF--NNIYTSGD-G 453

Query: 314 EVKIDGQITIDSNVAN---LARQDGSIHNLN-YKDDTRITGATVSDRGLV-----AIK 361
 V+++ + + N A+ G++ LN Y AT D G V +I
 Sbjct: 454 TVRLNAENALSGGEYNGIFFAKNGGTLDLNGYNQSFNKIAAT--DSGAVITNTSTKKSIL 511

Query: 362 PLNNTNIVADTIHYKG-----DVLAVNKGKVELDFTPNILLAGRLDNFSGLT 408
 LNNT AD I++ DVL ++ K E ++L G +D + ++
 Sbjct: 512 SLNNT---ADYIYHGNGINGNLDVLQHETKKE---NRRLILDGGVDTTNDIS 557

The protein was expressed in *E.coli* as an insoluble 95.92kDa His-fusion product and then purified.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 40

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 79> which encodes amino acid sequence <SEQ ID 80; NGS40>. Analysis of this protein sequence reveals the following:

GvH: Examining signal sequence (von Heijne)
 Signal Score (-7.5): -4.18
 Possible cleavage site: 17
 >>> Seems to have no N-terminal signal seq.
 Amino Acid Composition of Predicted Mature Form:
 calculated from 1
 ALOM: Finding transmembrane regions (Klein et al.)
 count: 0 value: 7.05 threshold: 0.0
 PERIPHERAL Likelihood = 7.05
 modified ALOM score: -1.91
 Rule: cytoplasmic protein

*** Reasoning Step: 2

----- Final Results -----

bacterial cytoplasm --- Certainty= 0.108(Affirmative) < succ>

The protein has no homology with sequences in the databases.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 41

- 5 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 81> which encodes amino acid sequence <SEQ ID 82; NGS41>. Analysis of this protein sequence reveals the following:

```

    GvH: Examining signal sequence (von Heijne)
          Signal Score (-7.5): -2.47
          Possible cleavage site: 17
10  >>> May be a lipoprotein
      Amino Acid Composition of Predicted Mature Form:
          calculated from 16
      ALOM: Finding transmembrane regions (Klein et al.)
          count: 0 value: 7.37 threshold: 0.0
15  PERIPHERAL Likelihood = 7.37
          modified ALOM score: -1.97
      Rule: inner or outer membrane protein
      Rule: inner or outer membrane protein

20  *** Reasoning Step: 2

      Lipoprotein?
      Inner membrane?

25  ----- Final Results -----

          bacterial outer membrane --- Certainty= 0.790(Affirmative) < succ>

```

The protein has no homology sequences in the databases.

- 30 Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 42

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 83> which encodes amino acid sequence <SEQ ID 84; NGS42>. Analysis of this protein sequence reveals the following:

```

35  GvH: Examining signal sequence (von Heijne)
          Signal Score (-7.5): -5.2
          Possible cleavage site: 14
      >>> Seems to have no N-terminal signal seq.
      Amino Acid Composition of Predicted Mature Form:
          calculated from 1
40  ALOM: Finding transmembrane regions (Klein et al.)
          count: 0 value: 6.58 threshold: 0.0
          PERIPHERAL Likelihood = 6.58
          modified ALOM score: -1.82
45  Rule: cytoplasmic protein

      *** Reasoning Step: 2

      ----- Final Results -----

50  bacterial cytoplasm --- Certainty= 0.514(Affirmative) < succ>

```

The protein has no homology with sequences in the databases.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 43

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 85> which encodes amino acid sequence

5 <SEQ ID 86; NGS43>. Analysis of this protein sequence reveals the following:

GvH: Examining signal sequence (von Heijne)
 Signal Score (-7.5): -4.34
 Possible cleavage site: 39
 >>> Seems to have no N-terminal signal seq.
 10 Amino Acid Composition of Predicted Mature Form:
 calculated from 1
 ALOM: Finding transmembrane regions (Klein et al.)
 count: 2 value: -4.78 threshold: 0.0
 15 INTEGRAL Likelihood = -4.78 Transmembrane 1881 -1897 (1876 -1898)
 INTEGRAL Likelihood = -1.01 Transmembrane 1966 -1982 (1966 -1982)
 PERIPHERAL Likelihood = 1.91
 modified ALOM score: 1.46
 Rule: cytoplasmic membrane protein
 20 *** Reasoning Step: 2
 ----- Final Results -----

25 bacterial inner membrane --- Certainty= 0.291(Affirmative) < succ>

The protein has no homology with sequences in the databases.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 44

30 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 87> which encodes amino acid sequence
 <SEQ ID 88; NGS44>. Analysis of this protein sequence reveals the following:

GvH: Examining signal sequence (von Heijne)
 Signal Score (-7.5): -3.49
 Possible cleavage site: 58
 35 >>> Seems to have no N-terminal signal seq.
 Amino Acid Composition of Predicted Mature Form:
 calculated from 1
 ALOM: Finding transmembrane regions (Klein et al.)
 count: 1 value: -1.33 threshold: 0.0
 40 INTEGRAL Likelihood = -1.33 Transmembrane 141 - 157 (140 - 157)
 PERIPHERAL Likelihood = 2.54
 modified ALOM score: 0.77
 Rule: cytoplasmic membrane protein
 45 *** Reasoning Step: 2
 ----- Final Results -----

50 bacterial inner membrane --- Certainty= 0.153(Affirmative) < succ>

The protein has no homology with sequences in the databases.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 45

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 89> which encodes amino acid sequence <SEQ ID 90; NGS45>. Analysis of this protein sequence reveals the following:

```

5  GvH: Examining signal sequence (von Heijne)
    Signal Score (-7.5): -4.07
    Possible cleavage site: 46
    >>> Seems to have no N-terminal signal seq.
    Amino Acid Composition of Predicted Mature Form:
    calculated from 1
10  ALOM: Finding transmembrane regions (Klein et al.)
    count: 0 value: 2.07 threshold: 0.0
    PERIPHERAL Likelihood = 2.07
    modified ALOM score: -0.91
    Rule: cytoplasmic protein
15  *** Reasoning Step: 2
    ----- Final Results -----
20  bacterial cytoplasm --- Certainty= 0.333(Affirmative) < succ>

```

The protein has homology with the following sequences in the databases:

```

25  >ref|NP_049512.1| putative portal protein [Bacteriophage 933W]
    ref|NP_050550.1| hypothetical protein [Bacteriophage VT2-Sa]
    gb|AAD25457.1|AF125520_52 (AF125520) putative portal protein [Bacteriophage
    933W]
    dbj|BAA84334.1| (AP000363) hypothetical protein [Bacteriophage VT2-Sa]
    dbj|BAA94158.1| (AP000422) portal protein [Escherichia coli O157:H7]
    Length = 714
30  Score = 314 bits (805), Expect = 2e-84
    Identities = 213/658 (32%), Positives = 327/658 (49%), Gaps = 22/658 (3%)
35  Query: 7  ETGVLDPKNGEPLTIG----EYRLFVGEMMNQPAWRAVADKEMDYADGRQLDNELLQKQR 62
    ET + KN T + + ++ +QP WR A+K Y DG QL E+LQ +
    Sbjct: 4  ETNTMATKNDNGATPRFSQRQLQALCSDIDSQPKWRDAANKACAYYDGDQLPPEVLQVLK 63
40  Query: 63 ELGLPPAVENLITPTLLSVQGYEATIRTDWRVTADGETGGRD-VADALNFKLNRAERQSR 121
    + G P + NLI PT+ V G EA RTD V +D + +A+A+N + A R
    Sbjct: 64 DRGQPMTIHNLIAPTVDGVLGMEAKTRTDLVMSDEPDDETEKLAEAINAEFADACRLGN 123
45  Query: 122 ADKACSDAFRGQIACGIGWVEVTRNPNPFEPYBCGVIHRNAIHWDMKSYKYDLSARWL 181
    +KA SDA+ QI G+ WVEV RN +PF ++ + RN + WD S + DLSR RWL
    Sbjct: 124 MNKARSDAYAEQIKAGLSWVEVRRNSDPFGPEFKVSTVSRNEVFWDLWSREADLSDCRWL 183
50  Query: 182 IRRRWLLPERLAQFFPEYAGHFKAMGRGGSDDR-ISGEMLDGGGNTGLADAWGISGRNTV 240
    +RRRW+ + FP G + + DWR + G + L AW
    Sbjct: 184 MRRRWMDTDEAKATFP---GMAQVIDYAIIDWRGFVDTTVTEGQPSPLMSAWEEYQSWDR 240
55  Query: 241 SEEFWFNETTRELAFAEVWYRRVVTADCLRDKKTGRTEVFDGANPNHREMAANGAV-LFA 299
    + W R + + V+YR + + + GR V FD N A+G V +
    Sbjct: 241 QQNEWLQRRRRVLLQVVYYRTFERLPVI-ELSNGRVVAFDKNLMMQAVAVASGRVQVKV 299
60  Query: 300 ASVPRMRAFFVVDLVVRDEPTPYPHQKFFPYVPFFGFREDNTGIPYGYVRNMKYAQDNLN 359
    V R+R A+ VG + D P P FP VPF+G+R+D TG PYG + AQD +N
    Sbjct: 300 GRVSRIREAWFVGPHFIVDRPCSAPOGMFPLVPFWGYRKDKTGEPYGLISRAIPAQDEVN 359
    Query: 360 STNSKLRWGLSAIRTVRTKGIVDMSDEQFRNIARVDADIVLNKIEAAQPGAR--FDVSR 417
    'KL W L A R + + +SD I R D I LN + Q F V +
    Sbjct: 360 FRIKLTWLLQAKRVIMDEDATQLSDNDLMEQIERPDGIIKLNPRKNQKSVADVFRVEQ 419
    Query: 418 DFELSAQHWQMLQDSRATIRQISGITPSFMGNRGNATSGRQESIQVEQSNQSLGLVMDNF 477
    DF++++Q +Q++Q+S I+ G+ +F+G ATSG S VEQ +L + DN+
    Sbjct: 420 DFQVASQQFQVMQSEKLIQDTMGVYSAFLQDQSGATSGVAISNLVEQGAATTLAEINDNY 479

```


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Query: 478 RQSRSLVGEILLAMITEDLGS-DEQTVVIEGDAVTOGRTVVINRPETDPVTGKAYLSNDL 536
 ++ VG LLLA +++DL VVI D + +T+V+N E D L+ND+
 Sbjct: 480 QFACQOVGRLLLAYLLDDLKRRNHAVVINRDDRRQRTIVLN-AEGD----NGELTNDI 534

Query: 537 QNIRLKVALEDVPSTNSYRSQQLGAMSEAVKSLPPEYQAAVLPPMVSLMDIPFKDKVIEK 596
 + +AL V T ++++Q MSE ++ LPP+ QA VL V+L+D+P K + +E+
 Sbjct: 535 SRLNTHIALAFVQQTAPFAKAQLAORMSEVIQGLPPQVQAVVLDLWVNLDDVPQKQEFVER 594

Query: 597 IK-EVRVQETPEQI--EARIAQAVQDALAKSGNDIKRRELALKEQRTASEIKEIEARA 651
 I+ + ++P+++ E + A Q AL + +++ RE+A + + ++ A A
 Sbjct: 595 IRAALGTPKSPDEMTPEEQEVAAQQQALQQQARLQMRMAGRVAKLEADAARAHAAA 652

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be
 useful antigens for vaccines or diagnostics.

Example 46

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 91> which encodes amino acid sequence
 <SEQ ID 92; NGS46>. Analysis of this protein sequence reveals the following:

GvH: Examining signal sequence (von Heijne)
 Signal Score (-7.5): -3.25
 Possible cleavage site: 37
 >>> Seems to have no N-terminal signal seq.
 Amino Acid Composition of Predicted Mature Form:
 calculated from 1

ALOM: Finding transmembrane regions (Klein et al.)
 count: 0 value: 4.77 threshold: 0.0
 PERIPHERAL Likelihood = 4.77
 modified ALOM score: -1.45
 Rule: cytoplasmic protein

*** Reasoning Step: 2

----- Final Results -----

bacterial cytoplasm --- Certainty= 0.281(Affirmative) < succ>

The protein has homology with the following sequences in the databases:

>sp|P44184|YE10_HAEIN HYPOTHETICAL PROTEIN HI1410
 pir||E64028 hypothetical protein HI1410 - Haemophilus influenzae (strain Rd
 KW20)
 gb|AAC23058.1| (U32820) H. influenzae predicted coding region HI1410
 [Haemophilus
 influenzae Rd]
 Length = 394

Score = 150 bits (379), Expect = 3e-35
 Identities = 75/168 (44%), Positives = 114/168 (67%), Gaps = 2/168 (1%)

Query: 57 REIQKSMRDSVHRLKDKVAQLGLGHFYBITDFEIRGANGTLFVFSGLQSHTVDSIKSFE 116
 REIQKS+ DSV ++L D++ L L F+++ +I G NG+ F F+GL+++ + SIKS
 Sbjct: 3 REIQKSISDSVIQMLADQIEMLSLQAFDQVQKTQIIGQNGSRFTFAGLKTN-ITSIKSMT 61

Query: 117 GIDIVWVEEGHGVSKKSWDVLPTIRKEGSEIWIITLNPDMETDETYRRFIAMPSEDTWLC 176
 GID+VWVEEG VSK+SWD+L PTIR++GS+I ++ NP D+TY+RF+ P E
 Sbjct: 62 GIDVWVEEGENVSKESWDILPTIREDGSQIIVSFNPKNILDDTYQRFVIHPERCKSV 121

Query: 177 EINWRDNPWFPEALNRERLKAQRSMNKEDYGNIEWGRPRMVSEGAAYR 224
 +NW+DNP+FP+ L E ++ R + E Y +++EG P S+ A+ +
 Sbjct: 122 LVNWQDNPFYFKEL-MEDMEQMRERDYELYRHVYEGEPVADSDLAIIK 168

>ref|NP_050979.1| P18 [Bacteriophage APSE-1]

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gb|AAF03961.1|AF157835_18 (AF157835) P18 [Bacteriophage APSE-1]
Length = 469

Score = 117 bits (294), Expect = 2e-25
Identities = 72/233 (30%), Positives = 110/233 (46%), Gaps = 13/233 (5%)

Query: 17 LFKPCRYKVMYXXXXXXXXXXXXXXXXXXXXXQRPRLRLCAREIQKSMRDSVHRLKDKVA 76
+FKP R KV + R LC RE S+ DS H +L+ +V
Sbjct: 1 MFKPKRIKVYFGGRGGMKTVSPAKIALITASMHKRRFLCLREFMNSIEDSGHAVLQAEVE 60

Query: 77 QLGLGHFYEITDFEIRGANGTLFVFSGLQSHTVDSIKSFEGIDIVWVEBGHGVSKKSWDV 136
LGL + + I + I G N ++F + L + + SIKS D+ WVEE VS+KS D
Sbjct: 61 TLGLQNRFRILNTYIEGINDSIFKYGQL-ARNIASIKSKHDFDVAWVEEAETVSEKSLDS 119

Query: 137 LPTPTIRKEGSEIWTILNPDMEYTYRRFIA-----MPSEDTWLCEINWRDNPW 185
L PTIRK GSE+W + NP E Y+RF+ +D ++ ++++ DNPW
Sbjct: 120 LIPTIRKPGSELWFSFNPAEEDGAVYKRFVKPYKELIDTQGYIEDDLVVGKVSYLDPNPW 179

Query: 186 FPEALNRERLKAQRSMNKEDYGNIEWGRPRMVSEGAVYRHEIQDAFHSGRVTL 238
P L + K +R N + + +++ G E A + + E +A + L
Sbjct: 180 LPAELKNDQAQMKRE-NYKKWRHVYGGCEDANYEDALIQPEWVEAIDAHIKL 231

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

25 Example 47

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 93> which encodes amino acid sequence <SEQ ID 94; NGS47>. Analysis of this protein sequence reveals the following:

GvH: Examining signal sequence (von Heijne)
Signal Score (-7.5): -4.87
Possible cleavage site: 31
>>> Seems to have no N-terminal signal seq.
Amino Acid Composition of Predicted Mature Form:
calculated from 1
ALOM: Finding transmembrane regions (Klein et al.)
count: 0 value: 4.88 threshold: 0.0
PERIPHERAL Likelihood = 4.88
modified ALOM score: -1.48
Rule: cytoplasmic protein

*** Reasoning Step: 2

----- Final Results -----

bacterial cytoplasm --- Certainty= 0.313(Affirmative) < succ>

The protein has homology with the following sequences in the databases:

>ref|NP_037739.1| Gp54 [Bacteriophage HK97]
gb|AAF31132.1| (AF069529) Gp54 [Bacteriophage HK97]
Length = 273

Score = 47.4 bits (111), Expect = 3e-04
Identities = 33/123 (26%), Positives = 52/123 (41%), Gaps = 20/123 (16%)

Query: 242 NGGLSGKPKNANVPRRRKTHGVPLQEIADLYNEVLGGRLPSVQVLNDTRKRAIANRWCEM 301
NGG G+ K P RRK + + + YN +G RLP +N+ RKR + +
Sbjct: 160 NGGGDGQVK----PERRKAERIDYESFLNAYNTEVGDRLPHAVAVNEKRRRL-KKIIPQ 214

Query: 302 LGTAAPNGKVRFGDKETGLAWFAGFFRKVA---MNPFFWMGENQTGFVAGFDWIFKAGNFVK 359
L T +G F + R PF+ G+N TG+ FD++ + +
Sbjct: 215 LKTPNVDG-----FRAYVRAVFHQAKPFYFGDNDTGWTADFDYLLREDSLTG 261

Query: 360 ILE 362
 + E
 Sbjct: 262 VRE 264

- 5 Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 48

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 95> which encodes amino acid sequence <SEQ ID 96; NGS48>. Analysis of this protein sequence reveals the following:

10 GvH: Examining signal sequence (von Heijne)
 Signal Score (-7.5): -6.85
 Possible cleavage site: 15
 >>> Seems to have no N-terminal signal seq.
 Amino Acid Composition of Predicted Mature Form:
 15 calculated from 1
 ALOM: Finding transmembrane regions (Klein et al.)
 count: 0 value: 7.16 threshold: 0.0
 PERIPHERAL Likelihood = 7.16
 modified ALOM score: -1.93
 20 Rule: cytoplasmic protein
 *** Reasoning Step: 2
 ----- Final Results -----
 25 bacterial cytoplasm --- Certainty= 0.379(Affirmative) < succ>

The protein has homology with the following sequences in the databases:

30 >dbj|BAA36059.1| (D90754) Outer membrane protein P.69 precursor [Escherichia coli]
 Length = 762
 Score = 64.7 bits (156), Expect = 1e-09
 Identities = 79/292 (27%), Positives = 121/292 (41%), Gaps = 55/292 (18%)
 35 Query: 3 NGARWTVTND SMLKELDLSEDAQVEFSDNNK----FVKVSVSKLKG DGGVFKMYGDIV-- 56
 N + W VT++S L L LS V+F+ + F ++V L G+ F M D+V
 Sbjct: 289 NNSVWNVTNSNLDTLALSHST-VDFASHGSTAGTFATLNVENLSGNS-TFIMRADVVGE 346
 40 Query: 57 ----KGESDKLITRK GSEGTTHIEYMDDAKATTGREYLKLVENKGNQEDNKASNKASYK 112
 + D L S G H++ + TTG E L +V+ D AS AS +
 Sbjct: 347 GNGVNNKGDLLNISGSSAGNHVLAIRNQSEATTGNEVLTVVKTT----DGAASFSASSQ 402
 45 Query: 113 LNVRC TEQGGWCFALGESG-----ASKKVNISTDGKRDF-----YLYPD----- 151
 + E GG+ + + ++G AS V T + PD
 Sbjct: 403 V-----ELGGYLYDVRKNGTNWEL YASGTVPEPTPNPEPTPAPAQPPIVNPDPPTPEPAPT 457
 Query: 152 ----TLTPGASSSVLFGEALYQLNAVSDETLVQRMGEIHADGMPQEDNNVWIKRVGKFGSG 208
 T T A + L Y LN V + TL+QRMG++ +D N+W++ GG
 50 Sbjct: 458 PKPTTTADAGGNYL--NVGYLLNYVENRTLMQRMGDLRNQ---SKDGNIWLRSYGGSLS 512
 Query: 209 SRSDYRVGGYGNRYWGFAGGFNRTGFGDKWIHYKGLMLRHLQSSYASEDYVG 260
 S ++ G+ Y G G ++ D Y GL ++ S++AS DY G
 55 Sbjct: 513 FASG-KLSGFDMGYSIGI QFGGDKR-LSDVMPLYVGL---YIGSTHASPDYSG 559

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 49

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 97> which encodes amino acid sequence <SEQ ID 98; NGS49>. Analysis of this protein sequence reveals the following:

```

5      GvH: Examining signal sequence (von Heijne)
          Signal Score (-7.5): -8.37
          Possible cleavage site: 15
          >>> Seems to have no N-terminal signal seq.
          Amino Acid Composition of Predicted Mature Form:
              calculated from 1
10     ALOM: Finding transmembrane regions (Klein et al.)
          count: 0 value: 4.93 threshold: 0.0
          PERIPHERAL Likelihood = 4.93
          modified ALOM score: -1.49
15     Rule: cytoplasmic protein

          *** Reasoning Step: 2

          ----- Final Results -----

20     bacterial cytoplasm --- Certainty= 0.355(Affirmative) < succ>
          bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
          bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
          bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

25     The protein has homology with the following sequences in the databases:

          gi|11282647|pir||H81959 patch repair protein (EC 3.1.-.-) NMA0429 [imported] -
          Neisseria meningitidis (group A strain Z2491)
          gi|7379179|emb|CAB83728.1| (AL162753) patch repair protein [Neisseria
          meningitidis Z2491]
30     Length = 140

          Score = 256 bits (628), Expect = 8e-68
          Identities = 131/140 (93%), Positives = 132/140 (93%)

35     Query: 1 MTDIPTPSKRFSVMSKIHSKETKPEVLVRKFLFSQGFRYRKNDKRYAGKPDIVLPKYKTV 60
          MTDIFT SKRSFVM KIHSKETKPEVLVRKFLF QGFRYRKNDKRY GKPDIVL KYKTV
          Sbjct: 1 MTDIFTTSKRFSVMLKIHSKETKPEVLVRKFLFFQGFRYRKNDKRYVGKPDIVLSKYKTV 60

          Query: 61 VFIHGCFWHGHCNKGHIKPSNMDFWLEKITKNRERDIKNETELEKIGFKVIVVWECELK 120
          VFIHGCFW+GHSCNKGHIKPSN DFWLEKITKN ERDIKNETELEKIGFKVIVVWECELK
40     Sbjct: 61 VFIHGCFWYGHCNKGHIKPSNTDFWLEKITKN CERDIKNETELEKIGFKVIVVWECELK 120

          Query: 121 NKAICRERLNRLVREIKDAV 140
          NKAICRERLNRLV EIKDAV
45     Sbjct: 121 NKAICRERLNRLVREIKDAV 140

```

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 50

50 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 99> which encodes amino acid sequence <SEQ ID 100; NGS50>. Analysis of this protein sequence reveals the following:

```

          GvH: Examining signal sequence (von Heijne)
          Signal Score (-7.5): -6.6
          Possible cleavage site: 50
55     >>> Seems to have no N-terminal signal seq.
          Amino Acid Composition of Predicted Mature Form:
              calculated from 1
          ALOM: Finding transmembrane regions (Klein et al.)

```


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count: 0 value: 7.80 threshold: 0.0
 PERIPHERAL Likelihood = 7.80
 modified ALOM score: -2.06
 Rule: cytoplasmic protein

5

*** Reasoning Step: 2

----- Final Results -----

10

bacterial cytoplasm --- Certainty= 0.398 (Affirmative) < succ>
 bacterial periplasmic space --- Certainty= 0.000 (Not Clear) < succ>
 bacterial outer membrane --- Certainty= 0.000 (Not Clear) < succ>
 bacterial inner membrane --- Certainty= 0.000 (Not Clear) < succ>

15 The protein has homology with the following sequences in the databases:

>gi|11352963|pir|G81959 conserved hypothetical protein NMA0428 [imported] -
 Neisseria meningitidis (group A strain Z2491)
 gi|7379178|emb|CAB83727.1| (AL162753) conserved hypothetical protein [Neisseria
 meningitidis

20

Z2491]
 Length = 548

Score = 371 bits (954), Expect = e-102
 Identities = 189/197 (95%), Positives = 194/197 (97%)

25

Query: 1 VKGESGVDIENWKNKLPEKEREPVEVILNRLEDSELTNKEQAEVISALHSIPEYPYHW 60
 VKGESGVDIE+WKNKLPEKEREPVEVILNRLEDSELTNKEQAEVISALHSIPEYPYHW
 Sbjct: 350 VKGESGVDIEDWKNKLPEKEREPVEVILNRLEDSELTNKEQAEVISALHSIPEYPYHW 409

30

Query: 61 RHLHQDLHTACNDFYNEKKDYLSAAIEAVKVFEDKVQKQTGLHSIDGRELIEKAFGSKKS 120
 RHLHQDLHTACNDFYNEKKDYLSAAIEAVKVFEDKVQKQTGLHSIDGRELIE+AFGSK S
 Sbjct: 410 RHLHQDLHTACNDFYNEKKDYLSAAIEAVKVFEDKVQKQTGLHSIDGRELIEQAFGSKNS 469

35

Query: 121 MLLLTNNKTQAEQNLEDGLEQLACGTWTGFRNPVQHELRLANLSPSIFNDKDALDLISLVS 180
 +LLLTNNKT+AEQNLEDGLEQLACGTWTGFRNPVQHELRLANLSPSIFNDKDALDLISLVS
 Sbjct: 470 ILLLTNNKTQAEQNLEDGLEQLACGTWTGFRNPVQHELRLANLSPSIFNDKDALDLISLVS 529

Query: 181 YLLRKVEQTKKRAKPTS 197
 YLLRKVEQTKKR+K S

40

Sbjct: 530 YLLRKVEQTKKRSKVVS 546

>gi|10955124|ref|NP_059780.1| ymh [Agrobacterium tumefaciens]
 gi|5738274|gb|AAB91582.2| (AF242881) ymh [Agrobacterium tumefaciens]
 Length = 266

45

Score = 58.7 bits (141), Expect = 5e-08
 Identities = 40/127 (31%), Positives = 69/127 (53%), Gaps = 5/127 (3%)

50

Query: 61 RHLHQDLHTACNDFYNEKKDYLSAAIEAVKVFEDKVQKQTGLHSIDGRELIEKAFGSKKS 120
 R +H D+ C + +Y A +EAVK DK++++TGL + DG L+++AF
 Sbjct: 137 RGVHPDVLRFCEEL-LVDNYFHAVLEAVKSVADKIRQRTGL-TDDGAVLVDRAFGSDAP 194

Query: 121 MLLLTNNKTQAEQNLEDGLEQLACGTWTGFRNPVQHELRLANLSPSIFNDKDALDLISLVS 180
 ML + ++++E+ + G L GT++ FRN H R + S +DA DL S+ S
 Sbjct: 195 MLAINELQSESEKGEQGFNSNLVKGTFSMFRNTTAHAPRIHWQMS---KEDAEDLFSMFS 251

55

Query: 181 YLLRKVE 187
 + R+++

Sbjct: 252 LMHRRID 258

60

As a homolog was found in serogroup A *N.meningitidis* but not in serogroup B, NGS50 protein and nucleic acid are useful for distinguishing between gonococcus and serogroup B *N.meningitidis*.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 51

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 101> which encodes amino acid sequence <SEQ ID 102; NGS51>. Analysis of this protein sequence reveals the following:

```

5   GvH: Examining signal sequence (von Heijne)
      Signal Score (-7.5): 0.14
      Possible cleavage site: 42
      >>> Seems to have no N-terminal signal seq.
      Amino Acid Composition of Predicted Mature Form:
          calculated from 1
10  ALOM: Finding transmembrane regions (Klein et al.)
      count: 0 value: 5.67 threshold: 0.0
      PERIPHERAL Likelihood = 5.67
      modified ALOM score: -1.63
15  Rule: cytoplasmic protein

      *** Reasoning Step: 2

      ----- Final Results -----

20      bacterial cytoplasm --- Certainty= 0.145(Affirmative) < succ>
      bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
      bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
      bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

25  The protein has homology with the following sequences in the databases:

      >pir||G81959 conserved hypothetical protein NMA0428 [imported] - Neisseria
          meningitidis (group A strain Z2491)
      emb|CAB83727.1| (AL162753) conserved hypothetical protein [Neisseria
          meningitidis
30      Z2491]
          Length = 548

      Score = 532 bits (1371), Expect = e-150
      Identities = 272/285 (95%), Positives = 280/285 (97%)

35  Query: 1 MSEEKLMSEFPTVIEHLGVKMYSHSTVPAIAELIANAYDACATEVEVRLFDKPEHKIVIK 60
      MSEEKLMSEFPTVIEHLGVKMYSHSTVPAIAELIANAYDACATEVEVRLFDKPEHKIVIK
      Sbjct: 1 MSEEKLMSEFPTVIEHLGVKMYSHSTVPAIAELIANAYDACATEVEVRLFDKPEHKIVIK 60

40  Query: 61 DNGIGMSFDEINDFYLRIGRNRREEKQASPCGRIPTGKKGLGKLALFRLGNKIEISTIQG 120
      DNGIGMSFDEINDFYLRIGRNRREEKQASPCGRIPTGKKGLGKLALF LGNKIEISTIQG
      Sbjct: 61 DNGIGMSFDEINDFYLRIGRNRREEKQASPCGRIPTGKKGLGKLALFGLGNKIEISTIQG 120

45  Query: 121 NERVTFTLDYAEIKKSERIYQPEFQKESVRKPTENGTTITLTELTKKQGYPLDNYVGHLS 180
      NERVTFTLDYAEI++S+ IYQPEF+KESV+ N E+GTTITLTELTKKQGYPLDNYV HLS
      Sbjct: 121 NERVTFTLDYAEIRRSKGIYQPEFRKESVESNIESGTTITLTELTKKQGYPLDNYVEHLS 180

      Query: 181 RLFDFFPAQDFKIKVSLNGSEPRIIDGNLKYNLVTPQFEWEYQDLATNISSLSSKFEQY EY 240
      RLFDFFPAQDFKIKVSLNGSEP+IIDGNLKY+LVTPQFEWEYQDLATNISSLSSKFEQY EY
50  Sbjct: 181 RLFDFFPAQDFKIKVSLNGSEPKIIDGNLKYDLVTPQFEWEYQDLATNISSLSSKFEQY EY 240

      Query: 241 SGLIQGKFITTEKPLKNNMKGITLFANGRMVMNMEFFTDSESSH F 285
      SGLIQGKFITTEKPLKNNMKGITLFANGRMVMNMEFFTDSESSH F
      Sbjct: 241 SGLIQGKFITTEKPLKNNMKGITLFANGRMVMNMEFFTDSESSH F 285

55  >emb|CAC22276.1| (AJ302030) putative heat shock protein [Listeria monocytogenes]
      Length = 181

      Score = 70.2 bits (171), Expect = 2e-11
60  Identities = 57/173 (32%), Positives = 90/173 (51%), Gaps = 10/173 (5%)

      Query: 1 MSEEKLMSEFPTVIEHLGVKMYSHSTVPAIAELIANAYDACATEVEVRLFDKPEHKIVIK 60
      MSE++ + +P ++E LG +Y++ + ELIANAYDA A V V E+K++++
      Sbjct: 1 MSEKEYNLDIDPRILELLGPHLYTNIYYILGELIANAYDADAKNVYVIDRIDEENKLIVE 60

```


Query: 61 DNGIGMSFD--BINDFYLRIGRNRREEKQASPC---GRIPTGKGLGKLALFRLGNKIEI 115
 D+G GMS++ ++ +F L + + R S R G+KG+GKLA + + I
 Sbjct: 61 DDGSGMSYENKDVKNF-LSVAKESRTNAINSYTKLNNRRKMGKRGVGLASLSVSENVNI 119

Query: 116 STIQGNERVTFTLDYABI-KKSERIYQPEFQKESVKPNTENGTTITLTETLTKK 167
 TI+ E+ F L I KK E I + +K +GT I +T T K
 Sbjct: 120 KTIKDGEKSGFVLSRKVINKKLEAINEDTISFIKIK---NHGTAIEMTNPTYK 169

- 10 As a homolog was found in serogroup A *N.meningitidis* but not in serogroup B, NGS51 protein and nucleic acid are useful for distinguishing between gonococcus and serogroup B *N.meningitidis*.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 52

- 15 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 103> which encodes amino acid sequence <SEQ ID 104; NGS52>. Analysis of this protein sequence reveals the following:

GvH: Examining signal sequence (von Heijne)
 Signal Score (-7.5): -3.5
 Possible cleavage site: 49
 >>> Seems to have no N-terminal signal seq.
 Amino Acid Composition of Predicted Mature Form:
 calculated from 1
 ALOM: Finding transmembrane regions (Klein et al.)
 count: 0 value: 7.64 threshold: 0.0
 PERIPHERAL Likelihood = 7.64
 modified ALOM score: -2.03
 Rule: cytoplasmic protein

*** Reasoning Step: 2

----- Final Results -----

bacterial cytoplasm --- Certainty= 0.213(Affirmative) < succ>
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

The protein has homology with the following sequences in the databases:

2.1.1.73) NMA0427 [imported] - Neisseria meningitidis (group A strain Z2491)
 gi|7379177|emb|CAB83726.1| (AL162753) modification methylase (cytosine-specific
 DNA methylase)
 [Neisseria meningitidis Z2491]
 Length = 351

Score = 310 bits (794), Expect = 8e-84
 Identities = 152/154 (98%), Positives = 153/154 (98%)

Query: 1 LGMENGFPKIMAGHQDETDFMHSCAGLSNDINLKRLLALIPKNGGNRLAFAHIPQLQECFI 60
 LGMENGFPKI+AGHQDETDFMHSCAGLSNDINLKRLLALIPKNGGNRLAFAHIPQLQECFI
 Sbjct: 198 LGMENGFPKIIAGHQDETDFMHSCAGLSNDINLKRLLALIPKNGGNRLAFAHIPQLQECFI 257

Query: 61 GKDNSFKDTFGRLWWDKPAPTITTKFFSISNGRFAHPEEDRALSLREGATLQSFPRNYVF 120
 GKDNSFKDTFGRLWWDKPAPTITTKFFSISNGRFAHPEEDRALSLREGATLQSFPRNYVF
 Sbjct: 258 GKDNSFKDTFGRLWWDKPAPTITTKFFSISNGRFAHPEEDRALSLREGATLQSFPRNYVF 317

Query: 121 KAGSRDKIARLIGNAVPPMYTEKIGRAIVDNIEC 154
 KAGSRDKIARLIGNAVPPMY EKIGRAIVDNIEC
 Sbjct: 318 KAGSRDKIARLIGNAVPPMYAEKIGRAIVDNIEC 351

>gi|127441|sp|P25265|MTD2_HERAU MODIFICATION METHYLASE HGIDII (CYTOSINE-SPECIFIC METHYLTRANSFERASE
 HGIDII) (M.HGIDII)
 gi|538661|pir|JT0594 site-specific DNA-methyltransferase (cytosine-specific)
 5 (EC 2.1.1.73) - Herpetosiphon aurantiacus
 gi|48773|emb|CAA38941.1| (X55141) methyltransferase [Herpetosiphon aurantiacus]
 Length = 354

10 Score = 95.6 bits (237), Expect = 3e-19
 Identities = 62/142 (43%), Positives = 82/142 (57%), Gaps = 9/142 (6%)

Query: 12 AGHQDETDPMHSCAGLS DINLKR LALIPKNGGNRLAFAHIP-ELQLECFIGKD-NSFKDT 69
 +G E D MH+ + L DINL+R+ G +A P EL EC + S+
 15 Sbjct: 200 SGGHWEGD SMHAASRL EDINLRR IQHSVP GG-----TWADWPEELIAECHKKESGESYGSV 255

Query: 70 FGRLWWDKPAPTITTTKFFSISNGRFAHPPEEDRALSLREGATLQSFPRNYVFKAGSRDK-- 127
 +GR+ WDK APTITT+ NGRF HPE+DRA+SLRE A LQ+FPR+Y F + K
 Sbjct: 256 YGRMEWDK VAPTITTTQCNGYGNRFGHPEQDRAISLREAALLQTFFRSYQFAPEGQLKFK 315

20 Query: 128 -IARLIGNAVPPMYTEKIGRAI 148
 ++R IGNAV P I ++I
 Sbjct: 316 TVSRQIGNAVPVALGRVIAKSI 337

- 25 As a homolog was found in serogroup A *N.meningitidis* but not in serogroup B, NGS52 protein and nucleic acid are useful for distinguishing between gonococcus and serogroup B *N.meningitidis*.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 53

- 30 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 105> which encodes amino acid sequence <SEQ ID 106; NGS53>. Analysis of this protein sequence reveals the following:

GvH: Examining signal sequence (von Heijne)
 Signal Score (~7.5): -7.56
 Possible cleavage site: 31
 35 >>> Seems to have no N-terminal signal seq.
 Amino Acid Composition of Predicted Mature Form:
 calculated from 1
 ALOM: Finding transmembrane regions (Klein et al.)
 count: 0 value: 5.36 threshold: 0.0
 40 PERIPHERAL Likelihood = 5.36
 modified ALOM score: -1.57
 Rule: cytoplasmic protein

45 *** Reasoning Step: 2

----- Final Results -----

50 bacterial cytoplasm --- Certainty= 0.189(Affirmative) < succ>
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

The protein has homology with the following sequences in the databases:

55 >gi|11256915|pir|F81959 site-specific DNA-methyltransferase (cytosine-specific)
 (EC2.1.1.73) NMA0427 [imported] - Neisseria meningitidis (group A strain Z2491)
 gi|7379177|emb|CAB83726.1| (AL162753) modification methylase (cytosine-specific
 DNA methylase)
 [Neisseria meningitidis Z2491]
 Length = 351

Score = 247 bits (606), Expect = 5e-65
Identities = 124/149 (83%), Positives = 127/149 (85%)

5 Query: 1 LQPETLEKELGLKKNDDDLILIGCSPQYWSVIQTDKRKSEKSKSLLEFQRFVEYFNPG 60
LQPETLEKELGLKKNDDDLILIGCSPQYWSVIQTDKRKSEKSKSLLEFQRFVEYFNPG
Sbjct: 59 LQPETLEKELGLKKNDDDLILIGCSPQYWSVIQTDKRKSEKSKSLLEFQRFVEYFNPG 118

10 Query: 61 YVVVENVPGILSRMKESGLDNFIKLLLEKGFTVHFGIHNNTADYGIPQSRKRFTLIANRIT 120
YVVVENVPGILSRMKES LDNFIKLLLEKGFTVHFGIHNNTADYGIPQSRKRFTLIANRIT
Sbjct: 119 YVVVENVPGILSRMKESRLDNFIKLLLEKGFTVHFGIHNNTADYGIPQSRKRFTLIANRIT 178

Query: 121 KKSQNSIRANGLRYAMFWEWKTAFFPKL 149
K+ L + FPK+
15 Sbjct: 179 KEKLEPVKYSGKRLTVRDVLGMENGFPKI 207

>gi|127441|sp|P25265|MTD2_HERAU MODIFICATION METHYLASE HGIDII (CYTOSINE-SPECIFIC
METHYLTRANSFERASE
20 gi|538661|pir|JT0594 site-specific DNA-methyltransferase (cytosine-specific)
(EC
2.1.1.73) - Herpetosiphon aurantiacus
gi|48773|emb|CAA38941.1| (X55141) methyltransferase [Herpetosiphon aurantiacus]
25 Length = 354

Score = 71.9 bits (169), Expect = 4e-12
Identities = 39/105 (37%), Positives = 57/105 (54%), Gaps = 1/105 (0%)

30 Query: 12 LKKNDDDLILIGCSPQYWSVIQTDKRKSEKSKSLLEFQRFVEYFNPGYVVVENVPGIL 71
L N+ IL+GC+PCQ +S T K ++ LL EF R + P + +ENVP +
Sbjct: 64 LYPNNQHKILVGCAPCQDFSQY-TKKSRTGKTWQLLTFEFSRLIREIEPDIISMENVPEVR 122

Query: 72 SRMKESGLDNFIKLLLEKGFTVHFGIHNNTADYGIPQSRKRFTLIA 116
+ + +NFI+ LE+ G+ V + + DYGIQ R R L A
35 Sbjct: 123 TFNRGVEVFNNFIQSLEQLGYHVSHSVHCPDYGIQQORDRLVLFA 167

As a homolog was found in serogroup A *N.meningitidis* but not in serogroup B, NGS53 protein and nucleic acid are useful for distinguishing between gonococcus and serogroup B *N.meningitidis*.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be
40 useful antigens for vaccines or diagnostics.

Example 54

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 107> which encodes amino acid sequence <SEQ ID 108; NGS54>. Analysis of this protein sequence reveals the following:

45 GvH: Examining signal sequence (von Heijne)
Signal Score (-7.5): -6.82
Possible cleavage site: 50
>>> Seems to have no N-terminal signal seq.
Amino Acid Composition of Predicted Mature Form:
calculated from 1
50 ALOM: Finding transmembrane regions (Klein et al.)
count: 0 value: 6.89 threshold: 0.0
PERIPHERAL Likelihood = 6.89
modified ALOM score: -1.88
Rule: cytoplasmic protein

55 *** Reasoning Step: 2

----- Final Results -----

60 bacterial cytoplasm --- Certainty= 0.253(Affirmative) < succ>

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bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

5 The protein has homology with the following sequences in the databases:

gi|1074456|pir||D64155 hypothetical protein HI0597 - Haemophilus influenzae
 (strain Rd KW20)
 gi|1573586|gb|AAC22254.1| (U32741) conserved hypothetical protein [Haemophilus
 influenzae Rd]
 10 Length = 272

Score = 188 bits (459), Expect = 2e-47
 Identities = 95/100 (95%), Positives = 97/100 (97%)

15 Query: 1 MNLFFRAMVSDLG GTLLTPEHLVGDLTIDTLRLVLEQKGVDIILATGRNHTDMSSILGKIG 60
 MNLFFRAMVSDL GTLLTPEHLVGDLTIDTLR LEQKGVDIILATGRNHTD+SSILGKIG
 Sbjct: 1 MNLFFRAMVSDLDG TLLTPEHLVGDLTIDTLRALEQKGVDIILATGRNHTDVSSILGKIG 60

20 Query: 61 AERAVMITSNGARVRDLQGNLLYSNSLPEELVLELYKTSY 100
 AERAVMITSNGARVRDLQGNLLYSNSLPEELVLELYKT +
 Sbjct: 61 AERAVMITSNGARVRDLQGNLLYSNSLPEELVLELYKTPF 100

A homolog was found in serogroup A *N.meningitidis* but not in serogroup B, so NGS54 protein and nucleic acid are useful for distinguishing between gonococcus and serogroup B *N.meningitidis*.

25 Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 55

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 109> which encodes amino acid sequence <SEQ ID 110; NGS55>. Analysis of this protein sequence reveals the following:

30 GvH: Examining signal sequence (von Heijne)
 Signal Score (-7.5): -4.46
 Possible cleavage site: 37
 >>> Seems to have no N-terminal signal seq.
 Amino Acid Composition of Predicted Mature Form:
 35 calculated from 1
 ALOM: Finding transmembrane regions (Klein et al.)
 count: 0 value: 3.02 threshold: 0.0
 PERIPHERAL Likelihood = 3.02
 modified ALOM score: -1.10
 40 Rule: cytoplasmic protein

*** Reasoning Step: 2

----- Final Results -----

45 bacterial cytoplasm --- Certainty= 0.311(Affirmative) < succ>
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

50

The protein has homology with the following sequences in the databases:

aeruginosa (strain PAO1)
 gi|9948791|gb|AAG06104.1|AE004699_9 (AE004699) probable FMN oxidoreductase
 [Pseudomonas aeruginosa]
 55 Length = 411

Score = 279 bits (686), Expect = 2e-74
 Identities = 157/375 (41%), Positives = 228/375 (59%), Gaps = 10/375 (2%)

Query: 1 MEEQLAQNDQ-PSEKLVRLYGAWAEGGAGVLVTGNVMVAESGKGSINDVLISDDRALEML 59
 MEE +A Q PSE+L+RLY AWA+GGAG+L++GNVMV V++ DD LE
 Sbjct: 24 MEENMADAAQAPSERLMRLYQAWADGGAGLLISGNVMVDSRAMTGGGVVLEDDAQLEKF 83

5 Query: 60 KKWAKARTQNDTLLIMQINHAGKQSPAVVNKTPLAPSAVPLV--GMNGFINPPRELSADE 117
 ++WA+ +QINH G+Q A + + APSAVPL GM+ P+ +
 Sbjct: 84 RRWARIGRSAGAQFWLQINHPGRQMQLNGQQAWAPSAVPLELGGMSRHFATPKAMDEAM 143

10 Query: 118 INGLIQQFVQTAKIAEQAGFSGVQIYAVHGYLISQFLSPHHNRRQDQWGGSGLENRMRFLL 177
 I +IQ+F ++A +AE+AGFSGV+I+A HGYL+SQFLSP NRR D WGGSGLENR R LL
 Sbjct: 144 IAEVIQRFARSAGLAERAGFSGVEIHAAHGYLLSQFLSPLSNRRSDAWGGSGLENRRARLLL 203

15 Query: 178 ETYTAIRAAAGKDFLVGVKLSADFOKGGFDESESVQVVQKLEMGIDFIEVSGGNYESP 237
 E A+RA F V VKLSADFO+GGF ++ +VV+ L +G+D +E+SGG+YE+P
 Sbjct: 204 EIVRAVRAEVAPGFAVAVKLSADFOKGGFSADDAREVVRMLDGLGVDLVELSGGSYEAP 263

20 Query: 238 QMLA-AKDS-TRKREAFFIDYAEKARAASQAPLIITGGFRSQTAMEDALSSGHLDLVGIA 295
 M A+D T REA+F+++A RAA++ P+++TGG R + E L+SG +D+VGI
 Sbjct: 264 AMQGEARDGRTLAREAYFVEFARDIRAAARMPVMVTGGIRRRPVAEQVLASG-VDMVGIG 322

25 Query: 296 RPFALVPDLANKMQNRTYQTVQADRIQTGVAFVDKKAGAMLEMNWYMTQMDLIGQKQSN 355
 A+ P+L + Q I + +K ++ M Q+ + +G+ +N
 Sbjct: 323 TALAIEPNLPRDWRAGKDSAPQLRPI-----TWRNKFLASLANMAAVKFLRLKLSRGRATN 378

Query: 356 PRIVGVESIAENFAG 370
 P++ + ++ AG
 Sbjct: 379 PRVSPLCALLAQAG 393

30 Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 56

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 111> which encodes amino acid sequence <SEQ ID 1:12; NGS56>. Analysis of this protein sequence reveals the following:

35 GvH: Examining signal sequence (von Heijne)
 Signal Score (-7.5): -4.69
 Possible cleavage site: 54
 >>> Seems to have an uncleavable N-term signal seq
 Amino Acid Composition of Predicted Mature Form:
 40 calculated from 1
 ALOM: Finding transmembrane regions (Klein et al.)
 count: 0 value: 4.29 threshold: 0.0
 PERIPHERAL Likelihood = 4.29
 modified ALOM score: -1.36

45 *** Reasoning Step: 2
 ----- Final Results -----

50 bacterial inner membrane --- Certainty= 0.042(Affirmative) < succ>
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
 bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

55 The protein has homology with the following sequences in the databases:

>gi|7444004|pir||D70029 transcription regulator ArsR family homolog yvbA -
 Bacillus subtilis
 gi|2635892|emb|CAB15384.1| (Z99121) similar to transcriptional regulator (ArsR
 60 family)
 [Bacillus subtilis]

Length = 90

Score = 51.3 bits (118), Expect = 3e-06

Identities = 24/65 (36%), Positives = 42/65 (63%), Gaps = 1/65 (1%)

5

Query: 15 IFTVLSDENRHQILHVLWKHGRMNVNELTEHLHLSPAVSHHLKIMLQAGAVAVEQVGKE 74

+F +SD R +IL +L K G M ++ EH ++S+P++SHHL I+ QA ++ + G+

Sbjct: 4 VFKAISDPTRRKILDLL-KGGDMTAGDIAEHFNISKPSISHHLNILKQAEVISDHRKQGF 62

10

Query: 75 RFYSI 79

+YS+

Sbjct: 63 IYYSI 67

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 57

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 113> which encodes amino acid sequence <SEQ ID 114; NGS57>. Analysis of this protein sequence reveals the following:

20 GvH: Examining signal sequence (von Heijne)

Signal Score (-7.5): -2.57

Possible cleavage site: 55

>>> Seems to have no N-terminal signal seq.

Amino Acid Composition of Predicted Mature Form:

calculated from 1

25

ALOM: Finding transmembrane regions (Klein et al.)

count: 0 value: 5.67 threshold: 0.0

PERIPHERAL Likelihood = 5.67

modified ALOM score: -1.63

Rule: cytoplasmic protein

30

*** Reasoning Step: 2

----- Final Results -----

35

bacterial cytoplasm --- Certainty= 0.160(Affirmative) < succ>

bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>

bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>

bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

40 The protein has homology with the following sequences in the databases:

>gi|10444407|gb|AAG17897.1|AF297971_1 (AF297971) restriction endonuclease
R.NgoMIII [Neisseria gonorrhoeae]
Length = 213

45

Score = 319 bits (818), Expect = 1e-86

Identities = 156/156 (100%), Positives = 156/156 (100%)

Query: 1 LYKQYADWNRLSYNAPIYVGKAVPGWRQARNSDNALNQSTELFHRLKEHSRSIAAVSDL 60

LYKQYADWNRLSYNAPIYVGKAVPGWRQARNSDNALNQSTELFHRLKEHSRSIAAVSDL

50

Sbjct: 58 LYKQYADWNRLSYNAPIYVGKAVPGWRQARNSDNALNQSTELFHRLKEHSRSIAAVSDL 117

Query: 61 DPSPDFMCRFVIFEGAGSDMIGTIEAALIKLHKPLWNSCVDGFGNHDPGKGRYEQAQSDWD 120

DPSPDFMCRFVIFEGAGSDMIGTIEAALIKLHKPLWNSCVDGFGNHDPGKGRYEQAQSDWD

Sbjct: 118 DPSPDFMCRFVIFEGAGSDMIGTIEAALIKLHKPLWNSCVDGFGNHDPGKGRYEQAQSDWD 177

55

Query: 121 VLHSGRVWADRLNGIPNSYESILENINTHLEIKRK 156

VLHSGRVWADRLNGIPNSYESILENINTHLEIKRK

Sbjct: 178 VLHSGRVWADRLNGIPNSYESILENINTHLEIKRK 213

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 58

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 115> which encodes amino acid sequence
5 <SEQ ID 116; NGS58>. Analysis of this protein sequence reveals the following:

GvH: Examining signal sequence (von Heijne)
Signal Score (-7.5): -1.92
Possible cleavage site: 16
>>> Seems to have no N-terminal signal seq.
10 Amino Acid Composition of Predicted Mature Form:
calculated from 1
ALOM: Finding transmembrane regions (Klein et al.)
count: 0 value: 5.41 threshold: 0.0
PERIPHERAL Likelihood = 5.41
15 modified ALOM score: -1.58
Rule: cytoplasmic protein
*** Reasoning Step: 2
20 ----- Final Results -----
bacterial cytoplasm --- Certainty= 0.107(Affirmative) < succ>
bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
25 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

The protein has homology with the following sequences in the databases:

>gi|10444408|gb|AAG17898.1|AF297971_2 (AF297971) DNA cytosine methyltransferase
M.NgoMIII [Neisseria gonorrhoeae]
30 Length = 377
Score = 759 bits (1960), Expect = 0.0
Identities = 377/377 (100%), Positives = 377/377 (100%)
35 Query: 1 MKSLEIFSGAGGLAKGLELAGFQHASFIELNKDACNSLRSNFNPKLVIYQGDVADFDLSSQ 60
MKSLEIFSGAGGLAKGLELAGFQHASFIELNKDACNSLRSNFNPKLVIYQGDVADFDLSSQ
Sbjct: 1 MKSLEIFSGAGGLAKGLELAGFQHASFIELNKDACNSLRSNFNPKLVIYQGDVADFDLSSQ 60
40 Query: 61 EGIEVIAGGPPCQPFSLGGKHLAHDERRDMFPHAVRYVEYYRPKAFIFENVKGLLRKSFA 120
EGIEVIAGGPPCQPFSLGGKHLAHDERRDMFPHAVRYVEYYRPKAFIFENVKGLLRKSFA
Sbjct: 61 EGIEVIAGGPPCQPFSLGGKHLAHDERRDMFPHAVRYVEYYRPKAFIFENVKGLLRKSFA 120
45 Query: 121 DYFEYILLRLTYPNLGILQNEWDKGHLTRLKEIEFNLYKGIKYKVSQLLNAADYGVPOK 180
DYFEYILLRLTYPNLGILQNEWDKGHLTRLKEIEFNLYKGIKYKVSQLLNAADYGVPOK
Sbjct: 121 DYFEYILLRLTYPNLGILQNEWDKGHLTRLKEIEFNLYKGIKYKVSQLLNAADYGVPOK 180
50 Query: 181 RERVVIVGIRADLDIDWKFPKRTHSEDRLNWEKYVTGEYWEKHNEPKRFNKDIAEKLQKK 240
RERVVIVGIRADLDIDWKFPKRTHSEDRLNWEKYVTGEYWEKHNEPKRFNKDIAEKLQKK
Sbjct: 181 RERVVIVGIRADLDIDWKFPKRTHSEDRLNWEKYVTGEYWEKHNEPKRFNKDIAEKLQKK 240
55 Query: 241 YGIFEPEKKPWQTVRDTLSDIPHLGNHKITGHEYRDGARIYPGHTGSGIDEPSKTIKAG 300
YGIFEPEKKPWQTVRDTLSDIPHLGNHKITGHEYRDGARIYPGHTGSGIDEPSKTIKAG
Sbjct: 241 YGIFEPEKKPWQTVRDTLSDIPHLGNHKITGHEYRDGARIYPGHTGSGIDEPSKTIKAG 300
60 Query: 301 GHGVPGENMIRYDDGTVRYFTSYEAKLLQTFPEEFVISGAWGEAMRQIGNAVPVKLSEI 360
GHGVPGENMIRYDDGTVRYFTSYEAKLLQTFPEEFVISGAWGEAMRQIGNAVPVKLSEI
Sbjct: 301 GHGVPGENMIRYDDGTVRYFTSYEAKLLQTFPEEFVISGAWGEAMRQIGNAVPVKLSEI 360
Query: 361 LGKHLMGVLSEKSSLHN 377
LGKHLMGVLSEKSSLHN
Sbjct: 361 LGKHLMGVLSEKSSLHN 377

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 59

- 5 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 117> which encodes amino acid sequence <SEQ ID 118; NGS59>. Analysis of this protein sequence reveals the following:

```

    GvH: Examining signal sequence (von Heijne)
          Signal Score (-7.5): -3.82
          Possible cleavage site: 60
10  >>> Seems to have no N-terminal signal seq.
    Amino Acid Composition of Predicted Mature Form:
          calculated from 1
    ALOM: Finding transmembrane regions (Klein et al.)
          count: 0 value: 2.86 threshold: 0.0
15  PERIPHERAL Likelihood = 2.86
          modified ALOM score: -1.07
    Rule: cytoplasmic protein

    *** Reasoning Step: 2

20  ----- Final Results -----

          bacterial cytoplasm --- Certainty= 0.197(Affirmative) < succ>
          bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
25  bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
          bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

```

The protein has homology with the following sequences in the databases:

```

30  >gi|11353338|pir|F81882 hypothetical protein NMA1155 [imported] - Neisseria
    meningitidis
          (group A strain Z2491)
    gi|7379848|emb|CAB84417.1| (AL162755) hypothetical protein NMA1155 [Neisseria
    meningitidis
35  Z2491]
    Length = 120

    Score = 131 bits (329), Expect = 2e-30
    Identities = 64/68 (94%), Positives = 67/68 (98%)

40  Query: 1 LSDISASRAAYMDVQKQYPFETVAVCVLPNHIHAIWTLPPDDADYSLRRLIKTKFSAYS 60
    +S+ISASRAAYMDVQKQYPFETVAVCVLPNHIHAIWTLPPDDADYSLRRLIKTKFSAYS
    Sbjct: 1 MSNISASRAAYMDVQKQYPFETVAVCVLPNHIHAIWTLPPDDADYSLRRLIKTKFSAYS 60

    Query: 61 PHTKNLGA 68
45  P+TKNL A
    Sbjct: 61 PYTKNLSA 68

```

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

50 Example 60

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 119> which encodes amino acid sequence <SEQ ID 120; NGS60>. Analysis of this protein sequence reveals the following:

```

55  GvH: Examining signal sequence (von Heijne)
          Signal Score (-7.5): -3.14
          Possible cleavage site: 16

```


-86-

>>> Seems to have no N-terminal signal seq.
 Amino Acid Composition of Predicted Mature Form:
 calculated from 1
 ALOM: Finding transmembrane regions (Klein et al.)
 count: 0 value: 2.76 threshold: 0.0
 PERIPHERAL Likelihood = 2.76
 modified ALOM score: -1.05
 Rule: cytoplasmic protein

*** Reasoning Step: 2

----- Final Results -----

bacterial cytoplasm --- Certainty= 0.330(Affirmative) < succ>
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

The protein has homology with the following sequences in the databases:

>gi|11281269|pir||D81804 hypothetical protein NMA1789 [imported] - Neisseria
 meningitidis (group A strain Z2491)
 gi|7380430|emb|CAB85016.1| (AL162757) hypothetical protein [Neisseria
 meningitidis Z2491]
 Length = 243

Score = 154 bits (389), Expect = 5e-37
 Identities = 82/85 (96%), Positives = 82/85 (96%)

Query: 12 MNTKTELQKLLLEEDISTLKETLIRVDALPPRYVRSIATPIVRRWLIDKQLNILAKEIGLT 71
 MNTKTELQKLLLEEDISTL ETLI DALPPRYVRSIATPIVRRWLIDKQLNILAKEIGLT
 Sbjct: 1 MNTKTELQKLLLEEDISTLTETLICADALPPRYVRSIATPIVRRWLIDKQLNILAKEIGLT 60

Query: 72 IELPILDTSLVFEKLSLTLENKVNIFY 96
 IELPILDTSLVFEKLSLTLENKVNIFY

Sbjct: 61 IELPILDTSLVFEKLSLTLENKVNIFY 85

As a homolog was found in serogroup A *N.meningitidis* but not in serogroup B, NGS60 protein and nucleic acid are useful for distinguishing between gonococcus and serogroup B *N.meningitidis*.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 61

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 121> which encodes amino acid sequence <SEQ ID 122; NGS61>. Analysis of this protein sequence reveals the following:

GvH: Examining signal sequence (von Heijne)
 Signal Score (-7.5): -6.88
 Possible cleavage site: 32

>>> Seems to have no N-terminal signal seq.
 Amino Acid Composition of Predicted Mature Form:
 calculated from 1

ALOM: Finding transmembrane regions (Klein et al.)
 count: 0 value: 5.52 threshold: 0.0
 PERIPHERAL Likelihood = 5.52
 modified ALOM score: -1.60
 Rule: cytoplasmic protein

*** Reasoning Step: 2

----- Final Results -----

-87-

bacterial cytoplasm --- Certainty= 0.300(Affirmative) < succ>
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

5

The protein has homology with the following sequences in the databases:

>gi|11281269|pir||D81804 hypothetical protein NMA1789 [imported] - Neisseria
 meningitidis (group A strain Z2491)
 gi|7380430|emb|CAB85016.1| (AL162757) hypothetical protein [Neisseria
 meningitidis Z2491]
 Length = 243

10

Score = 193 bits (491), Expect = 5e-49
 Identities = 96/101 (95%), Positives = 97/101 (95%)

15

Query: 1 MAGGVYLGGKIISPIYHSSQEFSGEPIIYAETNIILCPAEKFLTTLKRVFHNGNIFNMNQI 60
 MAGGVYLGG+ IS IYHSSQEFSGEPIIYAE NIILCPAEKFLTTLKRVFHNGNIFNMNQI
 Sbjct: 86 MAGGVYLGGEFISSIYHSSQEFSGEPIIYAEPNIILCPAEKFLTTLKRVFHNGNIFNMNQI 145

20

Query: 61 ITFLSNKQGGVRFDKNYDKYKTWQVAIEKAANFLKLGPNYN 101
 ITFLSNKQGGV FDKNYDKYKTWQVAIEKAANFLKLGPNYN
 Sbjct: 146 ITFLSNKQGGVHFDKNYDKYKTWQVAIEKAANFLKLGPNYN 186)

25

As a homolog (amino acids 1-96) was found in serogroup A *N.meningitidis* but not in serogroup B,
 NGS61 protein and nucleic acid are useful for distinguishing between gonococcus and serogroup B
N.meningitidis.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be
 useful antigens for vaccines or diagnostics.

Example 62

30 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 123> which encodes amino acid sequence
 <SEQ ID 124; NGS62>. Analysis of this protein sequence reveals the following:

GvH: Examining signal sequence (von Heijne)
 Signal Score (-7.5): -2.43
 Possible cleavage site: 44
 35 >>> Seems to have no N-terminal signal seq.
 Amino Acid Composition of Predicted Mature Form:
 calculated from 1
 ALOM: Finding transmembrane regions (Klein et al.)
 count: 0 value: 4.72 threshold: 0.0
 40 PERIPHERAL Likelihood = 4.72
 modified ALOM score: -1.44
 Rule: cytoplasmic protein

45 *** Reasoning Step: 2

----- Final Results -----

50

bacterial cytoplasm --- Certainty= 0.324(Affirmative) < succ>
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

A homolog was found in serogroup A *N.meningitidis* but not in serogroup B, so NGS62 protein and
 nucleic acid are useful for distinguishing between gonococcus and serogroup B *N.meningitidis*.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 63

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 125> which encodes amino acid sequence <SEQ ID 126; NGS63>. Analysis of this protein sequence reveals the following:

```

5  GvH: Examining signal sequence (von Heijne)
      Signal Score (-7.5): 0.74
      Possible cleavage site: 24
10 >>> Seems to have a cleavable N-term signal seq.
      Amino Acid Composition of Predicted Mature Form:
      calculated from 25
      ALOM: Finding transmembrane regions (Klein et al.)
      count: 0 value: 10.72 threshold: 0.0
      PERIPHERAL Likelihood = 10.72
15 modified ALOM score: -2.64
      Score for OM-PP discrimination: -22.14
      Rule: outer membrane or periplasmic protein
      Score for OM-PP discrimination: -22.14
      Rule: outer membrane or periplasmic protein
20
      *** Reasoning Step: 2

      Periplasmic space? Score: 2.21378
      Periplasmic space? Score: 2.21378
25
      ----- Final Results -----

      bacterial periplasmic space --- Certainty= 0.931(Affirmative) < succ>
      bacterial outer membrane --- Certainty= 0.237(Affirmative) < succ>
30      bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>
      bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

```

The protein has homology with the following sequences in the databases:

```

35 >gi|11284146|pir||B81142 hypothetical protein NMB0912 [imported] - Neisseria
      meningitidis
      (group B strain MD58)
      gi|7226150|gb|AAF41320.1| (AE002443) hypothetical protein [Neisseria
      meningitidis MC58]
      Length = 208
40
      Score = 51.7 bits (119), Expect = 3e-06
      Identities = 30/72 (41%), Positives = 40/72 (54%)

      Query: 5 LLKNWKPLLILSAIAFFAVSWQLDRAAQYRRGYGAAVSEVSERLKAAAVEHAEHARKSSA 64
      LLK WKP+ +L I +W DRA +YR G AA +E+S RLK +E A+ AR +
45 Sbjct: 43 LLKYWKFPVGVLLILVLIPTAWHFDRAEKYRMGREAAAAEISNRLKDGYLEQAKQARSABQ 102

      Query: 65 AYQAQKAAREEK 76
      A A R+ K
50 Sbjct: 103 KAAAFERQTK 114

```

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 64

55 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 127> which encodes amino acid sequence <SEQ ID 128; NGS64>. Analysis of this protein sequence reveals the following:

-89-

5 McG: Examining signal sequence (McGeoch)
 Length of UR: 0
 Peak Value of UR: 2.99
 Net Charge of CR: 4
 Discriminant Score: 5.35
 10 GvH: Examining signal sequence (von Heijne)
 Signal Score (-7.5): -2.53
 Possible cleavage site: 33
 >>> Seems to have an uncleavable N-term signal seq
 15 Amino Acid Composition of Predicted Mature Form:
 calculated from 1
 ALOM: Finding transmembrane regions (Klein et al.)
 count: 0 value: 3.23 threshold: 0.0
 PERIPHERAL Likelihood = 3.23
 modified ALOM score: -1.15
 *** Reasoning Step: 2
 ----- Final Results -----
 20 bacterial inner membrane --- Certainty= 0.054(Affirmative) < succ>
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
 bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>
 25

The protein has no homology with sequences in the databases.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 65

30 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 129> which encodes amino acid sequence <SEQ ID 130; NGS65>. Analysis of this protein sequence reveals the following:

35 GvH: Examining signal sequence (von Heijne)
 Signal Score (-7.5): -5.61
 Possible cleavage site: 61
 >>> Seems to have no N-terminal signal seq.
 Amino Acid Composition of Predicted Mature Form:
 calculated from 1
 ALOM: Finding transmembrane regions (Klein et al.)
 count: 0 value: 3.34 threshold: 0.0
 40 PERIPHERAL Likelihood = 3.34
 modified ALOM score: -1.17
 Rule: cytoplasmic protein
 *** Reasoning Step: 2
 45 ----- Final Results -----
 bacterial cytoplasm --- Certainty= 0.236(Affirmative) < succ>
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
 50 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

The protein has homology with the following sequences in the databases:

55 >gi|1175791|sp|P44189|YE18_HABIN HYPOTHETICAL PROTEIN HI1418
 gi|1074769|pir|A64029 hypothetical protein HI1418 - Haemophilus influenzae
 (strain Rd
 KW20)
 gi|1574254|gb|AAC23068.1| (U32821) H. influenzae predicted coding region HI1418
 60 [Haemophilus
 influenzae Rd]

Length = 201

Score = 104 bits (251), Expect = 1e-21

Identities = 58/119 (48%), Positives = 72/119 (59%), Gaps = 4/119 (3%)

Query: 51 LKMONTISVFSFKSQNVRTQI-LGAEPWFCLGDVAEILQIQNAR---QLPLKDQGIQKSS 106
+K Q S F+FK VR + E WFC DV IL N+R Q K G+ K
Sbjct: 14 MKNQIQFSTFNFKDLPVRVILDPKGEFWFCGTDVCHILGYTNSRKALQDHCKQGQGVTKRY 73

Query: 107 VATKKGNQELLFINEPNLYRVIFRSRKAEAVKFQDWIFEVVPQIRKTTGGYQITPKTTA 165
TK +QE+ FINEPNLYR+I +SRK EA F+ W+FEV+PQIRKTG YQ+ P+ A
Sbjct: 74 TPTKSADQEMTFINEPNLYRLIIKSRKPEABPFEAWVFEEVLPQIRKTGKYQLQPQOLA 132

>gi|11281012|pir||A81144 hypothetical protein NMB0900. [imported] - *Neisseria meningitidis*

(group B strain MD58)

gi|7226137|gb|AAF41308.1| (AE002442) hypothetical protein [*Neisseria meningitidis* MC58]

Length = 305

Score = 104 bits (249), Expect = 2e-21

Identities = 73/137 (53%), Positives = 93/137 (67%), Gaps = 2/137 (1%)

Query: 190 YSMIHQRFNVEAVEGIPADKLEAVAYVHALTLHTG-LAGEVPDREPLPAPQPALPISGN 248
+S + +F E +PA++ PE ++ + + G L GEV DREPLPAPQPALPISGN
Sbjct: 164 WSAVKSFKGCSYKE-VPAEQFPEVLSVMGRVAVENGVLVYGEVLDREPLPAPQPALPISGN 222

Query: 249 ALADIAAMVYYGTRMIELGKDVSAPLKQLGCKQAVTMWTVWHETRSILKRSVAALEVLRG 308
AL D+A V YG I++G+DVS PLKQLGCKQAVTMWTVW ETRS LK + ALE L
Sbjct: 223 ALYDLAVAVRYGAWAIQMGDRVSLPLKQLGCKQAVTMWTVWAETRSRLKAAANALEALNA 282

Query: 309 YADKDASGRIACLEGI 325

+AD + + +I L I

Sbjct: 283 HADAEHAAKIRPMLPEI 299

>gi|7460273|pir||T13267 hypothetical protein - *Lactococcus lactis* phage BK5-T

gi|928839|gb|AAA98590.1| (L44593) ORF266; putative [*Lactococcus* phage BK5-T]

Length = 266

Score = 75.9 bits (179), Expect = 6e-13

Identities = 42/111 (37%), Positives = 63/111 (55%), Gaps = 3/111 (2%)

Query: 55 NTISVFSFKSQNVRTQILGAEPWFCLGDVAEILQIQNAR---QLPLKDQGIQKSSVATKK 111
N + F+F + VRT ++ EPWF DVA + +N R + +KD+ ++S + T

Sbjct: 2 NELQNFNFNNLPVRTVLINDEPWFVGKDVAIAIGYKNFRDALKSHVKDKYKRESRITTPS 61

Query: 112 GNQELLFINEPNLYRVIFRSRKAEAVKFQDWIFEVVPQIRKTTGGYQITPK 162

G Q + I+EP LY++ S+ A FQDW++EEV+P IRK G Y K

Sbjct: 62 GVQSVTVISEPGLYQLAGESKLPSAEPFQDWVYEEVLPITIRKHGAYMTDAK 112

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 66

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 131> which encodes amino acid sequence <SEQ ID 132; NGS66>. Analysis of this protein sequence reveals the following:

GvH: Examining signal sequence (von Heijne)

Signal Score (-7.5): -3.12

Possible cleavage site: 53

>>> Seems to have no N-terminal signal seq.

Amino Acid Composition of Predicted Mature Form:

calculated from 1

ALOM: Finding transmembrane regions (Klein et al.)

count: 0 value: 8.96 threshold: 0.0
 PERIPHERAL Likelihood = 8.96
 modified ALOM score: -2.29
 Rule: cytoplasmic protein

5

*** Reasoning Step: 2

----- Final Results -----

10

bacterial cytoplasm --- Certainty= 0.402(Affirmative) < succ>
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

15

The protein has no homology with sequences in the databases.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 67

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 133> which encodes amino acid sequence
 20 <SEQ ID 134; NGS67>. Analysis of this protein sequence reveals the following:

GvH: Examining signal sequence (von Heijne)
 Signal Score (-7.5): 5.71
 Possible cleavage site: 22
 >>> Seems to have a cleavable N-term signal seq.
 25 Amino Acid Composition of Predicted Mature Form:
 calculated from 23
 ALOM: Finding transmembrane regions (Klein et al.)
 count: 0 value: 2.81 threshold: 0.0
 PERIPHERAL Likelihood = 2.81
 30 modified ALOM score: -1.06
 Score for OM-PP discrimination: -32.34
 Rule: outer membrane or periplasmic protein
 Score for OM-PP discrimination: -32.34
 Rule: outer membrane or periplasmic protein

35

*** Reasoning Step: 2

Periplasmic space? Score: 3.23391
 Periplasmic space? Score: 3.23391

40

----- Final Results -----

bacterial periplasmic space --- Certainty= 0.928(Affirmative) < succ>
 bacterial outer membrane --- Certainty= 0.199(Affirmative) < succ>
 45 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>
 bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

The protein has homology with the following sequences in the databases:

50 >gi|7475078|pir|H69834 hypothetical protein yhjQ - Bacillus subtilis
 gi|2226189|emb|CAA74479.1| (Y14081) hypothetical protein [Bacillus subtilis]
 gi|2633396|emb|CAB12900.1| (Z99109) yhjQ [Bacillus subtilis]
 Length = 108

Score = 32.9 bits (74), Expect = 2.1
 55 Identities = 27/98 (27%), Positives = 44/98 (44%), Gaps = 4/98 (4%)

Query: 54 CLDAGQVCLTHCLSLLTQGDTSMSDCAVAVRQMLALCGAVHDLAAQNSPLTRDAARKVCLE 113
 C+ A C T CL Q +S C R+ +C +SP ++ +C +
 60 Sbjct: 15 CMKACNHCFTKCLEESVQ--HHLSCIRLDRECADICALAVKAMQTDSPFMKEICALCAD 72

-92-

Query: 114 ACKQCAKACKEHSAHAECKACYESCLDCIKECEKLAA 151
 C+ C C +H H C+AC ++C C ++C +AA
 Sbjct: 73 ICEACGTECGKHD--HDHCQACAKACFTCAEQCRSMAA 108

5 >gi|7479923|pir|T36241 hypothetical protein SCE39.31c - Streptomyces coelicolor
 gi|4582392|emb|CAB40339.1| (AL049573) hypothetical protein [Streptomyces
 coelicolor A3(2)]
 Length = 136

10 Score = 30.9 bits (69), Expect = 7.7
 Identities = 27/102 (26%), Positives = 43/102 (41%), Gaps = 6/102 (5%)

Query: 54 CLDAGQVCLTECLSLLTQGDTSMSDCAVAVRQMLALCGAVHDLAAQ-----NSPLTRDAAK 109
 C A C CLS T D ++ C +C A + ++ ++ +TR +

15 Sbjct: 34 CAQACTACADACLSEPTVAD--LTKCIRTDMDCADVCTATAAVLSRHTGYDANVTRAVLQ 91

Query: 110 VCLEACKQCAKACKEHSAHAECKACYESCLDCIKECEKLAA 151
 C C C C H+ H C+ C E+C C + C++L A

20 Sbjct: 92 ACATVCAACGDECARHAGMHEHCRVCAEACRSCEQACQBELLA 133

The protein was expressed in *E.coli* as a soluble 14.19kDa His-fusion product and then purified.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 68

25 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 135> which encodes amino acid sequence <SEQ ID 136; NGS68>. Analysis of this protein sequence reveals the following:

GvH: Examining signal sequence (von Heijne)
 Signal Score (-7.5): -4.05
 Possible cleavage site: 38

30 >>> Seems to have no N-terminal signal seq.
 Amino Acid Composition of Predicted Mature Form:
 calculated from 1

ALOM: Finding transmembrane regions (Klein et al.)
 count: 0 value: 5.25 threshold: 0.0

35 PERIPHERAL Likelihood = 5.25
 modified ALOM score: -1.55
 Rule: cytoplasmic protein

*** Reasoning Step: 2

40 ----- Final Results -----

bacterial cytoplasm --- Certainty= 0.220(Affirmative) < succ>
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
 45 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

The protein has homology with the following sequences in the databases:

50 >gi|11353493|pir|A81795 hypothetical protein NMA2214 [imported] - Neisseria
 meningitidis
 (group A strain Z2491)
 gi|7380833|emb|CAB85425.1| (AL162758) hypothetical protein [Neisseria
 meningitidis Z2491]
 Length = 208

55 Score = 263 bits (673), Expect = 3e-69
 Identities = 140/145 (96%), Positives = 143/145 (98%)

60 Query: 1 LDWRGNKPLGAAELADLKPLYKDFMYWERGLHMYKASAVVPTGYVRVGNTAPLCGEDTQR 60
 LDW+GNKPLGAAELADLKPLYKDFMYWERGLHMYKASAVVPTGYVRVGNTAPL GEDTQR

Sbjct: 44 LDWQGNKPLGAAELADLRPLYKDFMYWERGLHMYKASAVVPTGYVRVGNTAPLVGEDTQR 103
 Query: 61 YASFWGDGYDVYRQLRWRQIPEKQKAFKKAASKNTVMFAGREYGISKQNLSDVWDDFE 120
 YASFWGDGYDVYRQLRW+QIPEKQKAFKKAASK TVMFAGREYGISKQNLSDVWDDFE
 5 Sbjct: 104 YASFWGDGYDVYRQLRWQIPEKQKAFKKAASKNTVMFAGREYGISKQNLSDVWDDFE 163
 Query: 121 DAMELKAFPCLSLFLTKWHKNLYE 145
 DAMELKAFPCLSLFLTKWHKNLY+
 10 Sbjct: 164 DAMELKAFPCLSLFLTKWHKNLYD 188
 >gi|11280955|pir||B81219 hypothetical protein NMB0273 [imported] - Neisseria
 meningitidis
 (group B strain MD58)
 15 gi|7225497|gb|AAF40727.1| (AE002383) hypothetical protein [Neisseria
 meningitidis MC58]
 Length = 141
 Score = 216 bits (550), Expect = 5e-55
 Identities = 117/121 (96%), Positives = 119/121 (97%)
 20 Query: 25 MYWERGLHMYKASAVVPTGYVRVGNTAPLCGEDTQRYASFWGDGYDVYRQLRWRQIPEKQ 84
 MYWERGLHMYKASAVVPTGYVRVGNTAPL GEDTQRYASFWGDGYDVYRQLRW+QIPEKQ
 Sbjct: 1 MYWERGLHMYKASAVVPTGYVRVGNTAPLVGEDTQRYASFWGDGYDVYRQLRWQIPEKQ 60
 25 Query: 85 RKAFKKAASKNTVMFAGREYGISKQNLSDVWDDFEDAMELKAFPCLSLFLTKWHKNLY 144
 RKAFKKAASK TVMFAGREYGISKQNLSDVWDDFEDAMELKAFPCLSLFLTKWHKNLY
 Sbjct: 61 RKAFKKAASKNTVMFAGREYGISKQNLSDVWDDFEDAMELKAFPCLSLFLTKWHKNLY 120
 Query: 145 E 145
 30 +
 Sbjct: 121 D 121

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

35 Example 69

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 137> which encodes amino acid sequence <SEQ ID 138; NGS69>. Analysis of this protein sequence reveals the following:

GvH: Examining signal sequence (von Heijne)
 Signal Score (-7.5): -5.63
 40 Possible cleavage site: 43
 >>> Seems to have no N-terminal signal seq.
 Amino Acid Composition of Predicted Mature Form:
 calculated from 1
 45 ALOM: Finding transmembrane regions (Klein et al.)
 count: 0 value: 6.84 threshold: 0.0
 PERIPHERAL Likelihood = 6.84
 modified ALOM score: -1.87
 Rule: cytoplasmic protein
 50 *** Reasoning Step: 2
 ----- Final Results -----
 55 bacterial cytoplasm --- Certainty= 0.361(Affirmative) < succ>
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

The protein has homology with the following sequences in the databases:

60 >gi|7464552|pir||C64707 hypothetical protein HP1499 - Helicobacter pylori (strain
 26695)

-94-

gi|2314683|gb|AAD08545.1| (AE000648) *H. pylori* predicted coding region HP1499
Helicobacter pylori 26695]
 Length = 272

5 Score = 38.2 bits (88), Expect = 0.13
 Identities = 34/123 (27%), Positives = 58/123 (46%), Gaps = 10/123 (8%)

Query: 3 EFKFIFGQDFGLSKKEAIRKVLKWLPSHLKFTLMVAQGIQG-----FHPKAVFWKNDKN 56
 EF+ I G DF + ++IR +L ++ K + FHPK + N K

10 Sbjct: 54 EFETIVGLDFKMTDSKSIRFLDLNKTYYKLRFYCYGDKENNKTDIVFHPKIYMFNGK- 112

Query: 57 EYYALIGSSNLTHAAFNSNYEAN-ILTRISEQDFIKVKSWADEI--AMKSIPVSEDWLEE 113
 E ++IGS+NLT +N+E N I T+ + + + + I A +E++L+

15 Sbjct: 113 EKTSIIGSTNLTKGLENNFEVNTIFTEKKPLYTQLNATYNSIKYADSLFTPNEEYLQN 172

Query: 114 YQE 116
 Y E

Sbjct: 173 YNE 175

- 20 A homolog was found in serogroup A *N.meningitidis* but not in serogroup B, so NGS69 protein and nucleic acid are useful for distinguishing between gonococcus and serogroup B *N.meningitidis*.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 70

- 25 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 139> which encodes amino acid sequence <SEQ ID 140; NGS70>. Analysis of this protein sequence reveals the following:

GvH: Examining signal sequence (von Heijne)
 Signal Score (-7.5): -1.18
 Possible cleavage site: 22

30 >>> Seems to have a cleavable N-term signal seq.
 Amino Acid Composition of Predicted Mature Form:
 calculated from 23

ALOM: Finding transmembrane regions (Klein et al.)
 count: 0 value: 4.19 threshold: 0.0

35 PERIPHERAL Likelihood = 4.19
 modified ALOM score: -1.34
 Score for OM-PP discrimination: -5.89
 Rule: outer membrane or periplasmic protein
 Score for OM-PP discrimination: -5.89

40 Rule: outer membrane or periplasmic protein

*** Reasoning Step: 2

Periplasmic space? Score: 0.588927

45 Periplasmic space? Score: 0.588927

----- Final Results -----

50 bacterial periplasmic space --- Certainty= 0.849(Affirmative) < succ>
 bacterial outer membrane --- Certainty= 0.106(Affirmative) < succ>
 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>
 bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

The protein has homology with the following sequences in the databases:

- 55 >gi|11353344|pir||A81886 hypothetical protein NMA1183 [imported] - *Neisseria meningitidis*
 (group A strain Z2491)
 gi|7379875|emb|CAB84445.1| (AL162755) hypothetical protein NMA1183 [*Neisseria meningitidis*]

Z24911
Length = 74

Score = 58.7 bits (141), Expect = 2e-08
Identities = 30/43 (69%), Positives = 32/43 (73%)
Query: 62 IGGFGGVGGFGLKPAIVYRNFRITATNRPAATRARPRQTTVA 104
+G G+ G GGLKP LVY N IATNRPAATRA PR TTVA
Sbjct: 32 MGNIDGIDGSGGLKPTLVYWNHCIIATNRPAATRAHPRHTTVA 74

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 71

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 141> which encodes amino acid sequence
15 <SEQ ID 142; NGS71>. Analysis of this protein sequence reveals the following:

GvH: Examining signal sequence (von Heijne)
Signal Score (-7.5): -1.98
Possible cleavage site: 28
>>> Seems to have a cleavable N-term signal seq.
20 Amino Acid Composition of Predicted Mature Form:
calculated from 29
ALOM: Finding transmembrane regions (Klein et al.)
count: 0 value: 5.04 threshold: 0.0
PERIPHERAL Likelihood = 5.04
25 modified ALOM score: -1.51
Score for OM-PP discrimination: -9.17
Rule: outer membrane or periplasmic protein
Score for OM-PP discrimination: -9.17
Rule: outer membrane or periplasmic protein
30 *** Reasoning Step: 2
Periplasmic space? Score: 0.916744
Periplasmic space? Score: 0.916744
35 ----- Final Results -----
bacterial periplasmic space --- Certainty= 0.923(Affirmative) < succ>
bacterial outer membrane --- Certainty= 0.146(Affirmative) < succ>
40 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>
bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

The protein has no homology with sequences in the databases.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be
45 useful antigens for vaccines or diagnostics.

Example 72

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 143> which encodes amino acid sequence
<SEQ ID 144; NGS72>. Analysis of this protein sequence reveals the following:

GvH: Examining signal sequence (von Heijne)
Signal Score (-7.5): -3.18
Possible cleavage site: 42
>>> Seems to have an uncleavable N-term signal seq
Amino Acid Composition of Predicted Mature Form:
calculated from 1
55 ALOM: Finding transmembrane regions (Klein et al.)

-96-

count: 4 value: -8.76 threshold: 0.0
 INTEGRAL Likelihood = -8.76 Transmembrane 11 - 27 (8 - 37)
 INTEGRAL Likelihood = -6.90 Transmembrane 80 - 96 (75 - 102)
 INTEGRAL Likelihood = -2.39 Transmembrane 98 - 114 (98 - 114)
 5 INTEGRAL Likelihood = -1.12 Transmembrane 47 - 63 (47 - 64)
 PERIPHERAL Likelihood = 3.55
 modified ALOM score: 2.25
 Rule: cytoplasmic membrane protein

10 *** Reasoning Step: 2

----- Final Results -----

15 bacterial inner membrane --- Certainty= 0.450(Affirmative) < succ>
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
 bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

The protein has homology with the following sequences in the databases:

20 >gi|11354095|pir||H81995 probable transmembrane transport protein NMA0047
 [imported] - Neisseria meningitidis (group A strain Z2491)
 gi|7378822|emb|CAB83364.1| (AL162752) putative transmembrane transport protein
 [Neisseria meningitidis Z2491]
 Length = 405

25 Score = 257 bits (658), Expect = 5e-68
 Identities = 152/162 (93%), Positives = 154/162 (94%)

30 Query: 1 MTHTASKTPKLWAVIAAAAFILLITIGMRMTLGLFVQPVVNTTELNIAQFSLIITVFQLM 60
 MTHTASKTPK W I AAAFILLITIGMRMTLGLFVQPVVNTTEL+IAQFSLII VFQLM
 Sbjct: 1 MTHTASKTPKFWLTITAAAFILLITIGMRMTLGLFVQPVVNTTELSIAQFSLIIAVFQLM 60

Query: 61 WGVLPQLSGALADRFGAFRVLSGGALLVACLIASNIPTYWGLMIAVGLLLAFGTGSGG 120
 WGV QPLSGALADRFGAFRVLSGGA+LLVACLIA NIPTYWGLMIAVGLLLAFGTGSGG
 35 Sbjct: 61 WGVSQPLSGALADRFGAFRVLSGGAVLLVACLIAPNIPTYWGLMIAVGLLLAFGTGSGG 120

Query: 121 FSIIMGQVAAQVPTHKRGLASGLVNAGGSAGQFLFAPLVQGL 162
 FSIIMGQVAAQVP HKRGLASGLVNAGGSAGQFLFAPLVQGL
 Sbjct: 121 FSIIMGQVAAQVPAHKRGLASGLVNAGGSAGQFLFAPLVQGL 162

40 >gi|11351469|pir||F83484 probable MFS transporter PA1286 [imported] - Pseudomonas
 aeruginosa
 (strain PAO1)
 gi|9947221|gb|AAG04675.1|AE004558_4 (AE004558) probable MFS transporter
 45 [Pseudomonas aeruginosa]
 Length = 399

Score = 72.5 bits (177), Expect = 3e-12
 Identities = 53/149 (35%), Positives = 81/149 (53%)

50 Query: 14 VIAAAAFILLITIGMRMTLGLFVQPVVNTTELNIAQFSLIITVFQLMWGVLPQLSGALAD 73
 ++ + A IL +++G+R GLF+ P+ F+ I + L+WG+ QP +GALAD
 Sbjct: 8 ILLSGALILALSGLVRHGFGLFLAPMSADFGWGREVFFAFAIALQNLVWGLAQPF+TGALAD 67

55 Query: 74 RFGAFRVLSGGALLVACLIASNIPTYWGLMIAVGLLLAFGTGSGGFSIIMGQVAAQVP 133
 R+GA R + G LL ++ + GL ++ GLL+ G FS+I+G V VP
 Sbjct: 68 RYGAARAVLVGGLLYALGLVLMGLSQSASGLSLSAGLLIGLGLSCTSF+SVILGAVGRAVP 127

60 Query: 134 THKRGLASGLVNAGGSAGQFLFAPLVQGL 162
 +R +A G+ +A GS GQF P GL
 Sbjct: 128 AEQRSMAMGISSAAGSFGQFAMLP+GTLGL 156

As a homolog was found in serogroup A *N.meningitidis* but not in serogroup B, NGS72 protein and nucleic acid are useful for distinguishing between gonococcus and serogroup B *N.meningitidis*.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 73

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 145> which encodes amino acid sequence
5 <SEQ ID 146; NGS73>. Analysis of this protein sequence reveals the following:

GvH: Examining signal sequence (von Heijne)
Signal Score (-7.5): -4.26
Possible cleavage site: 52
>>> Seems to have no N-terminal signal seq.
10 Amino Acid Composition of Predicted Mature Form:
calculated from 1
ALOM: Finding transmembrane regions (Klein et al.)
count: 3 value: -3.72 threshold: 0.0
15 INTEGRAL Likelihood = -3.72 Transmembrane 172 - 188 (171 - 190)
INTEGRAL Likelihood = -2.97 Transmembrane 119 - 135 (114 - 137)
INTEGRAL Likelihood = -1.86 Transmembrane 209 - 225 (205 - 225)
PERIPHERAL Likelihood = 4.88
modified ALOM score: 1.24
20 Rule: cytoplasmic membrane protein
*** Reasoning Step: 2
----- Final Results -----
25 bacterial inner membrane --- Certainty= 0.249(Affirmative) < succ>
bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

30 The protein has homology with the following sequences in the databases:

>gi|11354095|pir||H81995 probable transmembrane transport protein NMA0047
[imported] - Neisseria meningitidis (group A strain Z2491)
gi|7378822|emb|CAB83364.1| (AL162752) putative transmembrane transport protein
35 [Neisseria meningitidis Z2491]
Length = 405
Score = 222 bits (567), Expect = 3e-57
Identities = 116/123 (94%), Positives = 117/123 (94%), Gaps = 4/123 (3%)
40 Query: 103 QGLVVLPEVGWGTGTFYVWGAIALLILPVSWWLAGGNNNGNNAHTQHTQATHGQSLGEAV 162
QGLVVLPEVGWGTGTFYVWGAIALL LPVSWWLA GGNNAHTQH QATHGQSLGEAV
Sbjct: 160 QGLVVLPEVGWGTGTFYVWGAIALLTLFVSWWLA----GGNNAHTQHAQATHGQSLGEAV 215
45 Query: 163 KTAFKTPSYILLHLSFFACGFHIAFLVTHLPTEVALCGLPATVASTSIAIIGLANIAGCV 222
KTAFKTPSYILLHLSFFACGFHIAFLVTHLPTEVALCGLPATVASTSIAIIGLANIAGC+
Sbjct: 216 KTAFKTPSYILLHLSFFACGFHIAFLVTHLPTEVALCGLPATVASTSIAIIGLANIAGCI 275
Query: 223 FSG 225
FSG
50 Sbjct: 276 FSG 278
>gi|11351469|pir||F83484 probable MFS transporter PA1286 [imported] - Pseudomonas
aeruginosa
(strain PAO1)
55 gi|9947221|gb|AAG04675.1|AE004558_4 (AE004558) probable MFS transporter
[Pseudomonas aeruginosa]
Length = 399
Score = 54.4 bits (130), Expect = 1e-06
60 Identities = 37/115 (32%), Positives = 56/115 (48%), Gaps = 10/115 (8%)

Query: 111 VGWTGTFYVWGAIALLILPVSWWLAGGNNGGNNAHTQHTQATHGQSLGEAVKTAFTKTPS 170
 +GW+ G + LI+P++ + H QSLGEA++ A
 Sbjet: 160 LGWSSALLALGLLVALIVPLAGLM-----KDRPLPPQGHEQSLGEALREACAHSG 209

5 Query: 171 YILLHLSFFACGFHIAFLVTHLPTEVALCGLPATVASTSIAIIGLANIAGCVFSG 225
 + LL L FF CGF + F+ HLP + LPA V +T +A++GL N+ G +G
 Sbjet: 210 FWLLALGFFVCGFQVVFIVGHLPAYLVDQHLPAQVGTTVLALVGLFNVFPTYIAG 264

As a homolog was found in serogroup A *N.meningitidis* but not in serogroup B, so NGS73 protein and
 10 nucleic acid are useful for distinguishing between gonococcus and serogroup B *N.meningitidis*.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be
 useful antigens for vaccines or diagnostics.

Example 74

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 147> which encodes amino acid sequence
 15 <SEQ ID 148; NGS74>. Analysis of this protein sequence reveals the following:

GvH: Examining signal sequence (von Heijne)
 Signal Score (-7.5): 0.41
 Possible cleavage site: 30
 >>> Seems to have no N-terminal signal seq.
 20 Amino Acid Composition of Predicted Mature Form:
 calculated from 1
 ALOM: Finding transmembrane regions (Klein et al.)
 count: 2 value: -1.49 threshold: 0.0
 INTEGRAL Likelihood = -1.49 Transmembrane 15 - 31 (15 - 31)
 25 INTEGRAL Likelihood = -1.28 Transmembrane 83 - 99 (83 - 99)
 PERIPHERAL Likelihood = 1.59
 modified ALOM score: 0.80
 Rule: cytoplasmic membrane protein

30 *** Reasoning Step: 2

----- Final Results -----

35 bacterial inner membrane --- Certainty= 0.160(Affirmative) < succ>
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
 bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

The protein has homology with the following sequences in the databases:

40 >pir||H81995 probable transmembrane transport protein NMA0047 [imported] -
 Neisseria meningitidis (group A strain Z2491)
 emb|CAB83364.1| (AL162752) putative transmembrane transport protein [Neisseria
 meningitidis Z2491]
 Length = 405

45 Score = 148 bits (374), Expect = 2e-35
 Identities = 97/106 (91%), Positives = 103/106 (96%)

50 Query: 1 MVLIYIFSPKTDNLNFIYFAAALGFTWLATVAPTAAVTGKLFGTRYLATLFLGLVMLTHQIG 60
 M+LIYIFSPKTDNLNFIYFAAALGFTWLATV PTA++TGKLFGTRYLATLFLGL ML+HQIG
 Sbjet: 300 MILIYIFSPKTDNLNFIYFAAALGFTWLATVPTASITGKLFGTRYLATLFLGLTMLSHQIG 359

Query: 61 GFLGSYIGGIVITQFGDYGWMWYADAVLAGTAALLVLPVREPRTAA 106
 GFLGSYIGGIVITQFGDYGWMWYADA+LAGTAALL LP+REPRTAA
 55 Sbjet: 360 GFLGSYIGGIVITQFGDYGWMWYADALLAGTAALLNLPVREPRTAA 405

>pir||F83484 probable MFS transporter PA1286 [imported] - Pseudomonas aeruginosa
 (strain PA01)

-99-

gb|AAG04675.1|AE004558_4 (AE004558) probable MFS transporter [Pseudomonas aeruginosa]

Length = 399

5 Score = 59.0 bits (142), Expect = 2e-08
Identities = 40/101 (39%), Positives = 61/101 (59%)

Query: 1 MVLIIYIFSPKTDLNFYIFAAALGFTWLATVAPTAAVTGKLFQTRYLATLFGVLVMLTHQIG 60
++++++ P + + Y F A+G WL+TV T LFG R L+ L G+V L HQ+G
10 Sbjct: 286 VIVLFLWLPLSVYSAYAFGVAMGLLWLSTVPLTNGTVATLFGVRNLSMLGGIVFLFHQLG 345

Query: 61 GFLGSYIGGIVITQFGDYGWMWYADAVLAGTAALLVLPVRE 101
FLG ++GG+V + G Y +W +L+ AALL FVRE
15 Sbjct: 346 AFLGGWLGGVVYDRTGSYDLVWQLSILLSLLAALLNWPVRE 386

As a homolog was found in serogroup A *N.meningitidis* but not in serogroup B, NGS74 protein and nucleic acid are useful for distinguishing between gonococcus and serogroup B *N.meningitidis*.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

20 Example 75

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 149> which encodes amino acid sequence <SEQ ID 150; NGS75>. Analysis of this protein sequence reveals the following:

GvH: Examining signal sequence (von Heijne)
Signal Score (-7.5): -5.2
25 Possible cleavage site: 22
>>> Seems to have no N-terminal signal seq.
Amino Acid Composition of Predicted Mature Form:
calculated from 1
ALOM: Finding transmembrane regions (Klein et al.)
30 count: 0 value: 4.45 threshold: 0.0
PERIPHERAL Likelihood = 4.45
modified ALOM score: -1.39
Rule: cytoplasmic protein

35 *** Reasoning Step: 2

----- Final Results -----

40 bacterial cytoplasm --- Certainty= 0.237(Affirmative) < succ>
bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

The protein has homology with the following sequences in the databases:

45 pir||S04419 type II site-specific deoxyribonuclease (EC 3.1.21.4) NgoPII -
Neisseria gonorrhoeae
emb|CAA36887.1| (X52661) NgoPII restriction and modification [N.gonorrhoeae]
prf||1613419A NgoPII endonuclease [Neisseria gonorrhoeae]
50 Length = 278

Score = 240 bits (614), Expect = 4e-63
Identities = 128/129 (99%), Positives = 128/129 (99%)

55 Query: 1 MNIIDAIINLANNPVVGVNSHSQSNNRANQAGDALEEFVKDLFSGSFNLTQRIARHAK 60
MNIIDAIINLANNPVVGV SHSQSNNRANQAGDALEEFVKDLFSGSFNLTQRIARHAK
Sbjct: 1 MNIIDAIINLANNPVVGVESHQSNNRANQAGDALEEFVKDLFSGSFNLTQRIARHAK 60

Query: 61 VFSYLGNNNSNPPDAMLNRNGDAIEVKKIESKDSALALNSSHPKSKLSVDDSMITKACKDAE 120
VFSYLGNNNSNPPDAMLNRNGDAIEVKKIESKDSALALNSSHPKSKLSVDDSMITKACKDAE

-100-

Sbjct: 61 VFSYLGNNNSPPDAMLRNGDAIEVKKIESKDSALALNSSHPKSKLSVDDSM LTKACKDAE 120

Query: 121 KWEEKDIY 129

KWEEKDIY

5 Sbjct: 121 KWEEKDIY 129

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 76

10 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 151> which encodes amino acid sequence <SEQ ID 152; NGS76>. Analysis of this protein sequence reveals the following:

GvH: Examining signal sequence (von Heijne)

Signal Score (-7.5): -1.73

Possible cleavage site: 13

15 >>> Seems to have no N-terminal signal seq.

Amino Acid Composition of Predicted Mature Form:
calculated from 1

ALOM: Finding transmembrane regions (Klein et al.)

count: 0 value: 9.39 threshold: 0.0

20 PERIPHERAL Likelihood = 9.39

modified ALOM score: -2.38

Rule: cytoplasmic protein

*** Reasoning Step: 2

25 ----- Final Results -----

bacterial cytoplasm --- Certainty= 0.272(Affirmative) < succ>
bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
30 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

The protein has homology with the following sequences in the databases:

35 pir||S04419 type II site-specific deoxyribonuclease (EC 3.1.21.4) NgoPII -
Neisseria gonorrhoeae
emb|CAA36887.1| (X52661) NgoPII restriction and modification [N.gonorrhoeae]
prf||1613419A NgoPII endonuclease [Neisseria gonorrhoeae]
Length = 278

40 Score = 268 bits (687), Expect = 2e-71
Identities = 136/136 (100%), Positives = 136/136 (100%)

45 Query: 1 LAMVYGIDYCADAE CYLKIKNQIKEGIGNIGGIQFAETKELGRVNRIDPLNITYLRVRGM 60
LAMVYGIDYCADAE CYLKIKNQIKEGIGNIGGIQFAETKELGRVNRIDPLNITYLRVRGM
Sbjct: 143 LAMVYGIDYCADAE CYLKIKNQIKEGIGNIGGIQFAETKELGRVNRIDPLNITYLRVRGM 202

Query: 61 WGIENPWFVFNYYIQRNMEKSFNFMAIINEDKWN SFNNTDKLLAIQDSKLAI SDIKIKNP 120
WGIENPWFVFNYYIQRNMEKSFNFMAIINEDKWN SFNNTDKLLAIQDSKLAI SDIKIKNP
50 Sbjct: 203 WGIENPWFVFNYYIQRNMEKSFNFMAIINEDKWN SFNNTDKLLAIQDSKLAI SDIKIKNP 262

Query: 121 NNPARLRNAKLITYHL 136
NNPARLRNAKLITYHL

Sbjct: 263 NNPARLRNAKLITYHL 278

55 Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 77

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 153> which encodes amino acid sequence <SEQ ID 154; NGS77>. Analysis of this protein sequence reveals the following:

```

5   GvH: Examining signal sequence (von Heijne)
      Signal Score (-7.5): -4.51
      Possible cleavage site: 58
      >>> Seems to have no N-terminal signal seq.
      Amino Acid Composition of Predicted Mature Form:
          calculated from 1
10  ALOM: Finding transmembrane regions (Klein et al.)
      count: 0 value: 3.18 threshold: 0.0
      PERIPHERAL Likelihood = 3.18
      modified ALOM score: -1.14
15  Rule: cytoplasmic protein

      *** Reasoning Step: 2

      ----- Final Results -----

20      bacterial cytoplasm --- Certainty= 0.127(Affirmative) < succ>
      bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
      bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
      bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

25  The protein has homology with the following sequences in the databases:

      >pir||CTNHP2 site-specific DNA-methyltransferase (cytosine-specific) (EC
          2.1.1.73) NgoPII - Neisseria gonorrhoeae
      emb|CAA30038.1| (X06965) NgoPII methylase (AA 1-341) [Neisseria gonorrhoeae]
      emb|CAA36888.1| (X52661) NgoPII restriction and modification [Neisseria
30  gonorrhoeae]
      gb|AAA17019.1| (L14564) cytosine methylase [Neisseria gonorrhoeae]
      prf||1613419B NgoPII methylase [Neisseria gonorrhoeae]
          Length = 341

35  Score = 682 bits (1761), Expect = 0.0
      Identities = 341/341 (100%), Positives = 341/341 (100%)

      Query: 1  MQNSSPTTYNPMKIIISLFSGCGGLDLGFEKAGFEIPAANEYDKTIWATFKANHPKTHLIE 60
      Sbjct: 1  MQNSSPTTYNPMKIIISLFSGCGGLDLGFEKAGFEIPAANEYDKTIWATFKANHPKTHLIE 60

      Query: 61  GDIRKIKEEDFPEEIDGIIGPPCQSWSEAGALRGIDDARGQLFFDYIRILKSKQPKFFL 120
      Sbjct: 61  GDIRKIKEEDFPEEIDGIIGPPCQSWSEAGALRGIDDARGQLFFDYIRILKSKQPKFFL 120

45  Query: 121  AENVSGMLANRHNGAVQNLLKMFDCGCGYDVTLTMANAKDYGVAQERKRVFYIGFRKDLEI 180
      Sbjct: 121  AENVSGMLANRHNGAVQNLLKMFDCGCGYDVTLTMANAKDYGVAQERKRVFYIGFRKDLEI 180

      Query: 181  KFSFPKGSTVEDKDKITLKDVIWDLQDTAVPSAPQNKTNPDVANNNEYFTGSPSIFMSR 240
      Sbjct: 181  KFSFPKGSTVEDKDKITLKDVIWDLQDTAVPSAPQNKTNPDVANNNEYFTGSPSIFMSR 240

50  Query: 241  NRVKAWDEQGFVQASGRQCQLHPQAPKMEKHGANDYRFAAGKETLYRRMTVREVARIQG 300
      Sbjct: 241  NRVKAWDEQGFVQASGRQCQLHPQAPKMEKHGANDYRFAAGKETLYRRMTVREVARIQG 300

55  Query: 301  FPDNFKFIYQNVNDAYKMIGNAVPVNLAYEIAAAIKKTLE 341
      Sbjct: 301  FPDNFKFIYQNVNDAYKMIGNAVPVNLAYEIAAAIKKTLE 341

60  Query: 301  FPDNFKFIYQNVNDAYKMIGNAVPVNLAYEIAAAIKKTLE 341
      Sbjct: 301  FPDNFKFIYQNVNDAYKMIGNAVPVNLAYEIAAAIKKTLE 341

```


Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 78

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 155> which encodes amino acid sequence
5 <SEQ ID 156; NGS78>. Analysis of this protein sequence reveals the following:

```

GvH: Examining signal sequence (von Heijne)
      Signal Score (-7.5): -8.33
      Possible cleavage site: 24
>>> Seems to have no N-terminal signal seq.
10 Amino Acid Composition of Predicted Mature Form:
      calculated from 1
      ALOM: Finding transmembrane regions (Klein et al.)
            count: 0 value: 2.17 threshold: 0.0
            PERIPHERAL Likelihood = 2.17
15 modified ALOM score: -0.93
      Rule: cytoplasmic protein

*** Reasoning Step: 2

20 ----- Final Results -----

            bacterial cytoplasm --- Certainty= 0.220(Affirmative) < succ>
            bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
            bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
25            bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

```

The protein has homology with the following sequences in the databases:

```

>pir||H82000 hypothetical protein NMA0089 [imported] - Neisseria meningitidis
      (group A strain Z2491)
30 emb|CAB83405.1| (AL162752) hypothetical protein NMA0089 [Neisseria meningitidis
      Z2491]
      Length = 226

      Score = 422 bits (1085), Expect = e-117
35 Identities = 217/228 (95%), Positives = 220/228 (96%), Gaps = 2/228 (0%)

Query: 1 MERYKNAVRKDKAAELYLLNLSLSRELFHVVSIFEIVLRNKIDICFRQEFKDRNRLYDSI 60
      MERYKNAV KDKAAELYLLNLSLSRELFHVVSIFEIVLRNKIDIC +Q FKD N LY+SI
Sbjct: 1 MERYKNAVGVKDKAAELYLLNLSLSRELFHVVSIFEIVLRNKIDICLQQAQFGDNWLYNSI 60

40 Query: 61 QPQTNPALKYQGCFLRNGTKESAEILKVALSKIQNNSSGGKFDHNQLVAGLGFGFWRYLFA 120
      QPQTNPALKYQGCFLRNGTKESAEILKVALSKIQNNSSGGKFDHNQLVAGLGFGFWRYLFA
Sbjct: 61 QPQTNPALKYQGCFLRNGTKESAEILKVALSKIQNNSSGGKFDHNQLVAGLGFGFWRYLFA 120

45 Query: 121 GSKDAQFDAAGKVLMMKVPKPKSTPSVQYNQKWIFRELSNINNFRNRLAHHEPICFSFK 180
      GSKDAQFDA GKVLMMKVPKPKSTPSVQ+QKWIFRELSNINNFRNRLAHHEPIC FK
Sbjct: 121 GSKDAQFDATGKVLMMKVPKPKSTPSVQHNNQKWIFRELSNINNFRNRLAHHEPIC--FK 178

50 Query: 181 GAIKDTGYARNIHQSIFELLNYMDVDTASVFSHFSDQVIACDEIDKL 228
      GAIKDTGYARNIHQSIFELLNYMDVDTASVFSHFSDQVIACDEIDKL
Sbjct: 179 GAIKDTGYARNIHQSIFELLNYMDVDTASVFSHFSDQVIACDEIDKL 226

>ref|NP_053274.1| Hypothetical gene [Agrobacterium tumefaciens]
dbj|BAA87659.1| (AB016260) Hypothetical gene [Agrobacterium tumefaciens]
55 Length = 380

      Score = 43.6 bits (102), Expect = 0.002
      Identities = 53/215 (24%), Positives = 86/215 (39%), Gaps = 42/215 (19%)

60 Query: 5 KNAVRKDKAAELYLLNLSLSRELFHVVSIFEIVLRNKIDICFRQEFKDRNRLYDSIQPQT 64
      K ++ A LYL N +++ + +++ E+ LRN +D F

```


Sbjct: 55 KGGNHEEYAMALYLYNARVAKAFLYPLNVAEVTLRNAVDGILVARFG----- 101

Query: 65 NPALKYQGCFLRNGTKESAEIKVALSKIQNNSGGKFDHNQLVAGLGFGFWRYLFAGGKD 124
 A +Q R+ T L L K +G +Q+VA L F FW LF

5 Sbjct: 102 --ANWHQDATFRDQTLTGNGL--ATLDKAIQRAGAGAARDQIVATLTFDFWSNLFR---- 153

Query: 125 AQFDAAGKVLKVPKPKSTPSVQYNQKWIFRELSN----INNFRNRLAHHEPICFSFK 180
 ++ + + + + P +Q+ + +B+ N IN FRNR+AHHEP+

10 Sbjct: 154 PEYGGWLWRTTVNI-----AFPHLQHGESR--QEIQNLVKPINVFRNRVAHHEFVL---- 201

Query: 181 GAIKDTGYARNIHQSIFELLNMYMDVDTASVFSHPS 215
 D +IH I L+ +TA+ H S

Sbjct: 202 ----DLNVT-DIHAKIVRLIELRCAETATWMKHHS 231

- 15 As a homolog was found in serogroup A *N.meningitidis* but not in serogroup B, so NGS78 protein and nucleic acid are useful for distinguishing between gonococcus and serogroup B *N.meningitidis*.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 79

- 20 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 157> which encodes amino acid sequence <SEQ ID 158; NGS79>. Analysis of this protein sequence reveals the following:

GvH: Examining signal sequence (von Heijne)
 Signal Score (-7.5): 2.07
 Possible cleavage site: 17

25 >>> Seems to have a cleavable N-term signal seq.
 Amino Acid Composition of Predicted Mature Form:
 calculated from 18

ALOM: Finding transmembrane regions (Klein et al.)
 count: 0 value: 9.49 threshold: 0.0

30 PERIPHERAL Likelihood = 9.49
 modified ALOM score: -2.40

Score for OM-PP discrimination: -11.72
 Rule: outer membrane or periplasmic protein

35 Score for OM-PP discrimination: -11.72
 Rule: outer membrane or periplasmic protein

*** Reasoning Step: 2

Periplasmic space? Score: 1.17242

40 Periplasmic space? Score: 1.17242

----- Final Results -----

45 bacterial periplasmic space --- Certainty= 0.932(Affirmative) < succ>
 bacterial outer membrane --- Certainty= 0.240(Affirmative) < succ>
 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>
 bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

- A homolog (amino acids 23-85) was found in serogroup A *N.meningitidis* but not in serogroup B, so
- 50 NGS79 protein and nucleic acid are useful for distinguishing between gonococcus and serogroup B *N.meningitidis*.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 80

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 159> which encodes amino acid sequence <SEQ ID 160; NGS80>. Analysis of this protein sequence reveals the following:

```

5   GvH: Examining signal sequence (von Heijne)
      Signal Score (-7.5): -8.49
      Possible cleavage site: 57
      >>> Seems to have no N-terminal signal seq.
      Amino Acid Composition of Predicted Mature Form:
      calculated from 1
10  ALOM: Finding transmembrane regions (Klein et al.)
      count: 0 value: 4.98 threshold: 0.0
      PERIPHERAL Likelihood = 4.98
      modified ALOM score: -1.50
      Rule: cytoplasmic protein
15  *** Reasoning Step: 2

      ----- Final Results -----

20      bacterial cytoplasm --- Certainty= 0.428(Affirmative) < succ>
      bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
      bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
      bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

25  The protein has homology with the following sequences in the databases:

      >pir||E81080 conserved hypothetical protein NMB1466 [imported] - Neisseria
      meningitidis (group B strain MD58)
      gb|AAF41823.1| (AE002496) conserved hypothetical protein [Neisseria meningitidis
      MC58]
30      Length = 243

      Score = 148 bits (375), Expect = 7e-35
      Identities = 82/189 (43%), Positives = 109/189 (57%)

35  Query: 120 VDRMFNMAGNHFARLGISGSGVHYWNARDFSEQAFHAEVGYRYRNSRLEWGFPRPFVKQNR 179
      + R N +HF GISG GVHYW+ +DFSEQ+ GY+ R+ +G PFV+QN
      Sbjct: 1 MSREINAGRHHFLYGGISGGGVHYWDNKFSEQSLRLSFGYKNRSVTRSFQIVPFVEQN 60

40  Query: 180 LGNNRYTANTGIVLDYSRRLNEKWRSTQSFQYGRKQYHDEYLAKRYNSKTISVSGTFSYY 239
      LG +RY G D+S+RL+E+WR T + K Y ++ A RY+S T Y
      Sbjct: 61 LGGSRYNFVGGFNADFQSLSERWRLTLNAGNMWKHYQEDRTAARYDSHMLAGATLMYS 120

      Query: 240 AMSAWQLYGGISGMFNDTVEKEQASRRYGVSLGTVKILDGGLGLKLGAGYTKRIFKAPAT 299
      A W LYGG + T E EQAS R G+ +G VK DGGLGL+ YT+R+F AP T
45  Sbjct: 121 APKDWLLYGGADWSHNITKEAQASIRKGLRVGAVKTFDGGLGLRANLRYTRRMFDAPGT 180

      Query: 300 LIYNFTRRD 308
      ++Y F R+D
      Sbjct: 181 IVYRFFRKD 189

50  >gb|AAD11779.1| (AF118122) putative outer membrane protein OmpU [Neisseria
      meningitidis]
      Length = 488

55  Score = 72.1 bits (176), Expect = 7e-12
      Identities = 71/300 (23%), Positives = 128/300 (42%), Gaps = 17/300 (5%)

      Query: 3 EAADLYRELLSERPDLVYPRFDLGVMLFEDKQYREALVQLHRAE-EVLPPDMRQLAREYI 61
      EA YREL++ +PD R L LF+++Q A Q R + E LPP + + Y
60  Sbjct: 136 EAISHYRELIAAQPDAPAVRMRLAAALFDNRQNEAAADQFDRLLKAENLPPQLMEQVELYR 195

      Query: 62 RQAEAVQAWHPSFNMNYEQTDNVNNAASLSDIVINGRKWIKSEDSLPKRA--IRYELG 119
      + AW + + + N+N A + KW + PK+ +G + Y LG
      Sbjct: 196 KALRERDAWKVNGGFSVTREHNNINQAPKRQY----GKW-----TFPKQVDGTAVNYRLG 246

```


Query: 120 VDRMPNMGHNFARLGISGSGVHYWNARDFSEQAFHAEVGYRYRNSRLEWGFPRPFVKQNR 179
 ++ +++ + G SG Y + F++ G + + R + G F ++
 5 Sbjct: 247 AEKKWSLKNWYTTAGGDVSGRVYPGNKKFNDMTAGVSGGIGFADRRKDAGLAVFHERRT 306

Query: 180 LGNNRYTANTGIVLDYSRRLNEKWRSTQSFQYGRKQYHDEYLAKRYNSKTISVSGTFSYY 239
 GN+ Y+ G L ++R KW++ S ++GR + R ++ + +S + +Y
 10 Sbjct: 307 YGNDAYSYTNGARLYFNRWQTPKWQTLSSAEWGRLK---NTRRARSNDNTHLQISNSLVFY 363

Query: 240 AMSAWQLYGGISGMFD-NTVEKEQASRRYGVSLGTVKILDG-GLGLKLGAGYTKRIFKAP 297
 + GG+ + N ++ RYG+ + G GL L G KR ++ P
 10 Sbjct: 364 RNARQYWMGGLDFYRERNPADRGDNFNRYGLRFAGWQEWGSGSLSSLLRLGAARHYEKP 423

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be
 15 useful antigens for vaccines or diagnostics.

Example 81

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 161> which encodes amino acid sequence
 <SEQ ID 162; NGS81>. Analysis of this protein sequence reveals the following:

20 GvH: Examining signal sequence (von Heijne)
 Signal Score (-7.5): -6.25
 Possible cleavage site: 15
 >>> Seems to have no N-terminal signal seq.
 Amino Acid Composition of Predicted Mature Form:
 calculated from 1
 25 ALOM: Finding transmembrane regions (Klein et al.)
 count: 0 value: 7.05 threshold: 0.0
 PERIPHERAL Likelihood = 7.05
 modified ALOM score: -1.91
 Rule: cytoplasmic protein
 30 *** Reasoning Step: 2
 ----- Final Results -----
 35 bacterial cytoplasm --- Certainty= 0.232(Affirmative) < succ>

The protein has homology with the following sequences in the databases:

gi|10803654|ref|NP_046052.1| putative ISH4 transposase [Halobacterium sp. NRC-1]
 40 gi|7484109|pir||T08324 probable transposase H1306 - Halobacterium sp. (strain
 NRC-1)
 insertion sequence ISH4 plasmid pNRC100
 gi|2822385|gb|AAC82891.1| (AF016485) putative ISH4 transposase [Halobacterium
 sp. NRC-1]
 45 gi|10580476|gb|AAG19350.1| (AE005029) Vng0918h [Halobacterium sp. NRC-1]
 Length = 294
 Score = 52.1 bits (124), Expect = 4e-06
 Identities = 36/139 (25%), Positives = 63/139 (44%), Gaps = 7/139 (5%)
 50 Query: 31 CPHCQSTHFVKNGKDCGNQRFLCRDCKKSFEVQTGTILYNTQKDIEVWEKYIHCMIK-KY 89
 CP C++ ++ G QR+LC+DC ++F +QTGT+ ++ + W ++ I
 Sbjct: 28 CPSCRAESVIRYGSYRVFQRYLCKDCDRTFNDQTGTVFEHSAVALRKWFLAVYTYIRLNT 87

Query: 90 PLRKCAEICKINLATAFTWRHKILDALQNMMEVELDGIVQADETYSTISYKGHHKKNFNL 149
 55 +R+ ++ T + + L AL L+G V+ DE Y KG ++
 Sbjct: 88 SIRQLDAEIDVSYKTVYRRVQRFLRALD--APRPHLEGPVEIDEFYVKAGLKGRRD--- 142

Query: 150 PRPAHKRGTRATKRGISKE 168
 +P+ RG RG E
 60 Sbjct: 143 -QPSRSRGLSTRGRGTAE 160

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 82

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 163> which encodes amino acid sequence <SEQ ID 164; NGS82>. Analysis of this protein sequence reveals the following:

```

5  GvH: Examining signal sequence (von Heijne)
    Signal Score (-7.5): -4.66
    Possible cleavage site: 57
    >>> Seems to have no N-terminal signal seq.
10 Amino Acid Composition of Predicted Mature Form:
    calculated from 1
    ALOM: Finding transmembrane regions (Klein et al.)
        count: 1 value: -0.85 threshold: 0.0
        INTEGRAL Likelihood = -0.85 Transmembrane 76 - 92 ( 76 - 92)
15 PERIPHERAL Likelihood = 1.75
        modified ALOM score: 0.67
    Rule: cytoplasmic membrane protein

    *** Reasoning Step: 2
20 ----- Final Results -----

        bacterial inner membrane --- Certainty= 0.134(Affirmative) < succ>

25 The protein has homology with the following sequences in the databases:

    >gi|586070|sp|Q07605|T4BA_BACCO RESTRICTION ENZYME BCGI ALPHA SUBUNIT [INCLUDES:
    ADENINE-SPECIFIC
        METHYLTRANSFERASE ACTIVITY ]
    gi|1075788|pir||A53125 restriction enzyme BcgI alpha chain - Bacillus coagulans
30 gi|304140|gb|AA16626.1| (L17341) restriction endonuclease alpha subunit
    [Bacillus
        coagulans]
        Length = 637

35 Score = 91.4 bits (226), Expect = 1e-17
    Identities = 78/256 (30%), Positives = 123/256 (47%), Gaps = 42/256 (16%)

    Query: 1 MFALAASNILRGDGRKANLHQSSCFMTDFQDLIKNPKPETGLKRPNVGFLNPPYAQSKSD 60
        +F +A +NMILRGDGK+NL + +C F + I N G+ N +NPPY+Q+K+D
40 Sbjct: 394 LPTIATTNMILRGDGRKSNLIRDNCLT--FDNTIMN---GYGI---NKILMNPPYSQARND 445

    Query: 61 ARLH--ELYFVKEMLDMLAEGGTGIAIIPVSCVIAPSK----AKSEIVKYHRLKAVMSMP 114
        H EL F+++ L+ML GG AI+P S ++ ++ K +I+K H L+ V+++
45 Sbjct: 446 QTQHLSELSFIQQAELMLVVGKLCIVPQSTMVGKNRHDKARKKQILKQHTLETVITLN 505

    Query: 115 SELFYPVGTVTCIVVFEAHKPHFQTVVIDPDTQBEISTKKACRKTWFGYWRDDGFETKHK 174
        + F+ VG CIV+F+A H + ++ F + DDG KH
50 Sbjct: 506 KDTFHGVGVNPCIVIFKAGIKHPEN-----KRVSFVNFEDDGHVVRKH 548

    Query: 175 LGRIDLYDRWQGIKARWLEHYL-----NNEVHTGESVTAFVTDNDEWVAEAYLETDYSKI 229
        +G + G + EH L + + T V + D DEW+ Y D
55 Sbjct: 549 VGLVG-----DGTEKGKREHLLAVLAGDEDDGTDLIVKTAIKDTDEWLHSFYFND-GIP 602

    Query: 230 TRADFEQVVREFALFQ 245
        + DF + V + FQ
    Sbjct: 603 SEDDFYKTVANYLTFQ 618
  
```

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 83

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 165> which encodes amino acid sequence <SEQ ID 166; NGS83>. Analysis of this protein sequence reveals the following:

```

5   GvH: Examining signal sequence (von Heijne)
      Signal Score (-7.5): -8.04
      Possible cleavage site: 43
      >>> Seems to have no N-terminal signal seq.
      Amino Acid Composition of Predicted Mature Form:
      calculated from 1
10  ALOM: Finding transmembrane regions (Klein et al.)
      count: 1 value: -1.44 threshold: 0.0
      INTEGRAL Likelihood = -1.44 Transmembrane 55 - 71 ( 55 - 71)
      PERIPHERAL Likelihood = 4.03
      modified ALOM score: 0.79
15  Rule: cytoplasmic membrane protein

      *** Reasoning Step: 2

      ----- Final Results -----
20  bacterial inner membrane --- Certainty= 0.157(Affirmative) < succ>

```

The protein has homology with the following sequences in the databases:

```

25  >gi|586071|sp|Q07606|T4BB_BACCO RESTRICTION ENZYME BGCI BETA SUBUNIT
      gi|1075789|pir||B53125 restriction enzyme BcgI beta chain - Bacillus coagulans
      gi|304141|gb|AAA16627.1| (L17341) restriction endonuclease beta subunit
      [Bacillus coagulans]
      Length = 341

30  Score = 44.0 bits (103), Expect = 0.002
      Identities = 46/195 (23%), Positives = 79/195 (39%), Gaps = 23/195 (11%)

      Query: 4  LQEIFDVSYGSKLDLNLKMSFNPTINFVGRSGKNNGVTASVDLLKNTKPYPAGLLTVALG 63
      + ++FDV G +D NK ++ R NG +D K K Y L + +G
35  Sbjct: 12  ISDLFDVVIGKTIDGNKAQRNENGTPYITRKATRNGFEFMIDGEKE-KLYSGKLPVITIG 70

      Query: 64  GSVLSTFLQNKPFYTAQNVAVLNPKTEMTQOKLFYCAAFANAYRFSACGREANRT-LR 122
      F+Q F+T V + PK ++ L Y + NA + + N T L+
40  Sbjct: 71  NETSKPFVQEFHFFTGTKVNICIPKLDLNRNH-LLYITMTIENATKMFYSYTYTINSTRLK 129

      Query: 123 QL--FVPSLDEIPSW-----VESVNLNPSAGVTEPKLKESLDLPVVRQSKR 166
      L +P E P W ++ ++ + GV++ + + L +
      Sbjct: 130 SLKILLPIKGEEPWDWYMNNTYISKILSNMEKNFDVQQNDGVSDLRSLKDLNLSW----SQFK 185

45  Query: 167 LDEIFTIQNGIAATK 181
      +DEIF+I +G+ TK
      Sbjct: 186 MDEIFSINSGVRLTK 200

```

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 84

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 167> which encodes amino acid sequence <SEQ ID 168; NGS84>. Analysis of this protein sequence reveals the following:

```

55  Signal Score (-7.5): 3.15
      Possible cleavage site: 33
      >>> Seems to have no N-terminal signal seq.
      Amino Acid Composition of Predicted Mature Form:
      calculated from 1

```


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ALOM: Finding transmembrane regions (Klein et al.)
 count: 0 value: 1.22 threshold: 0.0
 PERIPHERAL Likelihood = 1.22
 modified ALOM score: -0.74
 5 Rule: cytoplasmic protein

*** Reasoning Step: 2

----- Final Results -----

10 bacterial cytoplasm --- Certainty= 0.072(Affirmative) < succ>

The protein has homology with the following sequences in the databases:

15 >gi|2495432|sp|P55409|Y4DJ_RHISN HYPOTHETICAL TRANSCRIPTIONAL REGULATOR Y4DJ
 gi|7465604|pir||T02773 y4dJ protein - Rhizobium sp. plasmid pNGR234a
 gi|2182353|gb|AAB91639.1| (AE000069) Y4dJ [Rhizobium sp. NGR234]
 Length = 77

Score = 44.4 bits (104), Expect = 7e-04
 20 Identities = 25/61 (40%), Positives = 36/61 (58%)

Query: 92 KAGGETFVSLRMKKGFTQSELATAAGLPQPYLSRIENSKQSLQDKTVQKLANALGVSPLE 151
 K G F LR +KG TQ E+ +G Q YLS +E +++ T+ +LA ALGVS +E
 Sbjct: 5 KLVGSNFARLRREKGLTQEEVEARSGFSQQYLSSLERGRNPVTITLYELAQALGVSHVE 64

25 Query: 152 V 152
 +
 Sbjct: 65 L 65

30 Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 85

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 169> which encodes amino acid sequence <SEQ ID 170; NGS85>. Analysis of this protein sequence reveals the following:

35 Signal Score (-7.5): -6.09
 Possible cleavage site: 15
 >>> Seems to have no N-terminal signal seq.
 Amino Acid Composition of Predicted Mature Form:
 calculated from 1

40 ALOM: Finding transmembrane regions (Klein et al.)
 count: 0 value: 2.92 threshold: 0.0
 PERIPHERAL Likelihood = 2.92
 modified ALOM score: -1.08
 Rule: cytoplasmic protein

45 *** Reasoning Step: 2

----- Final Results -----

50 bacterial cytoplasm --- Certainty= 0.480(Affirmative) < succ>

The protein has no homology with sequences in the databases.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 86

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 171> which encodes amino acid sequence <SEQ ID 172; NGS86>. Analysis of this protein sequence reveals the following:

```

5   Signal Score (-7.5): -2.92
    Possible cleavage site: 21
    >>> Seems to have no N-terminal signal seq.
    Amino Acid Composition of Predicted Mature Form:
        calculated from 1
10  ALOM: Finding transmembrane regions (Klein et al.)
    count: 1 value: -2.76 threshold: 0.0
    INTEGRAL Likelihood = -2.76 Transmembrane 179 - 195 ( 179 - 195)
    PERIPHERAL Likelihood = 2.17
    modified ALOM score: 1.05
15  Rule: cytoplasmic membrane protein

    *** Reasoning Step: 2

    ----- Final Results -----

20  bacterial inner membrane --- Certainty= 0.210(Affirmative) < succ>

```

The protein has homology with the following sequences in the databases:

```

25  >sp|Q05205|PPB_LYSEN ALKALINE PHOSPHATASE PRECURSOR (APASE)
    pir||A42467 alkaline phosphatase (EC 3.1.3.1) phoA precursor - Lysobacter
        enzymogenes
    emb|CAA39978.1| (X56656) alkaline phosphatase [Lysobacter enzymogenes]
        Length = 539

    Score = 37.5 bits (86), Expect = 0.40
30  Identities = 28/82 (34%), Positives = 43/82 (52%), Gaps = 8/82 (9%)

    Query: 189 VALGLQAYWDVAGANNGATGQSPNIKTAQVPAKITRRNADGTTDTFGGGSARKSAAASVS 248
          V GL A W+V+ A + AQV +++ R+ GT D + G+A A AS S
    Sbjct: 458 VLRGLMA-WNVSSA-----AGKTLTGAQVKLQVSDRST-GTYDLYRAGAAWTEANASYS 509

35  Query: 249 GIEAGKKVTAVIPAVRGAVAYA 270
          G+ G K+ +V+P+ GA + A
    Sbjct: 510 GVSLGSKIGSVVPSATGAQSIA 531

```

40 Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 87

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 173> which encodes amino acid sequence <SEQ ID 174; NGS87>. Analysis of this protein sequence reveals the following:

```

45  Signal Score (-7.5): 0.18
    Possible cleavage site: 35
    >>> Seems to have no N-terminal signal seq.
    Amino Acid Composition of Predicted Mature Form:
        calculated from 1
50  ALOM: Finding transmembrane regions (Klein et al.)
    count: 0 value: 1.70 threshold: 0.0
    PERIPHERAL Likelihood = 1.70
    modified ALOM score: -0.84
55  Rule: cytoplasmic protein

    *** Reasoning Step: 2

    ----- Final Results -----

```


bacterial cytoplasm --- Certainty= 0.138(Affirmative) < succ>

The protein has homology with the following sequences in the databases:

5 >gi|12514207|gb|AAG55499.1|AE005289_17 (AE005289) unknown protein encoded by
cryptic prophage CP-933M
[Escherichia coli O157:H7]
gi|12514720|gb|AAG55907.1|AE005324_10 (AE005324) unknown protein encoded by
10 prophage CP-933N
[Escherichia coli O157:H7]
Length = 108

Score = 30.9 bits (69), Expect = 9.1
Identities = 21/55 (38%), Positives = 28/55 (50%), Gaps = 3/55 (5%)

15 Query: 1 MAAPVSLLEEFKQRIQIGVEHDDRDDFFLSVIDGVSAAAAYIGRSLLAADYVGRYDG 55
M A ++LEE K + V+HD DD + + +A AYI S D V R DG
Sbjct: 1 MTALLTLEEIKAHLRVDHDADDDMLMDKVRQATAVLLAYIQGS---RDKVIREDG 52

20 Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be
useful antigens for vaccines or diagnostics.

Example 88

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 175> which encodes amino acid sequence
<SEQ ID 176; NGS88>. Analysis of this protein sequence reveals the following:

25 Signal Score (-7.5): -3.69
Possible cleavage site: 43
>>> Seems to have no N-terminal signal seq.
Amino Acid Composition of Predicted Mature Form:
calculated from 1
30 ALOM: Finding transmembrane regions (Klein et al.)
count: 0 value: 6.05 threshold: 0.0
PERIPHERAL Likelihood = 6.05
modified ALOM score: -1.71
Rule: cytoplasmic protein
35 *** Reasoning Step: 2
----- Final Results -----

40 bacterial cytoplasm --- Certainty= 0.227(Affirmative) < succ>

The protein has no homology with sequences in the databases.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be
useful antigens for vaccines or diagnostics.

45 Example 89

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 177> which encodes amino acid sequence
<SEQ ID 178; NGS89>. Analysis of this protein sequence reveals the following:

50 Signal Score (-7.5): -4.77
Possible cleavage site: 26
>>> Seems to have no N-terminal signal seq.
Amino Acid Composition of Predicted Mature Form:
calculated from 1
ALOM: Finding transmembrane regions (Klein et al.)
count: 0 value: 1.38 threshold: 0.0

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PERIPHERAL Likelihood = 1.38
 modified ALOM score: -0.78
 Rule: cytoplasmic protein

5 *** Reasoning Step: 2

----- Final Results -----

10 bacterial cytoplasm --- Certainty= 0.284(Affirmative) < succ>

The protein has homology with the following sequences in the databases:

>gi|9634142|ref|NP_037684.1| gp24 [Enterobacteria phage HK022]
 gi|6863134|gb|AAF30375.1|AF069308_23 (AF069308) gp24 [Enterobacteria phage
 15 HK022]

Length = 1183

Score = 44.9 bits (102), Expect = 0.006

Identities = 38/127 (29%), Positives = 64/127 (49%), Gaps = 11/127 (8%)

20 Query: 851 NKALRDKINLIDGNGAGSVNERVEAVRSTADGNAAVQTHARSI---NG-LEAQYTVK-- 904
 NKA + +N + + ++ + +T +GN +A+ T+A++I NG L A Y +K
 Sbjct: 989 NKASINSLNQTFSQYQATATQINGITATVNGNTSAITTAQAIANVNGDLSAMYNKVG 1048

25 Query: 905 VDANGK--VAGFGLATTPKNGTPESKFIVNADRFGI-GAAGKADVFPFVVDQKNRVGIN 961
 V +NG+ AG G+ +S+ I ADRF + AAG + PFV+ Q + I
 Sbjct: 1049 VSSNGQYYAAGMGIGVENTPSGMQSQVIFLADRFAVTTAAGNSVALPFVI--QNGQTFIR 1106

Query: 962 GELVVNG 968
 + +G

30 Sbjct: 1107 ASFIQDG 1113

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 90

35 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 179> which encodes amino acid sequence <SEQ ID 180; NGS90>. Analysis of this protein sequence reveals the following:

Signal Score (-7.5): -2.82

Possible cleavage site: 24

40 >>> Seems to have no N-terminal signal seq.

Amino Acid Composition of Predicted Mature Form:
 calculated from 1

ALOM: Finding transmembrane regions (Klein et al.)

count: 4 value: -9.66 threshold: 0.0

45 INTEGRAL Likelihood = -9.66 Transmembrane 321 - 337 (317 - 349)
 INTEGRAL Likelihood = -6.48 Transmembrane 351 - 367 (340 - 371)
 INTEGRAL Likelihood = -5.73 Transmembrane 907 - 923 (903 - 926)
 INTEGRAL Likelihood = -0.00 Transmembrane 430 - 446 (430 - 446)
 PERIPHERAL Likelihood = 2.17

modified ALOM score: 2.43

50 Rule: cytoplasmic membrane protein

*** Reasoning Step: 2

----- Final Results -----

55 bacterial inner membrane --- Certainty= 0.486(Affirmative) < succ>

The protein has homology with the following sequences in the databases:

60 >gi|12514839|gb|AAG56002.1|AE005332_9 (AE005332) putative tail component of
 prophage CP-933X [Escherichia

-112-

coli 0157:H7]
Length = 1026

Score = 111 bits (279), Expect = 3e-23
Identities = 78/274 (28%), Positives = 146/274 (52%), Gaps = 10/274 (3%)

5 Query: 69 AAGNQAQQASEKVRAEVGKIGSGLTKLLAGLATADFAKSVLDTADAMQSINSQVRQV 128
AA + ++A ++ +++ +I + G+T AG A ++ AD S+N+++Q

10 Sbjct: 45 AAAREQRRALAEHLSQLTEIRASAVGMTGAFAG---AFATGHLISLADEWSSVNARLKQA 101

Query: 129 TSSETEYLAVQQQLLDTANRTRASLESTANLYVSTSRALKDYGTYQOEILKFTAEANNAM 188
+ S E+ + Q+ L+D + RT + A L+ ++ ++++YGY+ ++LK TEA + +

Sbjct: 102 SQSSDEFASSQKVLMDISQRTGTAFSDNAALFARSAASMREYGYSAADDVLKVTEAISTGL 161

15 Query: 189 TIGGVGAQQQAAALMQLSQALGSGVLQGEFKSISEAAPILLDTIAEYMGKSRDEIKKLG 248
I G + + + Q SQAL GVL+G+EF S++E+ ++ +A MG +R ++K +

Sbjct: 162 KISGASTAEAGSVITQFSQALAQGVLRGEEFNSVNESGDRIVRALAAGMGVARKDLKAMA 221

20 Query: 249 SEGKLTADVIFKAISGASEKFGEQAAKMPVTMGQALT VFSNNWQSMVSKLLNDSGTMSGI 308
+GKLTAD + A+ ++ A MP T+ ++T N + + V G +

Sbjct: 222 DDGKLTADKVVPAISQLGILRDEYAAMPETVSSSITKVENAFMAWV-----GGANEA 274

Query: 309 AAVIKLIADNLNLVVPPIVAGFAVAVAAVAPTLA 342
+ V K ++ LN V + A AV A VA +A

25 Sbjct: 275 SGVTKTLSGMLNGVAGQIDNVATAVGALVAVGVA 308

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 91

30 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 181> which encodes amino acid sequence <SEQ ID 182; NGS91>. Analysis of this protein sequence reveals the following:

Signal Score (-7.5): -0.63
Possible cleavage site: 36
>>> Seems to have no N-terminal signal seq.
35 Amino Acid Composition of Predicted Mature Form:
calculated from 1
ALOM: Finding transmembrane regions (Klein et al.)
count: 0 value: 0.16 threshold: 0.0
PERIPHERAL Likelihood = 0.16
40 modified ALOM score: -0.53
Rule: cytoplasmic protein
*** Reasoning Step: 2
45 ----- Final Results -----
bacterial cytoplasm --- Certainty= 0.250(Affirmative) < succ>

The protein has homology with the following sequences in the databases:

50 (AF237934) putative integrase/recombinase
[Pasteurella multocida]
Length = 329

55 Score = 449 (206.9 bits), Expect = 4.4e-91, Sum P(2) = 4.4e-91
Identities = 93/196 (47%), Positives = 129/196 (65%)

Query: 56 IFADLIRRYLSEVTPSKRGAREESYRIGRALKTPLAKVRLADLRPQDFADWRDQRLQEV 115
IF D+I RY +EV+ +K+GAR E R+ R L+ ++ + + DLR +DF +W RL EVS

60 Sbjct: 55 IFRDVIERYQNEVSITKKGARNEIIRLNRFLRYDISNLYIRDRLRKEDFEWIRIRL TEVS 114

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Query: 116 PTVGRELTTLSAVCEHAMKEWGLLRENVPVRKISKPKSRARTRRPTEQEIADICAALLY 175
SV REL T+S+V A+ +WG + +P+ I KPK S R R +EQ+I I Y

Sbjct: 115 DASVRRELVTISSVLTTAINKWGYISRHPMTGIEKPKNSAERKERYSEQDIKTILETARY 174

5 Query: 176 RPNEKPKMAVQRVAVAVLFAIETAMRAGEICGLKWADVNMRRIAHLPTKNGDSRDVPL 235
++ P QRVA+A+LFAIETAMRAGEI +KW +V + +RI HLP TKNG SRDVL

Sbjct: 175 CEDKLPITLKQRVAIAMLFIAIETAMRAGEIASIKWDNVFLEKRIVHLPTTKNGHSRDVPL 234

10 Query: 236 SLRAELIEQLRGIDD 251
S RA LI +++ +++

Sbjct: 235 SQRAVALILKMKEVEN 250

Score = 248 (114.3 bits), Expect = 4.4e-91, Sum P(2) = 4.4e-91
Identities = 48/76 (63%), Positives = 57/76 (75%)

15 Query: 254 VFSLDAKSLDVLFRARDNCGIQGLHFHDTREALTRLSKKVPVEVLAKISGHRDLRILL 313
VF +SL FR + CG++ LHFHDTREALTRLSKKV V LAKISGHRDLRIL

Sbjct: 254 VFQTPBSLSTTFRVLKKECGLEHLHFHDTREALTRLSKKVDVMTLAKISGHRDLRILQ 313

20 Query: 314 NVYYRPDMADIAKMLD 329
N YY P+M+++A +LD

Sbjct: 314 NTYYAPNMSEVANLLD 329

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be
25 useful antigens for vaccines or diagnostics.

Example 92

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 183> which encodes amino acid sequence
<SEQ ID 184; NGS92>. Analysis of this protein sequence reveals the following:

30 Signal Score (-7.5): -7.85
Possible cleavage site: 25
>>> Seems to have an uncleavable N-term signal seq
Amino Acid Composition of Predicted Mature Form:
calculated from 1.

35 ALOM: Finding transmembrane regions (Klein et al.)
count: 1 value: -8.33 threshold: 0.0
INTEGRAL Likelihood = -8.33 Transmembrane 6 - 22 (1 - 25)
PERIPHERAL Likelihood = 5.99
modified ALOM score: 2.17
Rule: cytoplasmic membrane protein

40 *** Reasoning Step: 2

----- Final Results -----

45 bacterial inner membrane --- Certainty= 0.433(Affirmative) < succ>

The protein has homology with the following sequences in the databases:

50 >gi|9632051|ref|NP_048840.1| A484L [Paramecium bursaria Chlorella virus 1]
gi|7461623|pir||T17986 hypothetical protein A484L - Chlorella virus PBCV-1
gi|1620155|gb|AAC96851.1| (U42580) A484L [Paramecium bursaria Chlorella virus 1]
Length = 155

Score = 31.6 bits (70), Expect = 3.5
Identities = 20/72 (27%), Positives = 36/72 (49%)
55 Frame = +1

Query: 52 LQINLKMLEKRIDFLVENIDKYYQQYGSYPNNFDFISTKTDFTTESYCDFWDKNIAGYGN 231
+ +NLKM I F +DKY +QY +Y N F T+ + + ++ + +I N

60 Sbjct: 23 IAVNLKMGVSIPF----VDKYSKQYPTYTKNALFHVTRFNAYQKTFEYKNISIDTINN 78

Query: 232 CYFVKNDKDYTI 267

+ +++D Y I
 Sbjct: 79 LFSIRDDVLYNI 90

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be
 5 useful antigens for vaccines or diagnostics.

Example 93

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 185> which encodes amino acid sequence
 <SEQ ID 186; NGS93>. Analysis of this protein sequence reveals the following:

10 GvH: Examining signal sequence (von Heijne)
 Signal Score (-7.5): -5.08
 Possible cleavage site: 14
 >>> Seems to have no N-terminal signal seq.
 Amino Acid Composition of Predicted Mature Form:
 calculated from 1
 15 ALOM: Finding transmembrane regions (Klein et al.)
 count: 0 value: 0.79 threshold: 0.0
 PERIPHERAL Likelihood = 0.79
 modified ALOM score: -0.66
 20 Rule: cytoplasmic protein
 *** Reasoning Step: 2
 ----- Final Results -----
 25 bacterial cytoplasm --- Certainty= 0.320(Affirmative) < succ>

The protein has homology with the following sequences in the databases:

>gb|AAG22017.1|AF288038_2 (AF288038) putative HsdR [Streptococcus thermophilus]
 Length = 740
 30 Score = 674 bits (1738), Expect = 0.0
 Identities = 364/746 (48%), Positives = 489/746 (64%), Gaps = 40/746 (5%)
 Query: 14 NENSrvKIPAVLHLMRLGYDYLsLKNANW---DRQTNIFFEIFVDSLcRINPDLPPDDAR 70
 +E +RV+IPA HLMRLGY YL D +TNI IF + + N D
 35 Sbjct: 8 SELTRVQIPAAFHLMRLGYTYLPHNGKEIMGRDPETNILISIFREQFLKFNNYATDLQVE 67
 Query: 71 RLLADIRLELDNEDLGQKFYERLTNQSGGKKLIDFQNFdNNSFHVVTElPCINGDEAFRP 130
 R L +I++ELD DLG+ FY R+ + SG +D++N +NN+PH+ E+ C NG + FRP
 40 Sbjct: 68 RELNNIKIELDQNDLGRAFYNRIVSDSG-PTYVDWENPENNTFHLALEVTCQNGGDEF RP 126
 Query: 131 DIALLVNGMPLVFIEVKKPEN---NRGGIGEERERMgKRAKNPKFRRFINITQFMIFSNN 186
 DI + +NG+PL +IEVK+PN K I E+ R R +N +FRRF NITQ + FS+N
 45 Sbjct: 127 DIVIFINGLPLSYIEVKQPNairdGKTaiQSEQSRTAVRFENRRFRFNITQLISFSDN 186
 Query: 187 MEYDDGATEPAQGAfYASSACGKpVFNYFREEHXXXXXXXXXXXXXXXXXVLQDNNLPV 246
 + Y G + QG+FY S+A K FN F+EE + VL+D N
 Sbjct: 187 LPYISGQGGQKQGSfYCSNAfSKTKFNAfKEEREELIYSIRSLGEEEBIDAVLKDVNRFA 246
 50 Query: 247 IKHSPEFISNKSPDTPtPtnRILtSLlCRERLSFLLQhGLTYVK--ASQGLVQ--KHIMRYP 302
 +K PEF +N+ P TP N ++SL ++RL FLL++GL YV+ + G +Q KH+MRYP
 Sbjct: 247 LKSQPEFKTNQDPSTPCNTFISSLYQKKRLLFLLRYGLAYVEEHsKDGtIQLQKhVMRYP 306
 Query: 303 QLFATLAIEKHLANGGKKGVIWHTQSGSKTALAYnTRYLTHYAKQGIVPKFYFIVDRL 362
 Q FAT AIE + G +KGVWHTQSGSKTAL+Y+N RYLT+Y++KQGIVP+FYF+VDRL
 55 Sbjct: 307 QFFATKAIEDAIGKGVKGVWHTQSGSKTALSYFNIRYLTNYFSKQGIVPQFYFVVDRL 366
 Query: 363 DLLKQAQREFTARDLVVHTIDSREAFADIKSAQTLHNHAGKAEITVVNIQKFQDDPDVV 422
 DL QA REFT R L V I+S Q L+ ++ VVNIQKF+D+ D+
 60 Sbjct: 367 DLADQATREFTKRGLKVKRINS-----PQELNEKHDayQVAVVNIQKFkdNSDLT 416

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Query: 423 ARNDYDLAIQRVYFLDEVHRSYNPKGSFLANLNQSDVNAVIGLTGTPLI-----GVTA- 476
 + YDL Q +YF+DE HRSYN KGS+L NL +D NA+KI LTGTPLI G T
 Sbjct: 417 DHSGYDLNRQNIYFIDEAHRSYNEKGSYLPNLYNADKNAIKIALTGTPLITYKKDGKTK 476

5 Query: 477 GNVNTRLEFGDYIHKYYYNASIADGYTLRLIREEIGSRYKAQLQEALAEIEKGSFDRK 536
 + TR++FGDYIHKYYYN SI DG+TLRL+RE+I + YK LQ EI +G +
 Sbjct: 477 SHATTRDIFGDYIHKYYYNQSIDDGFTLRMLREDIETSYKETLQTI--NEEILRGDLSKD 534

10 Query: 537 EIIYAHPHFVHPMLDYILDDFAKFRKTN-QDESLGAMVVCDSAEQARQL---FEHFQTASD 592
 +I+AHP +V PMLD+IL+DF + R D+S+G M+VCDS++QAR++ E ++ +
 Sbjct: 535 DIFAHPRYVSPMLDFILEDENRARDVVFDSDSIGGMIVCDSSKQAREIEKQLEERRSRGE 594

15 Query: 593 HNFTAALILHDVGTKEERDQWVKDFKAGKIDILFVYNMLLTGFDAPRLKKLYLGRLIK 652
 N T+ALILHD G KE + V+ ++ GKID++ VY+MLLTGFDAPRLK+LYLGR IKAH
 Sbjct: 595 TNITSALILHDEGDKEYKKDRVESYREGKIDLVIVYSMLLTGFDAPRLKRLYLGRKIKAH 654

20 Query: 653 NLLQTLTRVNRITYKSYRYGYVVDFAIEREFDKTNRAYWDELSNE-----LGDEIGS-YS 706
 NLLQTLTRVNR YK Y++GYV+DFADI +EFDKTNRAY +EL+ E G+++ + +
 Sbjct: 655 NLLQTLTRVNRPYKDYQPGYVIDFADISKEFDKTNRAYLEELNQEYDPKNTGEDVENVFG 714

Query: 707 QLFKTAEBIEQEIADIKNALFDFDTE 732
 LF +A+EI +++ + L ++ TE
 Sbjct: 715 SLFVSADEISKQLEKSETILMNYPT 740

25 Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 94

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 187> which encodes amino acid sequence <SEQ ID 188; NGS94>. Analysis of this protein sequence reveals the following:

30 Signal Score (-7.5): -3.19
 Possible cleavage site: 35
 >>> Seems to have no N-terminal signal seq.
 Amino Acid Composition of Predicted Mature Form:
 calculated from 1

35 ALOM: Finding transmembrane regions (Klein et al.)
 count: 0 value: 5.73 threshold: 0.0
 PERIPHERAL Likelihood = 5.73
 modified ALOM score: -1.65
 Rule: cytoplasmic protein

40 *** Reasoning Step: 2

----- Final Results -----

45 bacterial cytoplasm --- Certainty= 0.302(Affirmative) < succ>

The protein has homology with the following sequences in the databases:

50 >gi|10717100|gb|AAG22014.1|AF288037_3 (AF288037) putative HsdS [Streptococcus
 thermophilus]
 Length = 402

Score = 154 bits (389), Expect = 2e-36
 Identities = 123/348 (35%), Positives = 168/348 (47%), Gaps = 48/348 (13%)

55 Query: 73 GKTA FVDILDDGEVAFGSTEFIVLRKNET--NPEFLYFPAISPDRKRAIECMGTSGR 130
 GKT ++ DGE ++ IV +E+ +FLYYF + F G++ +
 Sbjct: 74 GKT----VIFDGEDSYFQDSNIVWIENDESKVTNQFLYYFLQTNPFIT-----TNGSTIK 124

60 Query: 131 QRVNENALKTLELPIPEPQIQQSIAAVLSALDKKIALNKQINARLEEMAKTLYDYWFVQF 190
 + N+N T +P Q Q I +L LDKKI +N QIN LE MAKTLTYDYWFVQF
 Sbjct: 125 RLYNDNLRDTKIPNVPSIQQQNQITDILGTLDDKKIQINNQNQINQELEAMAKTLYDYWFVQF 184

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Query: 191 DFPDANGKPYKSSGGDMVFDETLKREIPKGGWGSIELQSCL---AKIPNTTKILNKDIDKF 247
 DFPD NGKPYKSSGG MV++ LKREIP+GWG+ +L S L + N K N++ K +
 Sbjct: 185 DFPDQNGKPYKSSGGKMVYNPELKREIPEGWGAEKLSLLKIGKETTNPKKFPNEEFKYY 244

Query: 248 -----GKYFVVD-----QSQDFICGFTNDEKSILNPQDAHIIFGDHTRIVKLNVFOYA 295
 G Y + +S F + S LNP +I+ + F
 Sbjct: 245 SIPEFDTTGTYSLGERGESIKSNKFKVEKNLLVSKLNPWFNRTVYNLEENAIASTEF--- 301

Query: 296 RGADGTQVILSNERNMPNYLFYQIINQIDLSSY-----GYARHFK-----FLKEFKIIL 344
 ++ R YQ+ + Y G + K + F+I
 Sbjct: 302 -----IVWKTFRNFEKNFLYQVATGKEFIEYCTRATGTSNSHKRVSPDIMVGFQIPF 354

Query: 345 PSKDISQKYNEIANTFFVKVRNNLQONHHLTQLRDFLLPMLMNGQVSV 392
 I QK+ EI ++ +V N +QN LTQLRD++LPMLMNGQV V
 Sbjct: 355 EKTHI-QKGEIIDSIRTQVLQNNQONQELTQLRDWILPMLMNGQVKV 401

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

20 Example 95

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 189> which encodes amino acid sequence <SEQ ID 190; NGS95>. Analysis of this protein sequence reveals the following:

GvH: Examining signal sequence (von Heijne)
 Signal Score (-7.5): -6.12
 Possible cleavage site: 19
 >>> Seems to have an uncleavable N-term signal seq
 Amino Acid Composition of Predicted Mature Form:
 calculated from 1

ALOM: Finding transmembrane regions (Klein et al.)
 count: 3 value: -10.51 threshold: 0.0

INTEGRAL	Likelihood = -10.51	Transmembrane	112 - 128 (109 - 132)
INTEGRAL	Likelihood = -4.46	Transmembrane	50 - 66 (46 - 70)
INTEGRAL	Likelihood = -2.23	Transmembrane	7 - 23 (7 - 23)
PERIPHERAL	Likelihood = 4.19		

modified ALOM score: 2.60
 Rule: cytoplasmic membrane protein

*** Reasoning Step: 2

----- Final Results -----

bacterial inner membrane --- Certainty= 0.520(Affirmative) < succ>

The protein has homology with the following sequences in the databases:

>pir||G69096 hypothetical protein MTH1717 - Methanobacterium thermoautotrophicum
 (strain Delta H)
 gb|AAB86189.1| (AE000928) unknown [Methanothermobacter thermautotrophicus]
 Length = 557

Score = 35.4 bits (80), Expect = 0.50
 Identities = 25/80 (31%), Positives = 47/80 (58%), Gaps = 5/80 (6%)

Query: 52 LLFYFLIPFIATATVLWL SKYLKDEFKQGEVKELEYVNDNFLPSYLG YFFVALSIPDNN 111
 L+F+F+ P + TATVL + K + ++ F++ EV L + +PS++ ++ IP++
 Sbjct: 92 LVFFFISPLLGTATVLVIYK-VARETFEREEVALLSAFLFSMVPSFVAR--TSVFIPESM 148

Query: 112 LFLLFVYGIIFLLVSCSKS 131
 LL GI+++LV K+
 Sbjct: 149 GLLL--TSGILYMLVKYLKT 166

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 96

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 191> which encodes amino acid sequence

5 <SEQ ID 192; NGS96>. Analysis of this protein sequence reveals the following:

GvH: Examining signal sequence (von Heijne)
 Signal Score (-7.5): -7.76
 Possible cleavage site: 28
 >>> Seems to have no N-terminal signal seq.
 10 Amino Acid Composition of Predicted Mature Form:
 calculated from 1
 ALOM: Finding transmembrane regions (Klein et al.)
 count: 0 value: 6.15 threshold: 0.0
 PERIPHERAL Likelihood = 6.15
 15 modified ALOM score: -1.73
 Rule: cytoplasmic protein
 *** Reasoning Step: 2
 20 ----- Final Results -----
 bacterial cytoplasm --- Certainty= 0.362(Affirmative) < succ>

The protein has no homology with sequences in the databases.

25 Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 97

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 193> which encodes amino acid sequence
 <SEQ ID 194; NGS97>. Analysis of this protein sequence reveals the following:

30 GvH: Examining signal sequence (von Heijne)
 Signal Score (-7.5): -0.48
 Possible cleavage site: 13
 >>> Seems to have no N-terminal signal seq.
 Amino Acid Composition of Predicted Mature Form:
 35 calculated from 1
 ALOM: Finding transmembrane regions (Klein et al.)
 count: 0 value: 8.86 threshold: 0.0
 PERIPHERAL Likelihood = 8.86
 modified ALOM score: -2.27
 40 Rule: cytoplasmic protein
 *** Reasoning Step: 2
 ----- Final Results -----
 45 bacterial cytoplasm --- Certainty= 0.127(Affirmative) < succ>

The protein has homology with the following sequences in the databases:

50 >ref|NP_052265.1| P2 J homolog; baseplate or base of tail fibre [Enterobacteria
 phage
 186]
 gb|AAC34162.1| (U32222) P2 J homolog; baseplate or base of tail fibre
 [Enterobacteria phage 186]
 Length = 302

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Score = 112 bits (280), Expect = 3e-24
 Identities = 65/151 (43%), Positives = 85/151 (56%), Gaps = 1/151 (0%)

```

5  Query: 1  MGNSRSLSQLPAPAAIETDFEGIFARKKAALTALCPBSIRETVAQTLLESESEPLTIDLQQ 60
      M   LS LP P  +EE DFE I A + A L +L PE  +E VA+TL LESEP+  LQ+
      Sbjct: 1  MATVDLSLLFPDVPDVEELDFETILAERIATLISLYPEDQQEAVARTLALESEPIVKLLQE 60

10 Query: 61  QAYQELLVRNRINEAVKANLLAYAQGSDDLHIAAQVGLSRKTIRXXXXXXXXXXXXXEYET 120
      AY+E++ R R+NEA +A +LAYA+ SDLD++ A + + R +R          E E
      Sbjct: 61  NAYREVIWRQRVNEAARAGMLAYARDSLDNLGANFNVERLVVRPADDTTIPPTPAEMEL 120

      Query: 121 DDAFRARV-QAHPEKYAAGPRTAYEAHAIDA 150
      D FR R+ QA      AG  AYE H  A
15  Sbjct: 121 DADFRLRIQQAFEGMSVAGSTGAYEFHGRSA 151
  
```

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 98

20 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 195> which encodes amino acid sequence <SEQ ID 196; NGS98>. Analysis of this protein sequence reveals the following:

```

      Signal Score (-7.5): -3.68
      Possible cleavage site: 33
      >>> Seems to have no N-terminal signal seq.
25  Amino Acid Composition of Predicted Mature Form:
      calculated from 1
      ALOM: Finding transmembrane regions (Klein et al.)
      count: 0 value: 4.61 threshold: 0.0
      PERIPHERAL Likelihood = 4.61
30  modified ALOM score: -1.42
      Rule: cytoplasmic protein

      *** Reasoning Step: 2

35  ----- Final Results -----

      bacterial cytoplasm --- Certainty= 0.182(Affirmative) < succ>
  
```

The protein has no homology with sequences in the databases.

40 Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 99

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 197> which encodes amino acid sequence <SEQ ID 198; NGS99>. Analysis of this protein sequence reveals the following:

```

45  Signal Score (-7.5): -4.87
      Possible cleavage site: 19
      >>> Seems to have no N-terminal signal seq.
      Amino Acid Composition of Predicted Mature Form:
      calculated from 1
50  ALOM: Finding transmembrane regions (Klein et al.)
      count: 0 value: 4.93 threshold: 0.0
      PERIPHERAL Likelihood = 4.93
      modified ALOM score: -1.49
      Rule: cytoplasmic protein
55
  
```


*** Reasoning Step: 2

----- Final Results -----

5 bacterial cytoplasm --- Certainty= 0.189(Affirmative) < succ>

The protein has homology with the following sequences in the databases:

10 >gi|10172952|dbj|BAB04058.1| (AP001508) BH0339-unknown conserved protein in
others [Bacillus
halodurans]
Length = 283

Score = 83.7 bits (206), Expect = 1e-15

Identities = 59/156 (37%), Positives = 87/156 (54%), Gaps = 8/156 (5%)

15 Query: 10 VRGPFVQLAFAQSIDPIVPEVSITRMAVTNEKDLEKERTMGRKYIVPYVVYRVHGFISAN 69
VRGPFV + A SIDPI IT+ + D TMG K+ V + VY G I+
Sbjct: 129 VRGFSIHTATSIDPIDIVSTQITKSVNSVTGDKRSSDTMGMKHRVDFGVYVFKGSINTQ 188

20 Query: 70 LAAKTGFSDDDLAKLWQALTLMEHDSR--GEMAARKLVVFKHDSALGSQPAHKLFD 127
LA KTGF+++D K+ +AL +FE+D S+AR G M K+ ++H S LG + K+
Sbjct: 189 LAEKTGFTNEDAEEKIKRALITLFEENDSSSARPDGSMKVHVKVYVWEHSSKLGQYSSAKVHR 248

25 Query: 128 AVKVERVNGESGTPASGFGDYKISVVSDDLNGVSVE 163
++K+E ++ TP S F DY + + L+G+ VE
Sbjct: 249 SLKIE---SKTDTPKS-FDDYAVELYE--LDGLGVE 278

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

30 Example 100

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 199> which encodes amino acid sequence <SEQ ID 200; NGS100>. Analysis of this protein sequence reveals the following:

Signal Score (-7.5): -3.03
Possible cleavage site: 18
35 >>> Seems to have no N-terminal signal seq.
Amino Acid Composition of Predicted Mature Form:
calculated from 1
ALOM: Finding transmembrane regions (Klein et al.)
count: 0 value: 6.63 threshold: 0.0
40 PERIPHERAL Likelihood = 6.63
modified ALOM score: -1.83
Rule: cytoplasmic protein

45 *** Reasoning Step: 2

----- Final Results -----

bacterial cytoplasm --- Certainty= 0.185(Affirmative) < succ>

50 The protein has homology with the following sequences in the databases:

>gi|1175791|sp|P44189|YE18_HAEIN HYPOTHETICAL PROTEIN HI1418
gi|1074769|pir|A64029 hypothetical protein HI1418 - Haemophilus influenzae
(strain Rd
KW20)
55 gi|1574254|gb|AAC23068.1| (U32821) H. influenzae predicted coding region HI1418
[Haemophilus
influenzae Rd]
Length = 201

60 Score = 144 bits (364), Expect = 1e-33

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Identities = 71/109 (65%), Positives = 79/109 (72%)

Query: 8 NFOQNSVTVADNKGELWFLANDVCEILGYTNPRRTVDLHCKSRGVTKRYTPTTSGEQEM 67
 NF+ VR + D KGE WF DVC ILGYTN R+ + HCK GVTKRYTPT S +QEM
 5 Sbjct: 24 NFKDLFPVRVILDPKGEFWFCGTDVCHILGYTNSRKALQDHCKQGGVTKRYTPTKSADQEM 83

Query: 68 TYINEPNLYRLIIKSRKPAARAFEEVWVETVLPPIRKTGGCQVGPRTTA 116
 T+INEPNLYRLIIKSRKP AE FE WV E VLP IRKTG Q+ P+ A
 10 Sbjct: 84 TFINEPNLYRLIIKSRKPEAEFPAWVFEEVLPQIRKTGKYQLQPQOLA 132

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 101

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 201> which encodes amino acid sequence
 15 <SEQ ID 202; NGS101>. Analysis of this protein sequence reveals the following:

Signal Score (-7.5): -1.23
 Possible cleavage site: 47
 >>> Seems to have no N-terminal signal seq.
 Amino Acid Composition of Predicted Mature Form:
 20 calculated from 1
 ALOM: Finding transmembrane regions (Klein et al.)
 count: 0 value: 3.55 threshold: 0.0
 PERIPHERAL Likelihood = 3.55
 modified ALOM score: -1.21
 25 Rule: cytoplasmic protein

*** Reasoning Step: 2

----- Final Results -----

30 bacterial cytoplasm --- Certainty= 0.126(Affirmative) < succ>

The protein has homology with the following sequences in the databases:

35 >gi|9632520|ref|NP_049514.1| hypothetical protein [Bacteriophage 933W]
 gi|9633449|ref|NP_050552.1| hypothetical protein [Bacteriophage VT2-Sa]
 gi|4585431|gb|AAD25459.1|AF125520_54 (AF125520) hypothetical protein
 [Bacteriophage 933W]
 gi|5881645|dbj|BAA84336.1| (AP000363) hypothetical protein [Bacteriophage VT2-
 40 Sa]
 gi|7649882|dbj|BAA94160.1| (AP000422) hypothetical protein [Escherichia coli
 O157:H7]
 Length = 404

Score = 177 bits (449), Expect = 3e-43
 45 Identities = 130/425 (30%), Positives = 204/425 (47%), Gaps = 27/425 (6%)

Query: 7 TAYGDPQAMMKQAAGLFAMHMQRNSTLNRLAGKMPAGTA-GAEATLRKQTTQHMPVVRQC 65
 T QA LF + S +N L + A A + KQT+ PVVR
 50 Sbjct: 2 TTVTSAQANKLYQVALFTAANRNRSMVNILTEQQEAPKAVSPDKKSTKQTSAGAPVVRIT 61

Query: 66 DLTRGMGDEIRFNLVNPVSALPIMGDNTAEGRGVGMSLSEAGLRVNQARFPVDGGGTMTN 125
 DL + GDE+ F++++ +S P MGD EGRG +S ++ L++NQ R VD GG M+
 Sbjct: 62 DLNKQAGDEVTFSSIMHKLSKRPTMGDERVEGRGEDLSHADFSLKINQGRHLVDAGGRMSQ 121

55 Query: 126 QRSPADYRALIRPAAQSLMDRYADQTLVHVMAGARGFHDNIEWGVPLAGDPKFNDYAVNP 185
 QR+ + + R + + DQ +VH+AGARG + +P A P+F +N
 Sbjct: 122 QRTKFNLAASARTLLGTYFNDLQDQCAIVHLAARGDFVADDTILPTAEHPEFKKIMIND 181

60 Query: 186 VKAPSKNRHFTASGDAVTGVGDNGGELKIASTDLFTMDTVDSMRVLDQIPLPPPIVKFE 245
 V P+ +RHF GD +I + D+F++ VD++ +D++ P V+
 Sbjct: 182 VLPPTHDRHFFG-----GDATSFEQIEAADIFSIGLVDNLSLFIDEMAHPLQPVRLS 233

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Query: 246 GDKAAGDSPLRVWLLSPAQYNRF---AADPKFRQLQASAIARASQANQNPLFLGDAGLWN 302
 GD+ G+ P V ++P Q+N + + + Q+ A+ RA N +PLF G+ +W
 Sbjct: 234 GDELHGEDFYVLYVTPRQWWDWYTSTSGKDWNQMMVRAVNRAGFN-HPLFKGECAMWR 292

5 Query: 303 GFILVKMP-RPIRFYAGDEMYCADKFSABSGLKIPASFADKFAVDRSVILGGQAVLEA 361
 ++ K PIRFY G ++ + + A +DR+++LG QA+ A
 Sbjct: 293 NILVRKYAGMPIRFYQGSKVLVSENNLTATTK-----EVAAATNIDRAMLLGAQALANA 346

10 Query: 362 FANTGKHGGMPFFWSEKELDHGNRVETLVGTIRGVAKTRFAVDVGGGAKEITDYGVTVD 421
 + G+ G F EK+ D NR E + I G+ K RF G ++ D+GV VD
 Sbjct: 347 Y---GQKAGGHFNMVEKKTMDNRTETIAISWINGLKKIRFPEKSG----KMQDHGVIAVD 399

15 Query: 422 TVVPL 426
 T V L
 Sbjct: 400 TAVKL 404

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

20 Example 102

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 203> which encodes amino acid sequence <SEQ ID 204; NGS102>. Analysis of this protein sequence reveals the following:

Signal Score (-7.5): -6.09
 Possible cleavage site: 15
 25 >>> Seems to have no N-terminal signal seq.
 Amino Acid Composition of Predicted Mature Form:
 calculated from 1
 ALOM: Finding transmembrane regions (Klein et al.)
 count: 0 value: 2.92 threshold: 0.0
 30 PERIPHERAL Likelihood = 2.92
 modified ALOM score: -1.08
 Rule: cytoplasmic protein
 *** Reasoning Step: 2
 35 ----- Final Results -----
 bacterial cytoplasm --- Certainty= 0.480 (Affirmative) < succ

40 The protein has no homology with sequences in the databases.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 103

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 205> which encodes amino acid sequence <SEQ ID 206; NGS103>. Analysis of this protein sequence reveals the following:

Signal Score (-7.5): -1.29
 Possible cleavage site: 34
 >>> Seems to have no N-terminal signal seq.
 Amino Acid Composition of Predicted Mature Form:
 50 calculated from 1
 ALOM: Finding transmembrane regions (Klein et al.)
 count: 1 value: -0.00 threshold: 0.0
 INTEGRAL Likelihood = -0.00 Transmembrane 22 - 38 (22 - 38)
 PERIPHERAL Likelihood = 4.88
 55 modified ALOM score: 0.50

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Rule: cytoplasmic membrane protein

*** Reasoning Step: 2

5 ----- Final Results -----

bacterial inner membrane --- Certainty= 0.100(Affirmative) < succ>

The protein has homology with the following sequences in the databases:

10 >gi|11277848|pir||E81145 replicative DNA helicase NMB0885 [imported] - Neisseria
meningitidis (group B strain MD58)
gi|7226124|gb|AAF41296.1| (AE002441) replicative DNA helicase [Neisseria
meningitidis MC58]
Length = 468

15 Score = 233 bits (594), Expect = 5e-60
Identities = 158/456 (34%), Positives = 245/456 (53%), Gaps = 34/456 (7%)

20 Query: 15 SVGAEQNILGGILIEPTAIARCA-ILTPEKFYQAQHRIFRALLDMAAANEPIDIITLND 73
S+ AEQ++LGG+++E A R A +++ E FY+ +HR+IFR++ + + P D+IT+ +
Sbjct: 23 SMEAEQSVLGGMLLENPAWDRIADVSGEDFYRHEHRLIFRSIAKLINESRPADVITVQE 82

25 Query: 74 KLEARGEAEENAGGLAYLIDLNQNTPSAKNISRYVGIVNDRFVERGLLKASAAIEKIAVSK 133
L+ E E AGG YLI L QNTPSA NI RY IV +R + R L + I + A +
Sbjct: 83 DLQRNEELEAAGGFYDLITLAQNTPSAANIRRYAEIVRERSIMRQLAEVGTETIARSAYNP 142

30 Query: 134 DGGTVAEKLKSKADELAAVGKDAVKRETKTFGQTVEDLIGGLDKRLDGVR-----FG 185
G + L +A +++ + + K +K + DL+ + +R+D + G
Sbjct: 143 QGRDAGQLLDEAENKVFQIAESTAK--SKQGFLFEMPDLLEKVVQRIDMLYSRDNPDVETG 200

35 Query: 186 LPTGLMKLDGMTGGLPDGNLIVIAARPSMGKTVAENIARFALKQGGK-AVHFQSYEMSAV 244
+PTG + LD T GL G+LI++A RPSMGKT + NIA +G+ V S EM
Sbjct: 201 VPTGFIDLDKKTSGLQPGDLIIIVAGRPSMGKTAFSINIAEHVAVEGRLPVAVFPMEMGGA 260

40 Query: 245 ELARRGMAAECNIPMQNLKLTGNLTQSDYANM-----PIYVSQAKWKFDVNCDDL 294
+L R + + + LKTG L + + P+Y+ +
Sbjct: 261 QLVMRMLGSVGRLDQSVLKTGRLEDEHWGRLEAVVKSLSAPVYIDETPGLTALELRARA 320

45 Query: 295 NVDELFLAKEKRLTTGLDLLVVDHLHIMPRAGRDE--VAELGNISRRLNLAELNTPV 352
F K L L+V+D+L +M +GR + +ELG ISR LK LA EL P+
Sbjct: 321 RRLARQFNK-----LGLIVIDYQLMAGSGRSDNRASELGEISRSLKALAKELQVPI 373

50 Query: 353 VLVAQLNRGNTKQADKRPNMADIRGSGAIEQDANIIMPHRESYYDGNENP--SIAELII 410
+ ++QL+R + DKRP M+D+R SGAIEQDA++I+ +R+ YY+ ++P +AE II
Sbjct: 374 IALSQLSRTVESRTDKRPMMSDLRESGAIEQDADLIMFMYRDEYYN-QDSPMKGLAECEII 432

55 Query: 411 AKNRDGEVGTVCVCGWKGQFMKFEEEPDLAWQAPKHD 446
K+R+G +G + W GQF KF+ + +A D
Sbjct: 433 GKHRNGPVGKIFLTWTGQFTKFDNAAYIPEEKIED 468

60 >gi|11277846|pir||E81876 probable replicative DNA helicase (EC 3.6.1.-) NMA1105
[imported] -
Neisseria meningitidis (group A strain Z2491)
gi|7379799|emb|CAB84367.1| (AL162755) putative replicative DNA helicase
[Neisseria
meningitidis Z2491]
Length = 468

65 Score = 230 bits (588), Expect = 2e-59
Identities = 158/456 (34%), Positives = 244/456 (52%), Gaps = 34/456 (7%)

Query: 15 SVGAEQNILGGILIEPTAIARCA-ILTPEKFYQAQHRIFRALLDMAAANEPIDIITLND 73
S+ AEQ++LGG+++E A R A +++ E FY+ +HR+IFR++ + + P D+IT+ +
Sbjct: 23 SMEAEQSVLGGMLLENPAWDRIADVSGEDFYRHEHRLIFRSIAKLINESRPADVITVQE 82

Query: 74 KLEARGEAEENAGGLAYLIDLNQNTPSAKNISRYVGIVNDRFVERGLLKASAAIEKIAVSK 133
L+ E E AGG YLI L QNTPSA NI RY IV +R + R L + I + A +

-123-

Sbjct: 83 DLQRNEELEAAGGFYLLITLAQNTPSAANIRRYAEIVRERSIMRQLAEVGTIARSAYNP 142

Query: 134 DGGTVAEKLSKAADELAAGVGDVAVKRETKTFGQTVEDLIGGLDKRLDGVR-----FG 185
 G + L + A +++ + + K +K + DL+ + +R+D + G

5 Sbjct: 143 QGRDAGQLLDEAENKVFQIAESTAK--SKQGFLEMPDLLKEVVQRIDMLYSRDNPDVETG 200

Query: 186 LPTGLMKLDGMTGGLPDGNLIVIAARPSMGKTVLAENIARFALKQGGK-AVHFQSYEMSAV 244
 + TG + LD T GL G+LI++A RPSMGKT + NIA +GK V S EM

10 Sbjct: 201 VSTGFIDLDKKTSGQLPGDLIIVAGRPSMGKTAFSINIAEHVAVEGKLPVAVFSMEMGGA 260

Query: 245 ELARRGMAAECNIPMQNLKTGNLTQSDYANM-----PIYVSQAKEWKFDVNCDDL 294
 +L R + + + LKTG L + + P+Y+ +

Sbjct: 261 QLVMRMLGSGVGRLDQSVLKTGRLEDEHWGRLEAVVKLSDAFVYIDETPGLTALELRARA 320

15 Query: 295 NVDELCEFLAKEKLLTTGLDLLVVDHLHIMPRAGRDE--VAELGNISRRKLNLAELNTPV 352
 F K L L+V+D+L +M +GR + +ELG ISR LK LA EL P+

Sbjct: 321 RRLARQFNK-----LGLIVIDYLQLMAGSGRSDNRASELGEISRSLKALAKELQVPI 373

20 Query: 353 VLVAQLNRGNTKQADKRPNMADIRGSGAIEQDANIIIMPHRESYYDGNENP--SIAELII 410
 + ++QL+R + DKRP M+D+R SGAIEQDA++I+ +R+ YY+ ++P +AE II

Sbjct: 374 IALSQLSRTVESRTDKRPMMSDLRESGAIEQDADLIMFYRDEYYN-QDSPMKGLAECII 432

Query: 411 AKNRDGMGTVVCGWKGQFMKFEEEPDLAWQAPKHD 446
 K+R+G +G + W GQF KF+ + +A D

25 Sbjct: 433 GKHRNGPVGKIFLTWTGQFTKFDNAAIPEEAKIED 468

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 104

30 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 207> which encodes amino acid sequence <SEQ ID 208; NGS104>. Analysis of this protein sequence reveals the following:

Signal Score (-7.5): -2.11
 Possible cleavage site: 15
 >>> Seems to have no N-terminal signal seq.

35 Amino Acid Composition of Predicted Mature Form:
 calculated from 1
 ALOM: Finding transmembrane regions (Klein et al.)
 count: 0 value: 5.04 threshold: 0.0
 PERIPHERAL Likelihood = 5.04

40 modified ALOM score: -1.51
 Rule: cytoplasmic protein

*** Reasoning Step: 2

45 ----- Final Results -----
 bacterial cytoplasm --- Certainty= 0.220(Affirmative) < succ

The protein has homology with the following sequences in the databases:

50 >gi|7515458|pir||T13296 hypothetical protein 8 - Streptococcus phage phi-01205
 gi|2444088|gb|AAC79524.1| (U88974) ORF8 [Streptococcus thermophilus temperate
 bacteriophage
 01205]
 Length = 157

55 Score = 62.1 bits (150), Expect = 3e-09
 Identities = 53/161 (32%), Positives = 86/161 (52%), Gaps = 8/161 (4%)

60 Query: 5 TLYRCAADVQAGLDYFFDSETEREDTLEAV--IGQFEVKAQSVIAYIKNQEITEKMLEGH 62
 TLY + + D ET + DTLEA+ +E K + + IK+ E + +
 Sbjct: 3 TLYELTDQLLEIYNMVDDET-KLDTLEAIDWTTDYENKVEGYVKVIKSLEADIEARKNE 61

Query: 63 IRQMTGKLKAAKARNQSLKDYLRNMQAAGITEIKADDGTFKASFRKSEAVVILDEAQIP 122
 +++ G K+ +++ LK LA +M G T + D FK FRKSEAVV+ +E ++P
 Sbjct: 62 KKRLDGLNKSDQSKIDKLKTALAVSMAETGQTRV--DTTLFKVGFVKSEAVVV-NEEKLP 118

Query: 123 AEFMREAVKTEPDKTAIRKAIESGRQVAGAKIEGRKNLQIR 163
 E+ K PDK +++ ++SG+ + GA +E R+NL IR
 Sbjct: 119 KEYQIATYK--PDKKTLKELLKSGKHIEGATLEERRNLNIR 157

- 10 Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 105

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 209> which encodes amino acid sequence <SEQ ID 210; NGS105>. Analysis of this protein sequence reveals the following:

- 15 Signal Score (-7.5): -5.52
 Possible cleavage site: 31
 >>> Seems to have no N-terminal signal seq.
 Amino Acid Composition of Predicted Mature Form:
 calculated from 1
- 20 ALOM: Finding transmembrane regions (Klein et al.)
 count: 0 value: 2.60 threshold: 0.0
 PERIPHERAL Likelihood = 2.60
 modified ALOM score: -1.02
 Rule: cytoplasmic protein
- 25 *** Reasoning Step: 2
- Final Results -----
- 30 bacterial cytoplasm --- Certainty= 0.135(Affirmative) < succ>

The protein has no homology with sequences in the databases.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

35 Example 106

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 211> which encodes amino acid sequence <SEQ ID 212; NGS106>. Analysis of this protein sequence reveals the following:

- Signal Score (-7.5): 4.8
 Possible cleavage site: 26
- 40 >>> Seems to have a cleavable N-term signal seq.
 Amino Acid Composition of Predicted Mature Form:
 calculated from 27
- ALOM: Finding transmembrane regions (Klein et al.)
 count: 0 value: 7.80 threshold: 0.0
- 45 PERIPHERAL Likelihood = 7.80
 modified ALOM score: -2.06
 Score for OM-PP discrimination: 4.38
 Rule: outer membrane or periplasmic protein
 Score for OM-PP discrimination: 4.38
- 50 Rule: outer membrane or periplasmic protein
- *** Reasoning Step: 2
- Outer membrane? Score: 0.437687
- 55 Outer membrane? Score: 0.437687

----- Final Results -----

bacterial outer membrane --- Certainty= 0.768(Affirmative) < succ>

5

The protein has no homology with sequences in the databases, although it is similar to HMW1 from *Haemophilus influenzae*.

The protein was expressed in *E.coli* as an insoluble 43.56kDa His-fusion product and then purified.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

10

Example 107

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 213> which encodes amino acid sequence <SEQ ID 214; NGS107>. Analysis of this protein sequence reveals the following:

Signal Score (-7.5): -3.83
Possible cleavage site: 51
>>> Seems to have no N-terminal signal seq.
Amino Acid Composition of Predicted Mature Form:
calculated from 1
ALOM: Finding transmembrane regions (Klein et al.)
count: 0 value: 4.61 threshold: 0.0
PERIPHERAL Likelihood = 4.61
modified ALOM score: -1.42
Rule: cytoplasmic protein

*** Reasoning Step: 2

----- Final Results -----

bacterial cytoplasm --- Certainty= 0.146(Affirmative) < succ>

30

The protein has no homology with sequences in the databases.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 108

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 215> which encodes amino acid sequence <SEQ ID 216; NGS108>. Analysis of this protein sequence reveals the following:

GvH: Examining signal sequence (von Heijne)
Signal Score (-7.5): -6.14
Possible cleavage site: 19
>>> Seems to have no N-terminal signal seq.
Amino Acid Composition of Predicted Mature Form:
calculated from 1
ALOM: Finding transmembrane regions (Klein et al.)
count: 0 value: 8.43 threshold: 0.0
PERIPHERAL Likelihood = 8.43
modified ALOM score: -2.19
Rule: cytoplasmic protein

*** Reasoning Step: 2

----- Final Results -----

50

-126-

bacterial cytoplasm --- Certainty= 0.574(Affirmative) < succ>
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

5

The protein has homology with the following sequences in the databases:

>pir||G81977 probable lipoprotein NMA0586 [imported] - Neisseria meningitidis
 (group A strain Z2491)
 emb|CAB83877.1| (AL162753) putative lipoprotein [Neisseria meningitidis Z2491]
 Length = 280

Score = 52.9 bits (126), Expect = 5e-06
 Identities = 43/134 (32%), Positives = 63/134 (46%), Gaps = 23/134 (17%)

15 Query: 174 LGDIRGVATDEDKLPKAGSFQYEGRAFGNGVLSKESLDNHNGVFRYTIDFDRRKSGSGI 233
 +GDI G T DKLP+ G Y G AFG D+ +G YTIDF ++G G I
 Sbjct: 156 IGDIAGEHTSFDKLPEGGRATYRGTAFGS-----DDASGKLTYTIDFAAKQGHGKI 206

20 Query: 234 EGMEQYQYKIKLEAAIERIPYRESGSSSLGLKDRVSYFGVNEGVMLEKDNEIKKYHLGIF 293
 E ++ ++ ++ AA + P ++ + + ++L E Y LGIF
 Sbjct: 207 EHLKS-PELNVDLAASDIKPKKRHAVI-----SGSVLYNQAEGKSYSLGIF 252

Query: 294 GEAANEVAGAVSQE 307
 G A EVAG+ E
 25 Sbjct: 253 GGQAQEVAGSAEVE 266

>pir||D81032 hypothetical protein NMB1870 [imported] - Neisseria meningitidis
 (group B strain MD58)
 gb|AAF42204.1| (AE002537) hypothetical protein [Neisseria meningitidis MC58]
 Length = 320

30 Score = 50.6 bits (120), Expect = 3e-05
 Identities = 50/168 (29%), Positives = 76/168 (44%), Gaps = 28/168 (16%)

35 Query: 136 VYEQPYSVVRGYFGYSRKDGNPIEGDQNPPEIIPFDLYLGDIVGVATDEDKLPKAGSFQY 195
 VY+Q +S + + +D E G+ + F +GDI G T DKLP+ G Y
 Sbjct: 163 VYKQSHSALTAFQTEQIQDS---EHSCKMVAKRQFR--IGDIAGEHTSFDKLPEGGRATY 217

40 Query: 196 EGRAFGNGVLSKESLDNHNGVFRYTIDFDRRKSGSIEGMEQYQYKIKLEAAIERIPYR 255
 G AFG D+ G YTIDF ++G+G IE ++ ++ ++ AA + P
 Sbjct: 218 RGTAFGS-----DDAGGKLTYTIDFAAKQGNKIEHLKS-PELNVDLAADIKPDG 267

Query: 256 ESGSSSLGLKDRVSYFGVNEGVMLEKDNEIKKYHLGIFGEAANEVAGA 303
 + + + ++L E Y LGIF A EVAG+
 45 Sbjct: 268 KRHAVI-----SGSVLYNQAEGKSYSLGIFGGKAQEVAGS 302

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 109

50 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 217> which encodes amino acid sequence <SEQ ID 218; NGS109>. Analysis of this protein sequence reveals the following:

GvH: Examining signal sequence (von Heijne)
 Signal Score (-7.5): -5.39
 Possible cleavage site: 25
 55 >>> Seems to have no N-terminal signal seq.
 Amino Acid Composition of Predicted Mature Form:
 calculated from 1
 ALOM: Finding transmembrane regions (Klein et al.)
 count: 0 value: 7.00 threshold: 0.0
 60 PERIPHERAL Likelihood = 7.00
 modified ALOM score: -1.90

-127-

Rule: cytoplasmic protein

*** Reasoning Step: 2

5 ----- Final Results -----

10 bacterial cytoplasm --- Certainty= 0.353(Affirmative) < succ>
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

The protein has homology with the following sequences in the databases:

15 >pir||A82012 hypothetical protein NMA0179 [imported] - Neisseria meningitidis
 (group A strain Z2491)
 emb|CAB83494.1| (AL162752) hypothetical protein NMA0179 [Neisseria meningitidis
 Z2491]
 Length = 97

20 Score = 183 bits (464), Expect = 1e-45
 Identities = 92/97 (94%), Positives = 95/97 (97%)

25 Query: 44 MKANDKLNKQIDVLQKQSAATHNEAYIEMNTLLYRHREVVS+HNRKADYAEKGKRIALF 103
 MK NDKLNKQIDVLQKQSAATHNEAYIEMNTLLYRHREVVS+HNRKADYAEKGKE+IALF
 Sbjct: 1 MKTNDKLNKQIDVLQKQSAATHNEAYIEMNTLLYRHREVVS+HNRKADYAEKGKEQIALF 60

Query: 104 PRGLNGITKLPAAVLLPERPYHFDKMEVLYIFSRIIPR 140
 PRGLNGITKLPAAVLLPERPYHFDKMEVL+IFS IPR
 Sbjct: 61 PRGLNGITKLPAAVLLPERPYHFDKMEVLHIFSWIPR 97

30 As a homolog was found in serogroup A *N.meningitidis* but not in serogroup B, NGS109 protein and nucleic acid are useful for distinguishing between gonococcus and serogroup B *N.meningitidis*.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 110

35 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 219> which encodes amino acid sequence <SEQ ID 220; NGS110>. Analysis of this protein sequence reveals the following:

40 GvH: Examining signal sequence (von Heijne)
 Signal Score (-7.5): -2.76
 Possible cleavage site: 41
 >>> Seems to have no N-terminal signal seq.
 Amino Acid Composition of Predicted Mature Form:
 calculated from 1
 ALOM: Finding transmembrane regions (Klein et al.)
 count: 1 value: -0.00 threshold: 0.0
 45 INTEGRAL Likelihood = -0.00 Transmembrane 88 - 104 (88 - 104)
 PERIPHERAL Likelihood = 7.69
 modified ALOM score: 0.50
 Rule: cytoplasmic membrane protein

50 *** Reasoning Step: 2

----- Final Results -----

55 bacterial inner membrane --- Certainty= 0.100(Affirmative) < succ>
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
 bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

The protein has no homology with sequences in the databases.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 111

- 5 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 221> which encodes amino acid sequence <SEQ ID 222; NGS111>. Analysis of this protein sequence reveals the following:

```

10 GvH: Examining signal sequence (von Heijne)
    Signal Score (-7.5): -5.89
    Possible cleavage site: 21
    >>> Seems to have no N-terminal signal seq.
    Amino Acid Composition of Predicted Mature Form:
        calculated from 1
    ALOM: Finding transmembrane regions (Klein et al.)
        count: 0 value: 2.44 threshold: 0.0
15    PERIPHERAL Likelihood = 2.44
        modified ALOM score: -0.99
    Rule: cytoplasmic protein

    *** Reasoning Step: 2

20 ----- Final Results -----

        bacterial cytoplasm --- Certainty= 0.293(Affirmative) < succ>
        bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
25        bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
        bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

```

The protein has homology with the following sequences in the databases:

```

30 >gb|AAC45840.1| (AF001598) restriction endonuclease [Neisseria gonorrhoeae]
    Length = 374

    Score = 539 bits (1390), Expect = e-152
    Identities = 285/285 (100%), Positives = 285/285 (100%)

35 Query: 1 MGFIEPFLSSYTPLSRDYVQARTNRKRQTLLSKIVYTHSGFQRSVTENSNIHQINFLIKT 60
    MGFIEPFLSSYTPLSRDYVQARTNRKRQTLLSKIVYTHSGFQRSVTENSNIHQINFLIKT
    Sbjct: 90 MGFIEPFLSSYTPLSRDYVQARTNRKRQTLLSKIVYTHSGFQRSVTENSNIHQINFLIKT 149

40 Query: 61 LVEHPQGKLNKKEIAAMMLVDLKTFFQDDYLTETELNDYFQQGIESGFIERKYNQISYLWN 120
    LVEHPQGKLNKKEIAAMMLVDLKTFFQDDYLTETELNDYFQQGIESGFIERKYNQISYLWN
    Sbjct: 150 LVEHPQGKLNKKEIAAMMLVDLKTFFQDDYLTETELNDYFQQGIESGFIERKYNQISYLWN 209

45 Query: 121 LLDKLDLKRVDGDDLYFAEDAQRIFGNLDEITVRKRDPLYHRLYKNQLQEESSEHYGNVK 180
    LLDKLDLKRVDGDDLYFAEDAQRIFGNLDEITVRKRDPLYHRLYKNQLQEESSEHYGNVK
    Sbjct: 210 LLDKLDLKRVDGDDLYFAEDAQRIFGNLDEITVRKRDPLYHRLYKNQLQEESSEHYGNVK 269

50 Query: 181 CMLEKLAYPVLIAASHIKPFILSDDTEAYDPNNGLLLSRTLDSLFDLKYISFDDEGNMVK 240
    CMLEKLAYPVLIAASHIKPFILSDDTEAYDPNNGLLLSRTLDSLFDLKYISFDDEGNMVK
    Sbjct: 270 CMLEKLAYPVLIAASHIKPFILSDDTEAYDPNNGLLLSRTLDSLFDLKYISFDDEGNMVK 329

    Query: 241 KRLSDDVWRRWCDVKLDNNLLNDRKRSYLAYHRELMLQEDQEFHI 285
    KRLSDDVWRRWCDVKLDNNLLNDRKRSYLAYHRELMLQEDQEFHI
    Sbjct: 330 KRLSDDVWRRWCDVKLDNNLLNDRKRSYLAYHRELMLQEDQEFHI 374

```

- 55 Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 112

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 223> which encodes amino acid sequence <SEQ ID 224; NGS112>. Analysis of this protein sequence reveals the following:

```

5   GvH Examining signal sequence (von Heijne)
      Signal Score (-7.5): -9.08
      Possible cleavage site: 54
      >>> Seems to have no N-terminal signal seq.
      Amino Acid Composition of Predicted Mature Form:
      calculated from 1
10  ALOM: Finding transmembrane regions (Klein et al.)
      count: 1 value: -1.22 threshold: 0.0
      INTEGRAL Likelihood = -1.22 Transmembrane 160 - 176 ( 160 - 177)
      PERIPHERAL Likelihood = 0.58
      modified ALOM score: 0.74
15  Rule: cytoplasmic membrane protein

      *** Reasoning Step: 2

      ----- Final Results -----

20      bacterial inner membrane --- Certainty= 0.149(Affirmative) < succ>
      bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
      bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
      bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>
25

The protein has homology to the following sequences in the databases:

      ^ **gbp_12644572 gi|12644572|sp|Q50973|T2B1_NEIGO TYPE II RESTRICTION
      ENZYME NGOBI (ENDONUCLEASE NGOBI) (R.NGOBI) (R.NGOI)
      gb|AAB03207.2| (U42459) NgoI restriction endonuclease R.NgoI [N.gonorrhoeae]
30      Length = 350

      Score = 694 bits (1791), Expect = 0.0
      Identities = 349/350 (99%), Positives = 349/350 (99%)

35  Query: 1 MTLEEQQAKEALDGIKKSRVHLYKPIQIAEILYHDCIKQLDFLNLDTYRNQSKRWDE 60
      MTLEEQQAKEALDGIKKSRVHLYKPIQIAEILYHDCIKQLDFLNLDTYRNQSKRWDE
      Sbjct: 1 MTLEEQQAKEALDGIKKSRVHLYKPIQIAEILYHDCIKQLDFLNLDTYRNQSKRWDE 60

40  Query: 61 ICRRFLGRISTSSAKFQDNLFKNAIPPEKLAVLGTNLNRSDDGGVESYIYKQFFNRFSQM 120
      ICRRFLGRISTSSAKFQDNLFKNAIPPEKLAVLGTNLNRSDDGGVESYIYKQFFNRFSQM
      Sbjct: 61 ICRRFLGRISTSSAKFQDNLFKNAIPPEKLAVLGTNLNRSDDGGVESYIYKQFFNRFSQM 120

      Query: 121 SEALAYVGNTDRYSFQLSEFLNLFWLEPGLKRSIDKIYEIVVYALFDALVSELGITVSID 180
      SE LAYVGNTDRYSFQLSEFLNLFWLEPGLKRSIDKIYEIVVYALFDALVSELGITVSID
45  Sbjct: 121 SERLAYVGNTDRYSFQLSEFLNLFWLEPGLKRSIDKIYEIVVYALFDALVSELGITVSID 180

      Query: 181 FPKENLFLWEEYQDFAEKIITMPKNEHLKLPKIHVRVGTNAADRGLDMWSNFGGLAIQVK 240
      FPKENLFLWEEYQDFAEKIITMPKNEHLKLPKIHVRVGTNAADRGLDMWSNFGGLAIQVK
      Sbjct: 181 FPKENLFLWEEYQDFAEKIITMPKNEHLKLPKIHVRVGTNAADRGLDMWSNFGGLAIQVK 240
50

      Query: 241 HLSLDEELAEDIVSSISADRVIVCKKAEQSVIVSLLTQIGWKSRIQNIIVTEDDLISWYE 300
      HLSLDEELAEDIVSSISADRVIVCKKAEQSVIVSLLTQIGWKSRIQNIIVTEDDLISWYE
      Sbjct: 241 HLSLDEELAEDIVSSISADRVIVCKKAEQSVIVSLLTQIGWKSRIQNIIVTEDDLISWYE 300

55  Query: 301 KALRGQYPIAEALLENIKTEIMREFFAVNEANEFLDFAQNRGYDITVTHF 350
      KALRGQYPIAEALLENIKTEIMREFFAVNEANEFLDFAQNRGYDITVTHF
      Sbjct: 301 KALRGQYPIAEALLENIKTEIMREFFAVNEANEFLDFAQNRGYDITVTHF 350

```

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 113

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 225> which encodes amino acid sequence <SEQ ID 226; NGS113>. Analysis of this protein sequence reveals the following:

```

5   GvH Examining signal sequence (von Heijne)
      Signal Score (~7.5): -1.7
      Possible cleavage site: 43
      >>> Seems to have no N-terminal signal seq.
      Amino Acid Composition of Predicted Mature Form:
          calculated from 1
10  ALOM: Finding transmembrane regions (Klein et al.)
      count: 4   value: -9.77 threshold: 0.0
      INTEGRAL   Likelihood = -9.77   Transmembrane 187 - 203 ( 183 - 208)
      INTEGRAL   Likelihood = -7.22   Transmembrane 25 - 41 ( 19 - 46)
      INTEGRAL   Likelihood = -4.14   Transmembrane 139 - 155 ( 138 - 155)
15  INTEGRAL   Likelihood = -2.87   Transmembrane 86 - 102 ( 85 - 102)
      PERIPHERAL Likelihood = 1.27
      modified ALOM score: 2.45
      Rule: cytoplasmic membrane protein

20  *** Reasoning Step: 2

      ----- Final Results -----

25  bacterial inner membrane --- Certainty= 0.491(Affirmative) < succ>
      bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
      bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
      bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

```

The protein has homology to the following sequences in the databases:

```

30  ^ **gbp_15902668 gi|15902668|ref|NP_358218.1| \ (NC_003098) ABC
      transporter membrane-spanning permease - glutamine
      transport [Streptococcus pneumoniae R6]
      gb|AAK99428.1| (AE008440) ABC transporter membrane-spanning permease - glutamine
      transport [Streptococcus pneumoniae R6]
35  Length = 226

      Score = 218 bits (556), Expect = 7e-56
      Identities = 113/218 (51%), Positives = 155/218 (70%)

40  Query: 1  MNWPYLIDAVPKFADA AKLTLELSVYG VVLSLLFGLPVAVVTAYRIRPFYALARAYIELS 60
      M+W +.. +P + A LTL ++V+G++ S L GL V+++ YRI +A AYIELS
      Sbjct: 1  MDWSIVEQYLPLYQKAFFLT LHI AVWGILGSFLLGLIVSIIRHYRIPVLAQVATAYIELS 60

      Query: 61 RNTPLLIQLFFLYYGLPKMGIKWDGFTCGVIALVFLGASYMAEAVRAGILAVPKQGVGAG 120
      RNTPLLIQLFFLY+GLP++GI C + LVFLG SYMAE+ R+G+ A+ + Q G
45  Sbjct: 61 RNTPLLIQLFFLYFGLPRIGIVLSSEVCATLGLVFLGGSYMAESFRSGLEAISQTQQEIG 120

      Query: 121 KAIGLSRFQVFRYVELPQVWAVAVPAIGANILFLMKETSVVSTVGIABLLFVTKDVIGMD 180
      AIGL+ QVFRYV LPQ AVA+P+ AN++FL+KETSV S V +A+L++V KD+IG+
50  Sbjct: 121 LAIGLTPLQVFRYVVLQPQATAVALPSPSANVIFLIKETSVFSAVALADLMYVAKDLIGLY 180

      Query: 181 YKTNEALFLLFAAYLIILLPVSL LARRIENRVRSAKYG 218
      Y+T+ AL +L AYLI+LLP+SL+ IE R+R A +G
      Sbjct: 181 YETDIALAMLVVAYLIMLLPISLVFSWIERRIRHAGFG 218
55

```

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 114

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 227> which encodes amino acid sequence <SEQ ID 228; NGS114>. Analysis of this protein sequence reveals the following:

```

5   GvH Examining signal sequence (von Heijne)
      Signal Score (-7.5): -0.46
      Possible cleavage site: 17
      >>> Seems to have a cleavable N-term signal seq.
      Amino Acid Composition of Predicted Mature Form:
      calculated from 18
10  ALOM: Finding transmembrane regions (Klein et al.)
      count: 3   value: -5.36 threshold: 0.0
      INTEGRAL   Likelihood = -5.36   Transmembrane 50 - 66 ( 47 - 67)
      INTEGRAL   Likelihood = -4.83   Transmembrane 183 - 199 ( 176 - 200)
      INTEGRAL   Likelihood = -1.81   Transmembrane 72 - 88 ( 72 - 88)
15  PERIPHERAL Likelihood = 0.26
      modified ALOM score: 1.57
      Rule: cytoplasmic membrane protein

      *** Reasoning Step: 2

20  ----- Final Results -----

      bacterial inner membrane --- Certainty= 0.314(Affirmative) < succ>
      bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
25  bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
      bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

```

The protein has homology to the following sequences in the databases:

```

30  ^ **gbp_15902667 gi|15902667|ref|NP_358217.1| \ (NC_003098) ABC
      transporter membrane-spanning permease - glutamine
      transport [Streptococcus pneumoniae R6]
      gb|AAK99427.1| (AE008440) ABC transporter membrane-spanning permease - glutamine
      transport [Streptococcus pneumoniae R6]
      Length = 225

35  Score = 218 bits (555), Expect = 9e-56
      Identities = 111/206 (53%), Positives = 151/206 (72%)

40  Query: 3  EGLLLTAQISLISVAASCVLGTLFGLVLRNRNLVRFVGRFYLETIRIVPILVWLFGLYF 62
      +GL +T IS++SV S + GT+ G+++ S +R++RF+ R YLE IRI+P LV LF +YF
      Sbjct: 20 QQLGVTIGISILSVLLSMMFGTVMGIIMTSHSRIIRFLTRLYLEFIRIMPQLVLLFIVYF 79

      Query: 63 GLSVWTGIHIGGFVVCVWVFSLWGV AEMGDLVRGALESIEKHQVESGLAPGLSRGQVFR 122
      GL+ I+I G + VF+LWG AEMGDLVRGA+ S+ KHQ ESG A GL+ Q++
45  Sbjct: 80 GLARNFNINISGETSAITVFTLWGTAEMGDLVRGAITSLPKHQFESGQALGLTNVQLYYH 139

      Query: 123 IELPQSIRRVLP GAVNLFTRMIKTSSLAWLIGVIEVVKVGQQIIE NSLLTQPNASFVWYG 182
      I +PQ +RR+LP A+NL TRMIKT+SL LIGV+EV KVGQQII+++ LT P ASFW+YG
50  Sbjct: 140 IIIPQVLRLLPQAINLVTRMIKTSSLVVLIGVVEVTKVGQQIIDS NRLLTIPTASFWTYG 199

      Query: 183 LIFMLYFFCCWPLSLLAAKLEQKWEH 208
      I +LYF C+P+S L+ LE+ W +
      Sbjct: 200 TILVLYFAVCYPISKLSHLEKHWRN 225

```

55 Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 115

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 229> which encodes amino acid sequence <SEQ ID 230; NGS115>. Analysis of this protein sequence reveals the following:

-132-

GvH Examining signal sequence (von Heijne).
 Signal Score (-7.5): -0.639999
 Possible cleavage site: 38
 >>> May be a lipoprotein
 5 Amino Acid Composition of Predicted Mature Form:
 calculated from 23
 ALOM: Finding transmembrane regions (Klein et al.)
 count: 0 value: 5.25 threshold: 0.0
 PERIPHERAL Likelihood = 5.25
 10 modified ALOM score: -1.55
 Rule: inner or outer membrane protein
 Rule: inner or outer membrane protein
 *** Reasoning Step: 2
 15 Lipoprotein?
 Inner membrane?
 ----- Final Results -----
 20 bacterial outer membrane --- Certainty= 0.790(Affirmative) < succ>
 bacterial inner membrane --- Certainty= 0.700(Affirmative) < succ>
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
 bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>
 25 The protein has homology to the following sequences in the databases:
 ^ **gbp_4588485 gi|4588485|gb|AAD26123.1| \ (AF109148) antigenic protein
 [Actinobacillus pleuropneumoniae]
 Length = 278
 30 Score = 407 bits (1045), Expect = e-112
 Identities = 212/282 (75%), Positives = 242/282 (85%), Gaps = 7/282 (2%)
 35 Query: 1 MKLNAKLKALLASAAIAVGLTACGGSGDAQSSQSSGAA-TVAAIKEKGVIRIGVFGDKP 59
 MKL+ LK LLA+A A LTAC +A ++QSS A +VA IKEKGVIRIGVFGDKP
 Sbjct: 1 MKLSTTLKTLTATAITAFALTACD-----NANNAQSSSTAKDSVAQIKEKGVIRIGVFGDKP 56
 40 Query: 60 PFGYVDANGKNQGF DVEIAKDLAKDLLGSPDKVEFVLTEAANRVEYVRSQKVDLILANFT 119
 PFGYVDANGK+QGF DVEIAK++A DLLGS DKVEFVLTEAANRVEY++S KVDLILANFT
 Sbjct: 57 PFGYVDANGKSQGF DVEIAKEIANDLLGSSDKVEFVLTEAANRVEYLKSNKVDLILANFT 116
 45 Query: 120 QTPERAFAVDFA PVMKVALGVVSPKNKPITDMAQLKDQTLVKNKGT TADAF FTKSHPEV 179
 +TPERA E VDFA PVM VALGVVSPK + I+D+ QL+ +TLLVKNKGT TADA+FTK+HPE+
 Sbjct: 117 KTPERA EVVDF A PVMNVALGVVSPK VRLISDLKQLEGKTLVKNKGT TADAYFTKNHPEI 176
 50 Query: 180 KLLKFDQNTETFDALKDGRGVALAHDNALWAWAKENPNFEVAIGNLGPAEFIAPAVQKG 239
 LLLKFDQNTETFDALKDGRGVALAHDNAL+WAWAKENP F+VAIG++GPAE IAPAVQKG
 Sbjct: 177 NLLKFDQNTETFDALKDGRGVALAHDNALVWAWAKENPTFDVAIGSVGP AEQIAPAVQKG 236
 Query: 240 NADLLNWVNGEIAAMKKDGR LKAAYEKTLLPVYGEKV KPEAL 281
 N LL+ +N EIA K +G+LKAAYEKT L+PVY G+ KPE L
 Sbjct: 237 NQALLDVINK EIAEFK TNGKLKAAYEKT LVPVYGD--KPELL 276

55 The protein was expressed in *E.coli* as a soluble 28.16kDa His-fusion product, lacking its leader peptide
 and its poly-glycine sequence (GGGSG), and then purified.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be
 useful antigens for vaccines or diagnostics.

Example 116

60 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 231> which encodes amino acid sequence
 <SEQ ID 232; NGS116>. Analysis of this protein sequence reveals the following:

-133-

GvH Examining signal sequence (von Heijne)
 Signal Score (-7.5): -7.13
 Possible cleavage site: 61
 >>> Seems to have no N-terminal signal seq.
 5 Amino Acid Composition of Predicted Mature Form:
 calculated from 1
 ALOM: Finding transmembrane regions (Klein et al.)
 count: 1 value: -1.86 threshold: 0.0
 INTEGRAL Likelihood = -1.86 Transmembrane 51 - 67 (51 - 67)
 10 PERIPHERAL Likelihood = 1.54
 modified ALOM score: 0.87
 Rule: cytoplasmic membrane protein
 *** Reasoning Step: 2
 15 ----- Final Results -----
 bacterial inner membrane --- Certainty= 0.174(Affirmative) < succ>
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
 20 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
 bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

The protein has no homology to sequences in the databases.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be
 25 useful antigens for vaccines or diagnostics.

Example 117

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 233> which encodes amino acid sequence
 <SEQ ID 234; NGS117>. Analysis of this protein sequence reveals the following:

GvH Examining signal sequence (von Heijne)
 Signal Score (-7.5): 0.25
 Possible cleavage site: 40
 >>> Seems to have a cleavable N-term signal seq.
 Amino Acid Composition of Predicted Mature Form:
 calculated from 41
 35 ALOM: Finding transmembrane regions (Klein et al.)
 count: 2 value: -4.57 threshold: 0.0
 INTEGRAL Likelihood = -4.57 Transmembrane 100 - 116 (99 - 118)
 INTEGRAL Likelihood = -1.59 Transmembrane 54 - 70 (54 - 70)
 40 PERIPHERAL Likelihood = 0.53
 modified ALOM score: 1.41
 Rule: cytoplasmic membrane protein
 *** Reasoning Step: 2
 45 ----- Final Results -----
 bacterial inner membrane --- Certainty= 0.283(Affirmative) < succ>
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
 50 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
 bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

The protein has homology to the following sequences in the databases:

^ **gbp_15793413 gi|15793413|ref|NP_283235.1| \ (NC_003116) putative
 integral membrane protein [Neisseria meningitidis Z2491]
 55 pir||C81957 probable integral membrane protein NMA0408 [imported] - Neisseria
 meningitidis (group A strain Z2491)
 emb|CAB83707.1| (AL162753) putative integral membrane protein [Neisseria
 meningitidis Z2491]
 Length = 550
 60

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Score = 1115 bits (2885), Expect = 0.0
Identities = 539/550 (98%), Positives = 545/550 (99%)

```

5  Query: 1  MVAYAFLEFLFVTAALVLLIRSHYRWTFYFFASALFVFLAGGMLMLTAQWQORALNFASVWFV 60
    Sbjct: 1  MVAYFLFLFVTAALVLLIRSHYRWTFYFFASALFVFLAGGMLMLTAQWQORALNFASVWFV 60

10 Query: 61  VLILFHRLKIHYYKQPLISDFLLIADWRNWETLFHYKEAVIGMAGLLALAGYAVFGWSG 120
    Sbjct: 61  VLILFHRLKIHYYKQPLISDFLLIADWRNWETLFHYKEAVIGMAGLLALAAAYAVFGWSG 120

15 Query: 121 ADSLGMPWRWAGAVLFAAAFVSVRHFSKHGPAVKTWLDLSDPDDGRDVFNLNPMSCRAVFF 180
    Sbjct: 121 ADSLDVFWWRWAGAVLFAAAFVSMRHFSKHGPAVKTWLDLSDPDDGRDVFNLNPMSCRAVFF 180

20 Query: 181 QVPVFECDGEAFARQMPSETRPYGMSDEKPDIVVTLMESTLDPHCDFDFAAAKIPDLKMFG 240
    Sbjct: 181 QVPVFECDGEAFARQMPSETRPCGMSDEKPDIVVTLMESTLDPHCDFDFAAAKIPDLKMFG 240

25 Query: 241 RQEDTVFSSPLRVHTFGGATWKSEFAFLAGVPSTDFGALASGVFYSVPHLQTGFVRNLR 300
    Sbjct: 241 RQEDTVFSSPLRVHTFGGATWKSEFAFLAGVPSTDFGALASGVFYSVPHLQTGFVRNLR 300

30 Query: 301 EHGFCVALSPFTKGNYNAAAYDHFNFNLMFQPDGLGYPAPMGKNLWHISSEEMMQYAR 360
    Sbjct: 301 EHGFCVALSPFTKGNYNAAAYDHFNFNLMFQPDGLGYPAPMGKNLWHISSEEMMQYAR 360

35 Query: 361 MILEKRHPDLENVRQPMFVYVLTMKHEGFPYRTDTDNVFDLADPDLNAKTVSALNDYIGRI 420
    Sbjct: 361 MILEKRHPDLENVRQPMFVYVLTMKHEGFPYRTDTDNVFDLADPDLNAKTVSALNDYIGRI 420

40 Query: 421 ADLDKAVESFDRLYHERGKPFVFGYFGDHQVPFEGVSVRKKWDYAQPDYVTQFAVRSNIA 480
    Sbjct: 421 ADLDKAVESFDRLYHERGKPFVFGYFGDHQVPFEGVSVRKKWDYAQPDYVTQFAVRSNIA 480

45 Query: 481 GGFVQRQDFLDLAFAGGVLMEAAAGLEAKDGFMRANMAMRGLCGGGLEDPCPNRELVGNYRN 540
    Sbjct: 481 GGFVQRQDFLDLAFAGGVLMEAAAGLEAKDGFMRANMAMRGLCGGGLEDPCPNELVGNYRN 540

50 Query: 541 YLYDVLKIA 550
    Sbjct: 541 YLYDVLKIA 550

```

45 A homolog was found in serogroup A *N.meningitidis* but not in serogroup B, so NGS117 protein and nucleic acid are useful for distinguishing between gonococcus and serogroup B *N.meningitidis*.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 118

50 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 235> which encodes amino acid sequence <SEQ ID 236; NGS118>. Analysis of this protein sequence reveals the following:

```

55  GVH Examining signal sequence (von Heijne)
    Signal Score (-7.5): 0.59
    Possible cleavage site: 19
    >>> May be a lipoprotein
    Amino Acid Composition of Predicted Mature Form:
    calculated from 22
    ALOM: Finding transmembrane regions (Klein et al.)
    count: 0 value: 8.33 threshold: 0.0
    PERIPHERAL Likelihood = 8.33
60  modified ALOM score: -2.17

```


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Rule: inner or outer membrane protein
 Rule: inner or outer membrane protein

*** Reasoning Step: 2

Lipoprotein?
 Inner membrane?

----- Final Results -----

bacterial outer membrane --- Certainty= 0.790(Affirmative) < succ>
 bacterial inner membrane --- Certainty= 0.700(Affirmative) < succ>
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
 bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

The protein has no homology to sequences in the databases.

The protein was expressed in *E.coli* as a soluble 12.98kDa His-fusion product and then purified.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 119

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 237> which encodes amino acid sequence <SEQ ID 238; NGS119>. Analysis of this protein sequence reveals the following:

GvH Examining signal sequence (von Heijne)
 Signal Score (-7.5): -4.75
 Possible cleavage site: 47
 >>> Seems to have no N-terminal signal seq.
 Amino Acid Composition of Predicted Mature Form:
 calculated from 1
 ALOM: Finding transmembrane regions (Klein et al.)
 count: 0 value: 7.69 threshold: 0.0
 PERIPHERAL Likelihood = 7.69
 modified ALOM score: -2.04
 Rule: cytoplasmic protein

*** Reasoning Step: 2

----- Final Results -----

bacterial cytoplasm --- Certainty= 0.213(Affirmative) < succ>
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

The protein has homology to the following sequences in the databases:

^ **gbp_2625122 gi|2625122|gb|AAB86635.1| \ (AF031495) putative
 hemoglobin receptor component precursor HpuA [*Neisseria gonorrhoeae*]
 Length = 360

Score = 668 bits (1724), Expect = 0.0
 Identities = 331/331 (100%), Positives = 331/331 (100%)

Query: 1 VSIPTATPLPAGEVTLSSDNGNIENINTAGAGSASDAPSRRRSLDAAPQNTSGISIRQR 60
 VSIPTATPLPAGEVTLSSDNGNIENINTAGAGSASDAPSRRRSLDAAPQNTSGISIRQR
 Sbjct: 30 VSIPTATPLPAGEVTLSSDNGNIENINTAGAGSASDAPSRRRSLDAAPQNTSGISIRQR 89

Query: 61 EVEKDYFGYKSKETSIFIKTPGGAQYALSSYADPITVSYSSPDFKIPDRHAGQRLADGSR 120
 EVEKDYFGYKSKETSIFIKTPGGAQYALSSYADPITVSYSSPDFKIPDRHAGQRLADGSR
 Sbjct: 90 EVEKDYFGYKSKETSIFIKTPGGAQYALSSYADPITVSYSSPDFKIPDRHAGQRLADGSR 149

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Query: 121 IFICCSDSGATSYAEITKQDYMKGAWIGPNGEIDLFAGGFPVGKTPPPAFSYGSSTPET 180
 IFICCSDSGATSYAEITKQDYMKGAWIGPNGEIDLFAGGFPVGKTPPPAFSYGSSTPET
 5 Sbjct: 150 IFICCSDSGATSYAEITKQDYMKGAWIGPNGEIDLFAGGFPVGKTPPPAFSYGSSTPET 209

Query: 181 ALSKKGKITYQVWGIRVRNGQFVTSSYTPPKSGSYGTLANTPVLSTFANFNSNTLAGKI 240
 ALSKKGKITYQVWGIRVRNGQFVTSSYTPPKSGSYGTLANTPVLSTFANFNSNTLAGKI
 Sbjct: 210 ALSKKGKITYQVWGIRVRNGQFVTSSYTPPKSGSYGTLANTPVLSTFANFNSNTLAGKI 269

10 Query: 241 LGNSDYGPDVDIQNATITGPTFSGDATSGGKSGKLEGGKFFGKFASTRSSEVSIGGKITFD 300
 LGNSDYGPDVDIQNATITGPTFSGDATSGGKSGKLEGGKFFGKFASTRSSEVSIGGKITFD
 Sbjct: 270 LGNSDYGPDVDIQNATITGPTFSGDATSGGKSGKLEGGKFFGKFASTRSSEVSIGGKITFD 329

15 Query: 301 GDRSLDTVFGGVSYEKKLDDTSQDTNHLTKQ 331
 GDRSLDTVFGGVSYEKKLDDTSQDTNHLTKQ
 Sbjct: 330 GDRSLDTVFGGVSYEKKLDDTSQDTNHLTKQ 360

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

20 Example 120

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 239> which encodes amino acid sequence <SEQ ID 240; NGS120>. Analysis of this protein sequence reveals the following:

GvH Examining signal sequence (von Heijne)
 Signal Score (-7.5): -7.24
 25 Possible cleavage site: 38
 >>> Seems to have no N-terminal signal seq.
 Amino Acid Composition of Predicted Mature Form:
 calculated from 1
 30 ALOM: Finding transmembrane regions (Klein et al.)
 count: 0 value: 6.42 threshold: 0.0
 PERIPHERAL Likelihood = 6.42
 modified ALOM score: -1.78
 Rule: cytoplasmic protein

35 *** Reasoning Step: 2

----- Final Results -----

40 bacterial cytoplasm --- Certainty= 0.280(Affirmative) < succ>
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

The protein has homology to the following sequences in the databases:

45 ^ **gsa_AAR91313 *N. gonorrhoeae* glycosyltransferase LgtC
 |WO9610086-A1|09-JUL-1996
 Length = 306

Score = 535 bits (1379), Expect = e-151
 50 Identities = 252/253 (99%), Positives = 252/253 (99%)

Query: 8 GGGNIRFIDVNPEDFAGFPLNIRHISITTYARLKLGEYIADCDKVLVLDTDVLVRDGLKP 67
 GGGNIRFIDVNPEDFAGFPLNIRHISITTYARLKLGEYIADCDKVLVLDTDVLVRDGLKP
 Sbjct: 54 GGGNIRFIDVNPEDFAGFPLNIRHISITTYARLKLGEYIADCDKVLVLDTDVLVRDGLKP 113

55 Query: 68 LWDTDLGGNWVGACIDLFVERQEGYKQKIGMADGEYYFNAGVLLINLKKWRRHDIKMSC 127
 LWDTDLGGNWVGACIDLFVERQEGYKQKIGMADGEYYFNAGVLLINLKKWRRHDIKMSC
 Sbjct: 114 LWDTDLGGNWVGACIDLFVERQEGYKQKIGMADGEYYFNAGVLLINLKKWRRHDIKMSC 173

60 Query: 128 EWVEQYKDVMQYQDQDILNGLFKGGVCYANSRNFNMPNTNYAFMANGFASRHTDPLVLDRT 187
 EWVEQYKDVMQYQDQDILNGLFKGGVCYANSRNFNMPNTNYAFMANGFASRHTDPLVLDRT

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Sbjct: 174 EWVEQYKDVMOYQDQDILNGLFKGGVCYANSRNFMPNTNYAFMANGFASRHTDPLYLDRT 233

Query: 188 NTAMPVAVSHYCGSAKPWHRDCTVWGAERFTELAGSLTTPPEWRGKLAVPPTKRLQRW 247

NTAMPVAVSHYCGSAKPWHRDCTVWGAERFTELAGSLTTPPEWRGKLAVPPTK MLQRW

5 Sbjct: 234 NTAMPVAVSHYCGSAKPWHRDCTVWGAERFTELAGSLTTPPEWRGKLAVPPTKMLQRW 293

Query: 248 RKKLSARFLRKIY 260

RKKLSARFLRKIY

10 Sbjct: 294 RKKLSARFLRKIY 306

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 121

15 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 241> which encodes amino acid sequence <SEQ ID 242; NGS121>. Analysis of this protein sequence reveals the following:

GvH Examining signal sequence (von Heijne)
Signal Score (-7.5): -6.22
Possible cleavage site: 37
>>> Seems to have no N-terminal signal seq.
20 Amino Acid Composition of Predicted Mature Form:
calculated from 1
ALOM: Finding transmembrane regions (Klein et al.)
count: 0 value: 3.23 threshold: 0.0
PERIPHERAL Likelihood = 3.23
25 modified ALOM score: -1.15
Rule: cytoplasmic protein
*** Reasoning Step: 2
30 ----- Final Results -----
bacterial cytoplasm --- Certainty= 0.402(Affirmative) < succ>
bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
35 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

The protein has homology to the following sequences in the databases:

40 ^ **gbp_15281345 gi|15281345|dbj|BAB63435.1| \ (AB058945) DNA adenine
methylase M.Ssu4109IB [Streptococcus suis]
Length = 271
Score = 269 bits (687), Expect = 4e-71
Identities = 127/211 (60%), Positives = 158/211 (74%), Gaps = 1/211 (0%)
45 Query: 1 MIFADPPYFLSNDGFSCQNGQMVSVNKGNWDKSKGMAADLEFYEEWLRRLCYALLKPNGTI 60
MIFADPPYFLSN G S GQ+VSV+KG+WDK + EF +W+RL +LKPNGTI
Sbjct: 44 MIFADPPYFLSNGGISNSGGQVVSVDKGDWDKVNLSLEEKHEFNRRKWIRLAKNVLPNGTI 103
Query: 61 WVCGTFHNIYILIGYLMQTVGYHILNNITWEKPNPPNLSRFFTHSTETILWAKK-NKKA 119
50 W+ G+FHNIY +G ++ G+ ILNNITW+K NP PNLSCR+FTHTSTETILWA+K +KKA
Sbjct: 104 WISGSFHNIYSVGMALQEGEFKILNNITWQKTNPAPNLSCRYFTHSTETILWARKDDKKA 163
Query: 120 KHTFHYEMKKAQNNGKQMKCVWTFAPPNKTEKTFGKHPTQKPLPLLERCILSASNIGDLI 179
+H ++YE+MK N+GQMK VW K+EK GKHPQKP LLER IL+++ GD I
55 Sbjct: 164 RHYYNYELMKELNDGKQMKDVVVGGLTKKSEKWAGKHPTQKPEYLLERIILASTREGDYI 223
Query: 180 FDPFMGSGTTGVAALKHGRRF CGCELEEDFL 210
DPF+GSGTTGV A + GR+F G + E D+L
60 Sbjct: 224 LDPFVSGSGTTGVVAKRLGRKFIGIDAERDYL 254

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 122

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 243> which encodes amino acid sequence
5 <SEQ ID 244; NGS122>. Analysis of this protein sequence reveals the following:

```

    GvH Examining signal sequence (von Heijne)
      Signal Score (-7.5): -2.55
      Possible cleavage site: 23
    >>> May be a lipoprotein
10  Amino Acid Composition of Predicted Mature Form:
      calculated from 15
    ALOM: Finding transmembrane regions (Klein et al.)
      count: 0 value: 11.46 threshold: 0.0
      PERIPHERAL Likelihood = 11.46
15  modified ALOM score: -2.79
    Rule: inner or outer membrane protein
    Rule: inner or outer membrane protein

    *** Reasoning Step: 2
20  Lipoprotein?
    Inner membrane?

    ----- Final Results -----
25  bacterial outer membrane --- Certainty= 0.790(Affirmative) < succ>
      bacterial inner membrane --- Certainty= 0.700(Affirmative) < succ>
      bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
      bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>
30
```

The protein has no homology to sequences in the databases:

The protein was expressed in *E.coli* as an insoluble 14.85kDa His-fusion product and then purified.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

35 Example 123

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 245> which encodes amino acid sequence
<SEQ ID 246; NGS123>. Analysis of this protein sequence reveals the following:

```

    GvH Examining signal sequence (von Heijne)
      Signal Score (-7.5): -5.65
      Possible cleavage site: 20
40  >>> Seems to have no N-terminal signal seq.
    Amino Acid Composition of Predicted Mature Form:
      calculated from 1
    ALOM: Finding transmembrane regions (Klein et al.)
45  count: 0 value: 4.24 threshold: 0.0
      PERIPHERAL Likelihood = 4.24
      modified ALOM score: -1.35
    Rule: cytoplasmic protein

    *** Reasoning Step: 2
50  ----- Final Results -----

      bacterial cytoplasm --- Certainty= 0.404(Affirmative) < succ>

```


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bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

5 The protein has no homology to the sequences in the databases.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 124

10 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 247> which encodes amino acid sequence <SEQ ID 248; NGS124>. Analysis of this protein sequence reveals the following:

GvH Examining signal sequence (von Heijne)
 Signal Score (-7.5): -5
 Possible cleavage site: 18
 >>> Seems to have no N-terminal signal seq.
 15 Amino Acid Composition of Predicted Mature Form:
 calculated from 1
 ALOM: Finding transmembrane regions (Klein et al.)
 count: 1 value: -1.59 threshold: 0.0
 INTEGRAL Likelihood = -1.59 Transmembrane 289 - 305 (289 - 305)
 20 PERIPHERAL Likelihood = 3.76
 modified ALOM score: 0.82
 Rule: cytoplasmic membrane protein
 *** Reasoning Step: 2
 25 ----- Final Results -----
 bacterial inner membrane --- Certainty= 0.164(Affirmative) < succ>
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
 30 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
 bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

The protein has homology to the following sequences in the databases:

35 ^ **gbp_1617515 gi|1617515|gb|AAC82509.1| \ (U65994) pilin gene inverting
 protein homolog PivNG [Neisseria gonorrhoeae]
 Length = 320
 Score = 614 bits (1584), Expect = e-175
 Identities = 311/320 (97%), Positives = 316/320 (98%)
 40 Query: 1 MRNTVGLDISKLTFTDATAMVGKTEHSAKFDNDSKGLDQFSDRLKSLGYQNLHICMEATGS 60
 MRN VGLDISKLTFA+AMVGKTEHSAKFDNDSKGLDQFSDRLKSLG QNLHICMEATG+
 Sbjct: 1 MRNAVGLDISKLTFTNASAMVGKTEHSAKFDNDSKGLDQFSDRLKSLGCQNLHICMEATGN 60
 45 Query: 61 YYEEVADYFAQYYSVYVVNPLKISKYAESRFKRTKTDKQDAKLIQYCRSAQESLVKRQ 120
 YYEEVADYFAQYYSVYVVNPLKISKYAESRFKRTKTDKQDAKLIQYCR A+ESLVKRQ
 Sbjct: 61 YYEEVADYFAQYYSVYVVNPLKISKYAESRFKRTKTDKQDAKLIQYCR LAKESLVKRQ 120
 50 Query: 121 KPTDEQYRLSRMTAAYAQAQIKSECAAMKNRHHAAKDEEAAKAYAEI IKAMNEQLEVLKEKI 180
 KPTDEQYRL RMTAAYAQAQIKSECAAMKNRHHAAKDEEAAKAYA+I IKAMNEQLEVLKEKI
 Sbjct: 121 KPTDEQYRLLRMTAAYAQAQIKSECAAMKNRHHAAKDERAAKAYAQI IKAMNEQLEVLKEKI 180
 Query: 181 KEQTEKPNCKEGVKRLETIPAIGRMTAAVLFFHHLTSSKFETSNKFAAFAGLSPQOKESGT 240
 KEQTEKPNCKEGVKRLETIPAIGRMTAAVLFFHHLTSSKFETSNKFAAFAGLSPQOKESGT
 55 Sbjct: 181 KEQTEKPNCKEGVKRLETIPAIGRMTAAVLFFHHLTSSKFETSNKFAAFAGLSPQOKESGT 240
 Query: 241 SVRGKGKLTGFGNRKLRVLFMPAMVAYRIRAFPDFIKRLEEKKKPKKVIIAALMRKLAV 300
 SVRGKGKLTGFGNRKLRVLFMPAMVAYRIRAFPDFIKRLEEKKKPKKVIIAALMRKLAV
 Sbjct: 241 SVRGKGKLTGFGNRKLRVLFMPAMVAYRIRAFPDFIKRLEEKKKPKKVIIAALMRKLAV 300
 60

Query: 301 IAYHVHKKGGDYDPSRYKSA 320
 IAYHVHKKGGDYDPSRYKSA
 Sbjct: 301 IAYHVHKKGGDYDPSRYKSA 320

- 5 Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 125

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 249> which encodes amino acid sequence <SEQ ID 250; NGS127>. Analysis of this protein sequence reveals the following:

10 GvH Examining signal sequence (von Heijne)
 Signal Score (~7.5): -5.8
 Possible cleavage site: 52
 >>> Seems to have no N-terminal signal seq.
 Amino Acid Composition of Predicted Mature Form:
 15 calculated from 1
 ALOM: Finding transmembrane regions (Klein et al.)
 count: 0 value: 1.70 threshold: 0.0
 PERIPHERAL Likelihood = 1.70
 modified ALOM score: -0.84
 20 Rule: cytoplasmic protein
 *** Reasoning Step: 2
 ----- Final Results -----
 25 bacterial cytoplasm --- Certainty= 0.383(Affirmative) < succ>
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>
 30

The protein has homology to the following sequences in the databases:

^ **gbp_1076012 gi|1076012|pir||B55225 stress-sensitive restriction
 system protein 2 - Corynebacterium glutamicum (ATCC 13032)
 35 gb|AAC00044.1| (U13922) This orf may encode a typeI or typeIII restriction
 endonuclease which is stress-sensitive and
 ATP-dependent. It contains a typical ATP binding region
 (Walker motif) [Corynebacterium glutamicum]
 Length = 632
 40 Score = 298 bits (764), Expect = 2e-79
 Identities = 199/633 (31%), Positives = 321/633 (50%), Gaps = 32/633 (5%)
 Query: 2 LRTYLNQLTP-PELADSVKNTVDGFMEKLSQTEPKIA-QNVLLLGNVQSGKTAQVLGVLS 59
 L Y+ L+ +L + V TVD F + I+ Q VLL G+VQSGKT+ +LG+++
 45 Sbjct: 7 LNNYITSLSDNADLREKVTATVDAFRHTVMDDFDYISDQQVLLYGDVQSGKTSMLGIIA 66
 Query: 60 ALADDGDHKVFLYLTTDSVDLQDQTVKRKANLKNFIVLSEADDRSFMEVMKAENP--IL 117
 D H + + LT+ + L QT R + +V F K+ P +
 50 Sbjct: 67 DCLDSTPHTIVI-LTSPNTRLVQQTYDRVAQAFPDTLVCDRDRGYNDFRANQKSLTPRKSI 125
 Query: 118 VVIKKNARVLKRWRNLFASQSSSLKGYPLVIVDDEADAASLNTNSDKPAKDASTINKLLND 177
 VV+ K VL W +F +L G+P++I+DDEADA SLNT ++ D STIN L
 Sbjct: 126 VVGKIPAVLGNWLRVFNDSGALSGHPVLIIDDEADATSLNTEKVNQ--SDVSTINEQLTS 183
 55 Query: 178 IKNSCCQSLFIQLTATPQSLLLQHEESDWQPEFIHFFEAGEKYIGGNFVFSPPS-YIVR 236
 I++ +++Q+T TPQ++LLQ ++S+W E + F GE YIGG FS+ + Y+
 Sbjct: 184 IRDLATGCIYLQVTGTPQAVLLQSDSNWAAEHVLFHAPGESYIGGQLFFSELNNPYLRL 243
 Query: 237 FIDSELDDMKDESGEIAEGAKQALLSFLITCAEFALCDKANCNFALHPSYKIQDHQAFSK 296
 F +++ D+ S A+ ++L+T A F L ++ C +HPS+ H+ F++
 60 Sbjct: 244 FANTQFDEDSRFS-----DAITYTYLLTAALFKLRGESLCTMLIHPSHTASSHRDFAQ 295

Query: 297 KIQAFNLNDLVQAVNNGEDLAGSFKESYLDLQKTKPDIIHFDEIYEKLTALLENKQISTLV 356
 ++ L + + +F+ +Y L +T ++ +I L + ++ I +
 Sbjct: 296 EARLQLTFAFERFYEPF-IQHNFRAYEQLAQTDSNLPPLRKILNLLGGMEDDFSIIH--I 352

Query: 357 VNSQTET-DFDLKGFNIIIGGNVIGRGLTIPKLQTVYYSRTAKKPNADTFWQHSRIFGY 415
 VNS T + D G+NII+GGN +GRGLT LQTV+Y R +K+P ADT WQH+R+FGY
 Sbjct: 353 VNSDNPTVEEDWADGYNIIVGGNSLGRGLTFNNLQTVFYVRESKRQPADTLWQHARMFGY 412

Query: 416 DRDKSLRLRYIPFDVYFFVQLNQAANNLIIGQAKNSG--GNIQVIYPKNINPTRKNVLKF 473
 R K +R+++P + F ++ N I Q + +I+VI + PTR NVL
 Sbjct: 413 KRHKDTMRVFMPTIAQTFFQEVYLGNEAIKNQLDHGTHINDIRVILGDGVAPTRANVLDK 472

Query: 474 DSINQIVGGVNYFPLHPNEDNLSEINKILPSILKDEIQSDLYQIDIEDLFLVLDRKGRYV 533
 + + GGVNYF P N+ ++K L + L + I + + +L+
 Sbjct: 473 RKGVNLGGVNYFAADPRIKNVEALDKKLLAYLDKHGEDS--TIGMRAITILNAF--TVD 529

Query: 534 PDDWNKEKFIAGVEALKAQRPSEFKTYVLIKTGRKLSRATGTMLSEDDRKLGEKYPNDLFL 593
 P+D + F A + + +P ++++T RK+++ TG +LS D+ L L
 Sbjct: 530 PNDLDLATFKAALLDFERNQPHLTARMVLRNTRKVNQGTGALLSPTDQALSRAEVAHPLL 589

Query: 594 TLYQVVGNDKKG-----WQGDFFWLPNIKLP 619
 LY++ G D W W+PNIKLP
 Sbjct: 590 ILYRIEGVNDAAAQRGEPTWSSDPIWVVPNIKLP 622

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 126

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 251> which encodes amino acid sequence <SEQ ID 252; NGS128>. Analysis of this protein sequence reveals the following:

GvH Examining signal sequence (von Heijne)
 Signal Score (-7.5): -4.98
 Possible cleavage site: 20
 >>> Seems to have no N-terminal signal seq.

Amino Acid Composition of Predicted Mature Form:
 calculated from 1
 ALOM: Finding transmembrane regions (Klein et al.)
 count: 0 value: 7.37 threshold: 0.0
 PERIPHERAL Likelihood = 7.37
 modified ALOM score: -1.97
 Rule: cytoplasmic protein

*** Reasoning Step: 2

----- Final Results -----

bacterial cytoplasm --- Certainty= 0.225(Affirmative) < succ>
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

The protein has homology to the following sequences in the databases:

^ **gbp_11387195 gi|11387195|sp|Q50976|T2F7_NEIGO TYPE II RESTRICTION
 ENZYME NGOFVII (ENDONUCLEASE NGOFVII) (R.NGOFVII)
 (R.NGOVII)

pir||T10166 restriction endonuclease (EC 3.1.21.-) NgoVII - *N.gonorrhoeae*
 gb|AAA86271.1| (U43736) R.NgoVII [*Neisseria gonorrhoeae*]
 Length = 326

Score = 651 bits (1679), Expect = 0.0
 Identities = 317/326 (97%), Positives = 320/326 (97%)

Query: 1 MNTVFSNIAKITEKSLNAVWMDLFSKSADEVLMATGYVSNDAVVELHKILELNDHIQKI 60
 MNTVFSNIAKITEKSLNAVWMDLFSKSADEVLMATGYVSNDAVVELHKILELNDHIQKI
 Sbjct: 1 MNTVFSNIAKITEKSLNAVWMDLFSKSADEVLMATGYVSNDAVVELHKILELNDHIQKI 60
 5
 Query: 61 DLLVGMHYLEGFSLQYDSLCKLNDFLRHEKRGAVVSPFVKFHGKMSFKNYQKINGLI 120
 DLLVGMHYLEGFSLQYDSLCKLNDFLRHEKRGAVVSPFVKFHGKMSFKNYQKINGLI
 Sbjct: 61 DLLVGMHYLEGFSLQYDSLCKLNDFLRHEKRGAVVSPFVKFHGKMSFKNYQKINGLI 120
 10
 Query: 121 GSANLTCFWDSTERTYETMLHLNGKPAQILQADIQSTIHLGKNIQEVERPSKFIHNSH 180
 GSANLTCFWDSTERTYETMLHLNGKPAQILQADIQSTIHLGKNIQEVERPSKFIHNSH
 Sbjct: 121 GSANLTCFWDSTERTYETMLHLNGKPAQILQADIQSTIHLGKNIQEVERPSKFIHNSH 180
 15
 Query: 181 LENC LGVQKIAPEQIRQLFAQTSEYHFSIPAKTEEKS NLNVFFGEGRRDKRGFVKPRPWY 240
 LENC LGVQKIAPEQIRQLFAQTSEYHFSIPAKTEEKS NLNVFFGEGRRDKRGFVKPRPWY
 Sbjct: 181 LENC LGVQKIAPEQIRQLFAQTSEYHFSIPAKTEEKS NLNVFFGEGRRDKRGFVKPRPWY 240
 20
 Query: 241 EVELIVSKDITSQEGYPVLKSFTVITDDGWQFQCKTSGDY SKNFRSENDLKT LGKWKIGR 300
 EVELIVSKDITSQEGYPVLKSFTVITDDGWQFQCKTSGDY SK + +LKT LGKWKIGR
 Sbjct: 241 EVELIVSKDITSQEGYPVLKSFTVITDDGWQFQCKTSGDY SKTSTQKMN LKT LGKWKIGR 300
 Query: 301 LESHGCLQNN EKITHETLREYGN DHF 326
 LESHGCLQNN EKITHETLREYGN+ F
 Sbjct: 301 LESHGCLQNN EKITHETLREYGN ESF 326
 25

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 127

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 253> which encodes amino acid sequence <SEQ ID 254; NGS129>. Analysis of this protein sequence reveals the following:

30 GvH Examining signal sequence (von Heijne)
 Signal Score (-7.5): -5.5
 Possible cleavage site: 48
 >>> Seems to have no N-terminal signal seq.
 35 Amino Acid Composition of Predicted Mature Form:
 calculated from 1
 ALOM: Finding transmembrane regions (Klein et al.)
 count: 0 value: 10.03 threshold: 0.0
 PERIPHERAL Likelihood = 10.03
 40 modified ALOM score: -2.51
 Rule: cytoplasmic protein
 *** Reasoning Step: 2
 45 ----- Final Results -----
 bacterial cytoplasm --- Certainty= 0.545(Affirmative) < succ>
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
 50 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

The protein has homology to the following sequences in the databases:

55 ^ **gbp_15804186 gi|15804186|ref|NP_290225.1| \ (NC_002655)
 DNA-damage-inducible protein [Escherichia coli O157:H7
 EDL933]
 ref|NP_312547.1| (NC_002695) DNA-damage-inducible protein [Escherichia coli
 O157:H7]
 gb|AAG58789.1|AE005591_13 (AE005591) DNA-damage-inducible protein [Escherichia
 coli O157:H7
 60 EDL933]

dbj|BAB37943.1| (AP002566) DNA-damage-inducible protein [Escherichia coli O157:H7]

Length = 278

5 Score = 340 bits (872), Expect = 2e-92
Identities = 161/266 (60%), Positives = 197/266 (73%)

Query: 1 MTTENNAFENAKHIDETGNEYWSARTLQQILEYSEWRNFQRAIDKAITACETSGNDKNHH 60
M + FE +H G E+WSAR L +L+Y +WRNFQ+ + +A ACE S + H
10 Sbjct: 5 MNEHHQPFEIRHYGTEGQEFWSARELAPLLDYRDWRNFQKVLARATQACEASNQAASDH 64

Query: 61 FVETNMIALGKGGQREVADYRLSRYACYLIVQNGDPSKSVIAAGQTYFAVQARRQELQD 120
FVET KM+ LG G QRE+ D LSRACYL+VQNGDP+K VIAAGQTYFA+Q RRQEL D
15 Sbjct: 65 FVETTKMVLGSGAQRELEVDVHLSRYACYLVVQNGDPAKPVIAAGQTYFAIQTTRQELAD 124

Query: 121 EAAFRSLGEDKQRLLLRRQLREHNTDLAAAKDAGVEKPVYAVFQNHGYRGLYGGLDKQ 180
+ AF+ L ED++RL LR +L+EHN L AA+ A V ++A+FQNHGY+GLYGGLD++
Sbjct: 125 DEAFKQLREDEKRLFLRNELKEHNKQLVEAAQQAAVATATDFAIFQNHGYQGGLYGGLDQK 184

20 Query: 181 GIHSRKLKKSQRILDHMNASEPAAANLFRATQTEKLRRKNIQKQTQANRVHFEVQKVR 240
IH KGLKKSQ+ILDHM ++E AANLFRATQTEKL+R + K QAN HF+VG KVR
Sbjct: 185 AIHQLKGLKKSQKILDHMGSTELAANLFRATQTEKLKRDGVNSKQQANTTHFDVGSKVR 244

Query: 241 QTIEELGGIMPENQPVPEKSIKQLEN 266
QTI+ELGG MPE P P+ SIKQLEN
25 Sbjct: 245 QTIQELGGTMPEELPTPQVSIKQLEN 270

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

30 Example 128

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 255> which encodes amino acid sequence <SEQ ID 256; NGS130>. Analysis of this protein sequence reveals the following:

GvH Examining signal sequence (von Heijne)
Signal Score (-7.5): -3.68
35 Possible cleavage site: 14
>>> Seems to have an uncleavable N-term signal seq
Amino Acid Composition of Predicted Mature Form:
calculated from 1

40 ALOM: Finding transmembrane regions (Klein et al.)
count: 3 value: -3.45 threshold: 0.0
INTEGRAL Likelihood = -3.45 Transmembrane 68 - 84 (68 - 92)
INTEGRAL Likelihood = -1.59 Transmembrane 10 - 26 (10 - 26)
INTEGRAL Likelihood = -1.44 Transmembrane 46 - 62 (45 - 62)
PERIPHERAL Likelihood = 1.48
45 modified ALOM score: 1.19
Rule: cytoplasmic membrane protein

*** Reasoning Step: 2

50 ----- Final Results -----

bacterial inner membrane --- Certainty= 0.238(Affirmative) < succ>
bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
55 bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

The protein has homology to the following sequences in the databases:

60 ^ **gbp_17988861 gi|17988861|ref|NP_541494.1| \ (NC_003318) hypothetical
protein [Brucella melitensis]
gb|AAL53758.1| (AB009687) hypothetical protein [Brucella melitensis]
Length = 99

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Score = 108 bits (270), Expect = 3e-23
 Identities = 59/91 (64%), Positives = 69/91 (74%)

5 Query: 11 LLFSCMLAVTCPTRLIGFFALNRNRLSRRRAQTVMEAAPGCVLISVIAPYFVSDKPHELIA 70
 L M +VT TR+ G+ LRNRTL S RA VMEAAPGCVLISVIAP FVSDKP LIA
 Sbjct: 8 LTLAMASVTYLTRIGGYVLLRNRTL SNRAMAVMEAAPGCVLISVIAPDFVSDKPANLIA 67

10 Query: 71 IALTAFAACRF SMLPTVLIGVGSSSGISGWL M 101
 +A+T FAA RFSML TVLIG+G++ I +L+
 Sbjct: 68 LAVTVFAATRF SMLPTVLIGMGAASICRYLI 98

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

15 Example 129

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 257> which encodes amino acid sequence <SEQ ID 258; NGS131>. Analysis of this protein sequence reveals the following:

GvH Examining signal sequence (von Heijne)
 Signal Score (-7.5): -1.65
 Possible cleavage site: 43
 >>> Seems to have no N-terminal signal seq.
 Amino Acid Composition of Predicted Mature Form:
 calculated from 1

20 ALOM: Finding transmembrane regions (Klein et al.)
 count: 0 value: 7.05 threshold: 0.0
 PERIPHERAL Likelihood = 7.05
 modified ALOM score: -1.91
 Rule: cytoplasmic protein

25 *** Reasoning Step: 2

30 ----- Final Results -----

35 bacterial cytoplasm --- Certainty= 0.152(Affirmative) < succ>
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

The protein has homology to the following sequences in the databases:

40 ^ **gbp_16760390 gi|16760390|ref|NP_456007.1| \ (NC_003198) hypothetical
 protein [Salmonella enterica subsp. enterica serovar
 Typhi]
 emb|CAD01841.1| (AL627270) hypothetical protein [Salmonella enterica subsp.
 enterica serovar Typhi]
 45 Length = 227

Score = 104 bits (259), Expect = 2e-21
 Identities = 68/221 (30%), Positives = 115/221 (51%), Gaps = 11/221 (4%)

50 Query: 2 DKEKVL D K I K K L A L G R S V N E H E A A Q A L R Q A Q A L M E K Y K V N A E D I A L S K V S E Q R A D -- R K 59
 D++K ++K+K K L A L S N H E A A A L R + A + L M + + + D I A + S + E +
 Sbjct: 3 D Q D K H I E K L K K L L A L A A S G N P H E A A L A L R R A R K L M D V H G I T H S D I A M S D I D E T I S H Y W P T 62

55 Query: 60 M A F K L A G W Q W G V A N M I A D I F G C K S Y Q R G K T --- M M F Y G I G N R A E T S A Y A F D V V Y R Q I S A D 116
 + + + G + N + I + F G S T + F Y G R A + A Y + V + R Q +
 Sbjct: 63 G S L R P P R Y M L G L M N I I R E A F G V N S I I H P G T Y P G V G F Y G N R E R A A L A A Y T W E V L A R Q L K K A 122

Query: 117 R R K F L K T - C R A G K P S H R T Y L A D R F C G G W I A S A W E T V K K F E M S D E E K A I M D G Y K K E Y P D M 175
 R + + + + + K + R T D + F G W + + + F + + D + E + + M + + + Y P
 60 Sbjct: 123 R Q Q Y I S A Q N K R I K T A T R T S R G D Q F A E G W V L A V I S E I Q S F A L T D D E R E L M Q Q W L E H K Y P Q T 182

Query: 176 AEARTRDAKSSILQSGKMEYEALTRGMESGKQVKLHYAVNG 216
 R R S G Y G G+ V+LH V+G
 Sbjct: 183 QTTRARKPGRS-RNGDASRY-----AGFREGQNVRLHRPVSG 218

- 5 Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 130

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 259> which encodes amino acid sequence <SEQ ID 260; NGS132>. Analysis of this protein sequence reveals the following:

10 GvH Examining signal sequence (von Heijne)
 Signal Score (-7.5): -4.06
 Possible cleavage site: 30
 >>> Seems to have no N-terminal signal seq.
 Amino Acid Composition of Predicted Mature Form:
 15 calculated from 1
 ALOM: Finding transmembrane regions (Klein et al.)
 count: 0 value: 2.49 threshold: 0.0
 PERIPHERAL Likelihood = 2.49
 modified ALOM score: -1.00
 20 Rule: cytoplasmic protein
 *** Reasoning Step: 2
 ----- Final Results -----
 25 bacterial cytoplasm --- Certainty= 0.075(Affirmative) < succ>
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>
 30

The protein has no homology to sequences in the databases.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 131

- 35 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 261> which encodes amino acid sequence <SEQ ID 262; NGS133>. Analysis of this protein sequence reveals the following:

GvH Examining signal sequence (von Heijne)
 Signal Score (-7.5): 1.64
 Possible cleavage site: 53
 40 >>> Seems to have no N-terminal signal seq.
 Amino Acid Composition of Predicted Mature Form:
 calculated from 1
 ALOM: Finding transmembrane regions (Klein et al.)
 count: 0 value: 3.82 threshold: 0.0
 45 PERIPHERAL Likelihood = 3.82
 modified ALOM score: -1.26
 Rule: cytoplasmic protein
 *** Reasoning Step: 2
 50 ----- Final Results -----
 bacterial cytoplasm --- Certainty= 0.068(Affirmative) < succ>
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
 55 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>

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bacterial inner membrane --- Certainty= 0.000 (Not Clear) < succ>

The protein has no homology to the following sequences in the databases:

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be
5 useful antigens for vaccines or diagnostics.

Example 132

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 263> which encodes amino acid sequence
<SEQ ID 264; NGS135>. Analysis of this protein sequence reveals the following:

10 GvH Examining signal sequence (von Heijne)
Signal Score (-7.5): -4.67
Possible cleavage site: 39
>>> Seems to have no N-terminal signal seq.
Amino Acid Composition of Predicted Mature Form:
calculated from 1
15 ALOM: Finding transmembrane regions (Klein et al.)
count: 0 value: 5.52 threshold: 0.0
PERIPHERAL Likelihood = 5.52
modified ALOM score: -1.60
20 Rule: cytoplasmic protein
*** Reasoning Step: 2
----- Final Results -----
25 bacterial cytoplasm --- Certainty= 0.457 (Affirmative) < succ>
bacterial periplasmic space --- Certainty= 0.000 (Not Clear) < succ>
bacterial outer membrane --- Certainty= 0.000 (Not Clear) < succ>
bacterial inner membrane --- Certainty= 0.000 (Not Clear) < succ>

30 The protein has no homology to sequences in the databases:

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be
useful antigens for vaccines or diagnostics.

Example 133

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 265> which encodes amino acid sequence
35 <SEQ ID 266; NGS136>. Analysis of this protein sequence reveals the following:

GvH Examining signal sequence (von Heijne)
Signal Score (-7.5): -3.97
Possible cleavage site: 15
40 >>> Seems to have no N-terminal signal seq.
Amino Acid Composition of Predicted Mature Form:
calculated from 1
ALOM: Finding transmembrane regions (Klein et al.)
count: 0 value: 11.35 threshold: 0.0
PERIPHERAL Likelihood = 11.35
45 modified ALOM score: -2.77
Rule: cytoplasmic protein
*** Reasoning Step: 2
50 ----- Final Results -----
bacterial cytoplasm --- Certainty= 0.523 (Affirmative) < succ>
bacterial periplasmic space --- Certainty= 0.000 (Not Clear) < succ>
bacterial outer membrane --- Certainty= 0.000 (Not Clear) < succ>

bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

The protein has no homology to sequences in the databases:

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be
5 useful antigens for vaccines or diagnostics.

Example 134

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 267> which encodes amino acid sequence
<SEQ ID 268; NGS137>. Analysis of this protein sequence reveals the following:

10 GvH Examining signal sequence (von Heijne)
Signal Score (-7.5): -8.52
Possible cleavage site: 51
>>> Seems to have no N-terminal signal seq.
Amino Acid Composition of Predicted Mature Form:
calculated from 1
15 ALOM: Finding transmembrane regions (Klein et al.)
count: 0 value: 2.81 threshold: 0.0
PERIPHERAL Likelihood = 2.81
modified ALOM score: -1.06
20 Rule: cytoplasmic protein
*** Reasoning Step: 2
----- Final Results -----
25 bacterial cytoplasm --- Certainty= 0.374(Affirmative) < succ>
bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

30 The protein has no homology to sequences in the databases.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be
useful antigens for vaccines or diagnostics.

Example 135

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 269> which encodes amino acid sequence
35 <SEQ ID 270; NGS138>. Analysis of this protein sequence reveals the following:

GvH Examining signal sequence (von Heijne)
Signal Score (-7.5): -7
Possible cleavage site: 36
40 >>> Seems to have no N-terminal signal seq.
Amino Acid Composition of Predicted Mature Form:
calculated from 1
ALOM: Finding transmembrane regions (Klein et al.)
count: 0 value: 10.66 threshold: 0.0
PERIPHERAL Likelihood = 10.66
45 modified ALOM score: -2.63
Rule: cytoplasmic protein
*** Reasoning Step: 2
50 ----- Final Results -----
bacterial cytoplasm --- Certainty= 0.415(Affirmative) < succ>
bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>

bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

The protein has homology to the following sequences in the databases:

```

5   ^ **gbp_13559865 gi|13559865|ref|NP_112075.1| \ (NC_002730) terminase
      small subunit [Bacteriophage HK620]
      gb|AAK28890.1|AF335538_42 (AF335538) terminase small subunit [Bacteriophage
      HK620]
      Length = 140

10  Score = 125 bits (313), Expect = 5e-28
      Identities = 56/122 (45%), Positives = 85/122 (68%)

Query: 4   TKRKLGRPTDYTKDMADKICEKIANGSLRSICAEDGVPPMKTIYRWLEANEFRHQYAR 63
      T+ K GRP+DY ++AD IC +++G SL +C G+P T++RWL +E+FR +YA+
15  Sbjct: 3   TEPKAGRPSDYMEVADDICSLSSGESLLKVCKRPGMPDKSTVFRWLAKHEDFRDKYAK 62

Query: 64   AREKQADYFAEEIIEIADSAQAESAASVSKAKLQIDARKWAASKIAPKKYGDKSELDVKSQDGD 125
      A E +AD EEI EIAD+A ++A V+KA+L++D RKWA +++ P+KYGDK ++ DG
20  Sbjct: 63   ATEARADSIFEEIFEIADNAIPDAAEVAKARLRVDTRKWALARMNPRKYGDKVTNELVGKDG 124

```

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 136

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 271> which encodes amino acid sequence <SEQ ID 272; NGS139>. Analysis of this protein sequence reveals the following:

```

25  GvH Examining signal sequence (von Heijne)
      Signal Score (-7.5): -1.49
      Possible cleavage site: 32
      >>> Seems to have no N-terminal signal seq.
30  Amino Acid Composition of Predicted Mature Form:
      calculated from 1
      ALOM: Finding transmembrane regions (Klein et al.)
      count: 0 value: 8.65 threshold: 0.0
      PERIPHERAL Likelihood = 8.65
35  modified ALOM score: -2.23
      Rule: cytoplasmic protein

      *** Reasoning Step: 2

40  ----- Final Results -----

      bacterial cytoplasm --- Certainty= 0.301(Affirmative) < succ>
      bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
45  bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
      bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

```

The protein has homology to the following sequences in the databases:

```

50  ^ **gbp_16127009 gi|16127009|ref|NP_421573.1| \ (NC_002696) hypothetical
      protein [Caulobacter crescentus]
      gb|AAK24741.1| (AE005943) hypothetical protein [Caulobacter crescentus]
      Length = 184

      Score = 59.7 bits (143), Expect = 4e-08
      Identities = 50/164 (30%), Positives = 74/164 (44%), Gaps = 20/164 (12%)

55  Query: 30   ASGREFRTAYTYTPQWRFSLSFEVLRTKASVNELEKLAGFFNARKGSFESFLYEDPAD-- 87
      ASG E RT+ ++ + R+ ++ ++E+ +L FF AR+G F + DPAD
      Sbjct: 5   ASGHERRTSPWSQSRRLYLIA----TAPRPLDEIAELVAFFEARRGLHGRFRDPADDFK 60

60  Query: 88   -----NAVTDQFVGNTVQGVAR-YQLVRSMSGGFIEPVSAVKERP-----AVKVGGTAL 134

```


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A DQ +G T GV + +QL ++ G E V+ +P V V G L
 Sbjct: 61 SCAPSVQPAAGDQAIG-TGDGVRKAFQLRRITYGAGGEAVARTIAKPVAGTVTVAVAGVVL 119
 Query: 135 AYGRDYTEVTDKGVLFVNTFPQPPGRIITWTGGFYFRVFRFTSDTVD 178
 5 A G G++ NT P G +T F VRF D +D
 Sbjct: 120 APGAFAVDVTGLITLNTAPPAGAAVTAGFAFDTPVRFDLRLD 163

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

10 Example 137

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 273> which encodes amino acid sequence <SEQ ID 274; NGS140>. Analysis of this protein sequence reveals the following:

GvH Examining signal sequence (von Heijne)
 Signal Score (-7.5): -3.86
 15 Possible cleavage site: 31
 >>> Seems to have no N-terminal signal seq.
 Amino Acid Composition of Predicted Mature Form:
 calculated from 1
 ALOM: Finding transmembrane regions (Klein et al.)
 20 count: 1 value: -4.94 threshold: 0.0
 INTEGRAL Likelihood = -4.94 Transmembrane 34 - 50 (31 - 54)
 PERIPHERAL Likelihood = 8.01
 modified ALOM score: 1.49
 Rule: cytoplasmic membrane protein
 25 *** Reasoning Step: 2
 ----- Final Results -----
 30 bacterial inner membrane --- Certainty= 0.297(Affirmative) < succ>
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
 bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

35 The protein has homology to the following sequences in the databases:

^ **gbp_17987625 gi|17987625|ref|NP_540259.1| \ (NC_003317) Hypothetical
 Phage Protein [Brucella melitensis]
 gb|AAL52523.1| (AE009572) Hypothetical Phage Protein [Brucella melitensis]
 40 Length = 144
 Score = 72.4 bits (176), Expect = 5e-12
 Identities = 43/119 (36%), Positives = 64/119 (53%), Gaps = 7/119 (5%)
 Query: 10 RIVEEARSWLGTFPYHHHAMVKAGVDCAMLLVAVYGAV-GLLPGEFDPFRYPQDWHLHRD 68
 45 R++ EA W+GTPY H A G DC L+ ++ A+ G+ PE +P Y DW
 Sbjct: 6 RVLAEAHRWIGTFYRHGASTLGVSCDCLGLVRGIWRALYGVPE--NPGVYAPDWAQVSQ 63
 Query: 69 CERYLGFTVQFC--RETESQAGDIIV--WRFGRSFSGGILAGGGKVIHSYIGRGVVS 123
 + L ++ RE +PQ GD+ V W+ G + H GI+A G+ IH+Y G GV++
 50 Sbjct: 64 GDPMLEAAVRYMVRREEHAPQPGDLLVFRWKPFGFAAKHMGIMAREGRFIHAYQGHGVL 122

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 138

55 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 275> which encodes amino acid sequence <SEQ ID 276; NGS141>. Analysis of this protein sequence reveals the following:

-150-

GvH Examining signal sequence (von Heijne)
 Signal Score (-7.5): 5.35
 Possible cleavage site: 28
 >>> Seems to have a cleavable N-term signal seq.
 5 Amino Acid Composition of Predicted Mature Form:
 calculated from 29
 ALOM: Finding transmembrane regions (Klein et al.)
 count: 0 value: 8.86 threshold: 0.0
 PERIPHERAL Likelihood = 8.86
 10 modified ALOM score: -2.27
 Score for OM-PP discrimination: 1.53
 Rule: outer membrane or periplasmic protein
 Score for OM-PP discrimination: 1.53
 Rule: outer membrane or periplasmic protein
 15 *** Reasoning Step: 2
 Outer membrane? Score: 0.152929
 Outer membrane? Score: 0.152929
 20 ----- Final Results -----
 bacterial outer membrane --- Certainty= 0.512(Affirmative) < succ>
 bacterial periplasmic space --- Certainty= 0.320(Affirmative) < succ>
 25 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>
 bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

The protein has homology to the following sequences in the databases:

30 ^ **gbp_5915870 gi|5915870|sp|Q50940|CAH_NEIGO Carbonic anhydrase
 precursor (Carbonate dehydratase)
 emb|CAA72038.1| (Y11152) carbonic anhydrase [Neisseria gonorrhoeae]
 Length = 252
 Score = 523 bits (1347), Expect = e-147
 35 Identities = 252/252 (100%), Positives = 252/252 (100%)
 Query: 1 MPRFPRTLPRLTAVLLLLACTAFSAAAHGNHHTHWGYTGHDSPESWGNLSEEFRLCSTGKNQ 60
 MPRFPRTLPRLTAVLLLLACTAFSAAAHGNHHTHWGYTGHDSPESWGNLSEEFRLCSTGKNQ
 40 Sbjct: 1 MPRFPRTLPRLTAVLLLLACTAFSAAAHGNHHTHWGYTGHDSPESWGNLSEEFRLCSTGKNQ 60
 Query: 61 SPVNIETVSGKLPKLVNYKPSMVDVENNGHTIQVNYPEGGNTLTVNGRTYTLKQFHFH 120
 SPVNIETVSGKLPKLVNYKPSMVDVENNGHTIQVNYPEGGNTLTVNGRTYTLKQFHFH
 45 Sbjct: 61 SPVNIETVSGKLPKLVNYKPSMVDVENNGHTIQVNYPEGGNTLTVNGRTYTLKQFHFH 120
 Query: 121 VPSENQIKGRTPMEAHFVHLDENKQPLVLAVLYEAGKTNGRLSSIWNVMPMTAGKVKLN 180
 VPSENQIKGRTPMEAHFVHLDENKQPLVLAVLYEAGKTNGRLSSIWNVMPMTAGKVKLN
 50 Sbjct: 121 VPSENQIKGRTPMEAHFVHLDENKQPLVLAVLYEAGKTNGRLSSIWNVMPMTAGKVKLN 180
 Query: 181 QPFDASTLLPKRLKYRFAGSLTTPPCTEGVSWVLKTYDHIDQAQAEKFTRAVGSENNR 240
 QPFDASTLLPKRLKYRFAGSLTTPPCTEGVSWVLKTYDHIDQAQAEKFTRAVGSENNR
 55 Sbjct: 181 QPFDASTLLPKRLKYRFAGSLTTPPCTEGVSWVLKTYDHIDQAQAEKFTRAVGSENNR 240
 Query: 241 FVQPLNARVVIE 252
 FVQPLNARVVIE
 Sbjct: 241 FVQPLNARVVIE 252

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 139

60 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 277> which encodes amino acid sequence <SEQ ID 278; NGS142>. Analysis of this protein sequence reveals the following:

-151-

GvH Examining signal sequence (von Heijne)
 Signal Score (-7.5): -0.49
 Possible cleavage site: 22
 >>> Seems to have no N-terminal signal seq.
 5 Amino Acid Composition of Predicted Mature Form:
 calculated from 1
 ALOM: Finding transmembrane regions (Klein et al.)
 count: 0 value: 1.22 threshold: 0.0
 PERIPHERAL Likelihood = 1.22
 10 modified ALOM score: -0.74
 Rule: cytoplasmic protein
 *** Reasoning Step: 2
 15 ----- Final Results -----
 bacterial cytoplasm --- Certainty= 0.145(Affirmative) < succ>
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
 20 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

The protein has homology to the following sequences in the databases:

^ **gbp_15794480 gi|15794480|ref|NP_284302.1| \ (NC_003116) hypothetical
 protein [Neisseria meningitidis Z2491]
 25 pir|F81851 hypothetical protein NMA1587 [imported] - Neisseria meningitidis
 (group A strain Z2491)
 emb|CAB84814.1| (AL162756) hypothetical protein [Neisseria meningitidis Z2491]
 Length = 181
 30 Score = 358 bits (919), Expect = 6e-98
 Identities = 173/181 (95%), Positives = 178/181 (97%)
 Query: 1 LKTD TARMNNLIPEHLAAYAHSDNLQIEGGHRCFSLSCQGRDTFHIRYYGEPFDGLITDT 60
 +KTDTA+MNNLIPEHLAAYAHSD+LQIEG HRCFSLSCQGRDTFHIRYYGEPFDGL+TDT
 35 Sbjct: 1 MKTD TAKMNNLIPEHLAAYAHSDSLQIEGVHRCFSLSCQGRDTFHIRYYGEPFDGLMTDT 60
 Query: 61 DKAPVKIVAVEAVSGDEIVLFDGAEHGYNAMFCDKYSNQKQNRNLTDLDEYTYRVPIHL 120
 DKAPVKIVAVEAVSGDEIVLFDGAEHGYNAMFCDKYS NQKQNRNLTDLDEYTYRV IHL
 40 Sbjct: 61 DKAPVKIVAVEAVSGDEIVLFDGAEHGYNAMFCDKYSPNQKQNRNLTDLDEYTYRVLIHL 120
 Query: 121 YYNIDYEDEYEDFVNSEGQVPLIDGRIISFDSLKRNGFDAISIDLIDEKHSVRELLNEELS 181
 YYNIDYEDEYEDFVNSEGQVPLIDGRIISFDSLKRNGFDAIS+DLIDEKHSVRELLNEELS
 Sbjct: 121 YYNIDYEDEYEDFVNSEGQVPLIDGRIISFDSLKRNGFDAISVDLIDEKHSVRELLNEELS 181

45 A homolog was found in serogroup A *N.meningitidis* but not in serogroup B, so NGS142 protein and nucleic acid are useful for distinguishing between gonococcus and serogroup B *N.meningitidis*.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 140

50 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 279> which encodes amino acid sequence <SEQ ID 280; NGS143>. Analysis of this protein sequence reveals the following:

GvH Examining signal sequence (von Heijne)
 Signal Score (-7.5): -2.51
 Possible cleavage site: 57
 55 >>> Seems to have no N-terminal signal seq.
 Amino Acid Composition of Predicted Mature Form:
 calculated from 1
 ALOM: Finding transmembrane regions (Klein et al.)
 count: 4 value: -15.23 threshold: 0.0

-152-

INTEGRAL Likelihood = -15.23 Transmembrane 84 - 100 (79 - 107)
 INTEGRAL Likelihood = -8.12 Transmembrane 259 - 275 (250 - 281)
 INTEGRAL Likelihood = -4.14 Transmembrane 159 - 175 (153 - 176)
 INTEGRAL Likelihood = -3.88 Transmembrane 216 - 232 (216 - 235)
 5 PERIPHERAL Likelihood = 1.11
 modified ALOM score: 3.55
 Rule: cytoplasmic membrane protein

*** Reasoning Step: 2

10

----- Final Results -----

bacterial inner membrane --- Certainty= 0.709(Affirmative) < succ>
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
 15 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
 bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

The protein has homology to the following sequences in the databases:

^ **gbp_5764059 gi|5764059|emb|CAB53350.1| \ (AJ010260) NosR protein
 20 [Paracoccus denitrificans]
 Length = 724
 Score = 393 bits (1009), Expect = e-108
 Identities = 191/379 (50%), Positives = 249/379 (65%), Gaps = 22/379 (5%)
 25
 Query: 1 LMVQRVLSVNDKAFVTADLDYELPQAYVDDPKAPPVEISAPVEAVPAAASDTASDGI AE 60
 L+VQR + +K F T DL Y+LPQ Y AP A PAA +D
 Sbjct: 358 LLVQREVGPPIEKVFHTFDLGYQLPQKYLRSIAPAPEA-----AAPAAQAD----- 402
 30
 Query: 61 DASAENGVS NQLWKQIWKAKQGQIVVVGIALTILLVFLPQDWIVRYEKWYDRFRAFLT 120
 E+ QLWK+IW + +I + L +L VF FQ + RYE+ + FR A+LT
 Sbjct: 403 -----ESQAQAQLWKRIWLDSKPKIAGLAAMLVLVTGTVFFQSFTRYERAFYVFRMAYLT 458
 35
 Query: 121 FTLFYIGWYAQAQLSVVNTLTLSAILTEFHWEFFLMDPIVFILWLFTAATMLLWNRGTF 180
 TL ++GWYA AQLSVVN + LF +++ F W+ FL+DP+ FILW AA +L W RG +
 Sbjct: 459 VTLVFLGWYANAQLSVVNLMLFGLSVNGFSWQAFLLDPLTFILWFAVAALLFWGRGAY 518
 Query: 181 CGWLCPFGLQELTNRIAKKLGKQITVPHMLHTRLNVIKYLILFGFLAISLYDLGTAEK 240
 CGWLCPFGLQELTN++A+KL + Q T+P LH RL +KY+I G +SL + AE
 40 Sbjct: 519 CGWLCPFGLQELTNQVARKLRIPQWTLPLWGLHERLWPKYMI FLGLFGVSLMSVEQA EH 578
 Query: 241 FAEVEPFKTAIILKFMCDWWFVFAVAALLIAGLFIERFFCRYLCPLGAGIALPGRFRVFD 300
 AEVEPFKTAIILKF+ W FVA+A ALLIAGLF+ERF+CRYLCPLGA +A+P R R+FD
 Sbjct: 579 LAEVEPFKTAIILKPIRAWPFVAYAAALLIAGLFVERFYCRYLCPLGAALAI PARMRMFD 638
 45
 Query: 301 WLRRYKMCGNPCQICTHECPVQAIAPGEDIHPNECIQCLHCQVMYHHDTRCPQVVAENKK 360
 WL+RY CGNPCQ C +CPVQ+I P G+I+PNECI CLHCQV+Y +T CP V+ KK
 Sbjct: 639 WLKRYHECGNPCQTCARQCPVQSIHPTGEINPNECINCLHCQVLYQSETTCPVVI---KK 695
 50
 Query: 361 KQKQAAAKSGELENVSKQP 379
 +++ A +G + + + P
 Sbjct: 696 LKRREAVAAGSMPKLGQPP 714

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be
 55 useful antigens for vaccines or diagnostics.

Example 141

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 281> which encodes amino acid sequence
 <SEQ ID 282; NGS144>. Analysis of this protein sequence reveals the following:

60 GvH Examining signal sequence (von Heijne)
 Signal Score (-7.5): 1.23
 Possible cleavage site: 21

>>> May be a lipoprotein.

Amino Acid Composition of Predicted Mature Form:
calculated from 20

ALOM: Finding transmembrane regions (Klein et al.)

5 count: 1 value: -0.37 threshold: 0.0

INTEGRAL Likelihood = -0.37 Transmembrane 90 - 106 (89 - 106)

PERIPHERAL Likelihood = 10.82

modified ALOM score: 0.57

10 Rule: inner or outer membrane protein

Rule: inner or outer membrane protein

Rule: cytoplasmic membrane protein

*** Reasoning Step: 2

15 Lipoprotein?

Inner membrane?

----- Final Results -----

20 bacterial outer membrane --- Certainty= 0.790(Affirmative) < succ>

bacterial inner membrane --- Certainty= 0.734(Affirmative) < succ>

bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>

bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

25 The protein has homology no to sequences in the databases.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 142

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 283> which encodes amino acid sequence
30 <SEQ ID 284; NGS145>. Analysis of this protein sequence reveals the following:

GvH Examining signal sequence (von Heijne)

Signal Score (-7.5): 1.5

Possible cleavage site: 19

35 >>> Seems to have a cleavable N-term signal seq.

Amino Acid Composition of Predicted Mature Form:
calculated from 20

ALOM: Finding transmembrane regions (Klein et al.)

count: 0 value: 8.70 threshold: 0.0

PERIPHERAL Likelihood = 8.70

40 modified ALOM score: -2.24

Score for OM-PP discrimination: -9.24

Rule: outer membrane or periplasmic protein

Score for OM-PP discrimination: -9.24

45 Rule: outer membrane or periplasmic protein

*** Reasoning Step: 2

Periplasmic space? Score: 0.924443

Periplasmic space? Score: 0.924443

50 ----- Final Results -----

bacterial periplasmic space --- Certainty= 0.931(Affirmative) < succ>

bacterial outer membrane --- Certainty= 0.231(Affirmative) < succ>

55 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

The protein has homology to the following sequences in the databases:

60 ^ **gbp_5051426 gi|5051426|emb|CAB45007.1| \ (AJ242839) OPCA protein
[Neisseria gonorrhoeae]

-154-

Length = 263

Score = 531 bits (1369), Expect = e-150
 Identities = 262/263 (99%), Positives = 263/263 (99%)

5 Query: 1 MKKALLALTIAAISGTAMAQLPDFLGKGEYTVRTDISKQTLKNADLKEKHVKQKNIGFRA 60
 MKKALLALTIAAISGTAMAQLPDFLGKGEYTVRTDISKQTLKNADLKEKHVKQKNIGFRA
 Sbjct: 1 MKKALLALTIAAISGTAMAQLPDFLGKGEYTVRTDISKQTLKNADLKEKHVKQKNIGFRA 60

10 Query: 61 DMPFDDIHHGMRFEVSHSRDKKDMYVVTESTTKPFGKDVEEKRTDVYAGYTYTQPISEAT 120
 DMPFDDIHHGMRFEVSHSRDKKDMYVVTESTTKPFGKDV+EKRRTDVYAGYTYTQPISEAT
 Sbjct: 61 DMPFDDIHHGMRFEVSHSRDKKDMYVVTESTTKPFGKDVEEKRTDVYAGYTYTQPISEAT 120

15 Query: 121 KLRAGLGLGYEKYKDAVANEKGTVSTEREAFYTKAHADLTSDLGGGWYLNPAEYKVDLD 180
 KLRAGLGLGYEKYKDAVANEKGTVSTEREAFYTKAHADLTSDLGGGWYLNPAEYKVDLD
 Sbjct: 121 KLRAGLGLGYEKYKDAVANEKGTVSTEREAFYTKAHADLTSDLGGGWYLNPAEYKVDLD 180

20 Query: 181 AKLKHNATVAGVSADINAKTRGWGVGVGANIGKQITDTVGIEAGPFYKHRHFKASGSFVL 240
 AKLKHNATVAGVSADINAKTRGWGVGVGANIGKQITDTVGIEAGPFYKHRHFKASGSFVL
 Sbjct: 181 AKLKHNATVAGVSADINAKTRGWGVGVGANIGKQITDTVGIEAGPFYKHRHFKASGSFVL 240

Query: 241 DGGNIRVDPTKINEYGVRVGVKF 263
 DGGNIRVDPTKINEYGVRVGVKF
 Sbjct: 241 DGGNIRVDPTKINEYGVRVGVKF 263

25

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 143

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 285> which encodes amino acid sequence
 30 <SEQ ID 286; NGS146>. Analysis of this protein sequence reveals the following:

GvH Examining signal sequence (von Heijne)
 Signal Score (-7.5): 0.1
 Possible cleavage site: 51
 >>> Seems to have a cleavable N-term signal seq.
 35 Amino Acid Composition of Predicted Mature Form:
 calculated from 52
 ALOM: Finding transmembrane regions (Klein et al.)
 count: 0 value: 3.50 threshold: 0.0
 PERIPHERAL Likelihood = 3.50
 40 modified ALOM score: -1.20
 Score for OM-PP discrimination: -15.70
 Rule: outer membrane or periplasmic protein
 Score for OM-PP discrimination: -15.70
 Rule: outer membrane or periplasmic protein

45 *** Reasoning Step: 2

Periplasmic space? Score: 1.56979
 Periplasmic space? Score: 1.56979

50 ----- Final Results -----

bacterial periplasmic space --- Certainty= 0.944(Affirmative) < succ>
 bacterial outer membrane --- Certainty= 0.375(Affirmative) < succ>
 55 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>
 bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

The protein has homology to the following sequences in the databases:

60 ^ **gbp_5051429 gi|5051429|emb|CAB45013.1| \ (AJ242839) hypothetical
 protein [Neisseria gonorrhoeae]
 length = 109

-155-

Score = 216 bits (549), Expect = 2e-55
 Identities = 109/109 (100%), Positives = 109/109 (100%)

5 Query: 1 MFKRPEEIIIVLILAVLWLAGTYFLAALFGADAYTVLKITALTLWSAASFLLWQKKPQPA 60
 MFKRPEEIIIVLILAVLWLAGTYFLAALFGADAYTVLKITALTLWSAASFLLWQKKPQPA
 Sbjct: 1 MFKRPEEIIIVLILAVLWLAGTYFLAALFGADAYTVLKITALTLWSAASFLLWQKKPQPA 60

10 Query: 61 YLAAARLPDHLVAVSESIGRTRFFTLACIMDVQNHLSPPDSRNRRLSV 109
 YLAAARLPDHLVAVSESIGRTRFFTLACIMDVQNHLSPPDSRNRRLSV
 Sbjct: 61 YLAAARLPDHLVAVSESIGRTRFFTLACIMDVQNHLSPPDSRNRRLSV 109

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

15 Example 144

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 287> which encodes amino acid sequence <SEQ ID 288; NGS147>. Analysis of this protein sequence reveals the following:

20 GvH Examining signal sequence (von Heijne)
 Signal Score (-7.5): -4.09
 Possible cleavage site: 40
 >>> Seems to have no N-terminal signal seq.
 Amino Acid Composition of Predicted Mature Form:
 calculated from 1

25 ALOM: Finding transmembrane regions (Klein et al.)
 count: 1 value: -2.28 threshold: 0.0
 INTEGRAL Likelihood = -2.28 Transmembrane 36 - 52 (36 - 52)
 PERIPHERAL Likelihood = 5.20
 modified ALOM score: 0.96
 Rule: cytoplasmic membrane protein

30 *** Reasoning Step: 2

----- Final Results -----

35 bacterial inner membrane --- Certainty= 0.191(Affirmative) < succ>
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
 bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

40 The protein has homology to the following sequences in the databases:

^ **gbp_6606516 gi|6606516|gb|AAF19189.1|AF200716_2 \ (AF200716)
 trafficking protein B [Neisseria gonorrhoeae]
 Length = 139

45 Score = 274 bits (700), Expect = 7e-73
 Identities = 139/139 (100%), Positives = 139/139 (100%)

50 Query: 2 MILLDTNVISEPLRPQPNERNVAVWLDLILEDVYLSAITVAELRLGVALLNGKKKNVLH 61
 MILLDTNVISEPLRPQPNERNVAVWLDLILEDVYLSAITVAELRLGVALLNGKKKNVLH
 Sbjct: 1 MILLDTNVISEPLRPQPNERNVAVWLDLILEDVYLSAITVAELRLGVALLNGKKKNVLH 60

Query: 62 ERLEQSILPLFAGRILPFDEPVAAIYAQIRSYAKTHGKEIAAADGYIAATAKQHS�TVAT 121
 ERLEQSILPLFAGRILPFDEPVAAIYAQIRSYAKTHGKEIAAADGYIAATAKQHS�TVAT
 Sbjct: 61 ERLEQSILPLFAGRILPFDEPVAAIYAQIRSYAKTHGKEIAAADGYIAATAKQHS�TVAT 120

55 Query: 122 RDTGSFFAADVAVFNPWHD 140
 RDTGSFFAADVAVFNPWHD
 Sbjct: 121 RDTGSFFAADVAVFNPWHD 139

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 145

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 289> which encodes amino acid sequence
5 <SEQ ID 290; NGS148>. Analysis of this protein sequence reveals the following:

```

GvH Examining signal sequence (von Heijne)
Signal Score (-7.5): 0.86
Possible cleavage site: 47
>>> Seems to have a cleavable N-term signal seq.
10 Amino Acid Composition of Predicted Mature Form:
    calculated from 48
ALOM: Finding transmembrane regions (Klein et al.)
    count: 5 value: -15.44 threshold: 0.0
15 INTEGRAL Likelihood = -15.44 Transmembrane 157 - 173 ( 142 - 181)
    INTEGRAL Likelihood = -12.15 Transmembrane 62 - 78 ( 56 - 83)
    INTEGRAL Likelihood = -6.32 Transmembrane 194 - 210 ( 191 - 212)
    INTEGRAL Likelihood = -4.30 Transmembrane 87 - 103 ( 85 - 104)
    INTEGRAL Likelihood = -2.60 Transmembrane 121 - 137 ( 121 - 142)
    PERIPHERAL Likelihood = 2.92
20 modified ALOM score: 3.59
Rule: cytoplasmic membrane protein

*** Reasoning Step: 2

25 ----- Final Results -----

    bacterial inner membrane --- Certainty= 0.718(Affirmative) < succ>
    bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
    bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
30    bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

```

The protein has homology to the following sequences in the databases:

```

^ **gbp_15777859 gi|15777859|gb|AAL05955.1| \ (AY048756) putative cadmium
binding protein [Staphylococcus aureus]
35 Length = 209

Score = 354 bits (908), Expect = 1e-96
Identities = 177/208 (85%), Positives = 194/208 (93%)

40 Query: 14 MRCFMFSTVITA AVL YIATAVDLLVILLIFFARANTRKEYRDIYIGQYLGSVILILVSLF 73
    MRC M TV+ AA VLYIATAVDLLVILLIFFARA TRKEYRDIY+GQYLGS+ILILVSLF
Sbjct: 1 MRCIMIQTVVAAAVLYIATAVDLLVILLIFFARAKTRKEYRDIYVGQYLGSIIILILVSLF 60

45 Query: 74 LAFVLNYVPKRWVLGGLGLPIYLGIKVAIYDDCEGEKRAKKELDEKGLSKLVGIVALVT 133
    LAFVLNYVPKRW+LGLLGLPIYLGIKVAIYDDCEGEKRAKKEL+EKGLSKLVG VA+VT
Sbjct: 61 LAFVLNYVPKRWILGGLGLPIYLGIKVAIYDDCEGEKRAKKELNEKGLSKLVGTVAIVT 120

Query: 134 VASCGADNIGLFVPYFVTLDDLVLVLLVFLILIFVLVYTAQRLANISGVGEIVEKFSR 193
+ASCGADNIGLFVPYFVTL + +LL+TL VFLILIF LV+TAQ+LANI G+GEIVEKFSR
50 Sbjct: 121 IASCGADNIGLFVPYFVTL SVTNLLLTLEFVFLILIFLVTQAQLANIPGIGEIVEKFSR 180

Query: 194 WIMAVIYIGLGLFIIENNTIRTIIISII 221
WIMA+IYI LGLFIIEN+TI+TI+ I
Sbjct: 181 WIMAIYIALGLFIIENDTIQTILGFI 208
55

```

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 146

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 291> which encodes amino acid sequence <SEQ ID 292; NGS149>. Analysis of this protein sequence reveals the following:

```

5   GvH Examining signal sequence (von Heijne)
      Signal Score (-7.5): -0.63
      Possible cleavage site: 43
      >>> Seems to have no N-terminal signal seq.
      Amino Acid Composition of Predicted Mature Form:
      calculated from 1
10  ALOM: Finding transmembrane regions (Klein et al.)
      count: 0 value: 2.12 threshold: 0.0
      PERIPHERAL Likelihood = 2.12
      modified ALOM score: -0.92
      Rule: cytoplasmic protein
15  *** Reasoning Step: 2

      ----- Final Results -----

20      bacterial cytoplasm --- Certainty= 0.122(Affirmative) < succ>
      bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
      bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
      bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

25  The protein has homology to the following sequences in the databases:
      ^ **gbp_15675455 gi|15675455|ref|NP_269629.1| \ (NC_002737) conserved
      hypothetical protein [Streptococcus pyogenes]
      [Streptococcus pyogenes M1 GAS]
      gb|AAK34350.1| (AE006588) conserved hypothetical protein [Streptococcus pyogenes
30  M1 GAS]
      Length = 224

      Score = 106 bits (264), Expect = 3e-22
      Identities = 63/151 (41%), Positives = 85/151 (55%), Gaps = 12/151 (7%)
35  Query: 20  LSALQHAFPCPRQCALIHNEQAWAENYLTAQKALHERVDSDE-PETCKGVRFEWTVHVL 78
      LS +QH+ FC RQ ALIH EQ W +N TA G+ LH + D+ E K + + +
      Sbjct: 11  LSGIQHFQFCKRQWALIHIEQQWLDNEATAHGQVLHTKADNPYIKEKRKELLVSRAMPIS 70

40  Query: 79  ADKLGISGILDVE-----VDTKTGRLEK--VEYKRGKPKPDGDEIQLCAQGLCL 127
      + +LG+SGI+D+VE + K G+ P VEYKRGKPK D D +QL AQ +CL
      Sbjct: 71  SAELGLSGIMDVVEFYKDDQGVSLRGKRGKWLPKVVEYKRGKPKKDTRDIVQLVAQTMCL 130

      Query: 128 EEMTGQTVSEGLWYMQTRHRVPVVFSDGLR 158
      EE ++EG L+Y RV V + LR
45  Sbjct: 131 EETLDCDINEGCLYYHSVNQRVIVPMTSALR 161

```

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

50 Example 147

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 293> which encodes amino acid sequence <SEQ ID 294; NGS150>. Analysis of this protein sequence reveals the following:

```

55  GvH Examining signal sequence (von Heijne)
      Signal Score (-7.5): -0.71
      Possible cleavage site: 19
      >>> Seems to have no N-terminal signal seq.
      Amino Acid Composition of Predicted Mature Form:
      calculated from 1

```


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ALOM: Finding transmembrane regions (Klein et al.)
 count: 1 value: -0.85 threshold: 0.0
 INTEGRAL Likelihood = -0.85 Transmembrane 79 - 95 (79 - 96)
 PERIPHERAL Likelihood = 6.52
 modified ALOM score: 0.67
 Rule: cytoplasmic membrane protein

*** Reasoning Step: 2

----- Final Results -----

bacterial inner membrane --- Certainty= 0.134(Affirmative) < succ>
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
 bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

The protein has no homology to sequences in the databases.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 148

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 295> which encodes amino acid sequence <SEQ ID 296; NGS151>. Analysis of this protein sequence reveals the following:

GvH Examining signal sequence (von Heijne)
 Signal Score (-7.5): 3.47
 Possible cleavage site: 23
 >>> Seems to have a cleavable N-term signal seq.
 Amino Acid Composition of Predicted Mature Form:
 calculated from 24
 ALOM: Finding transmembrane regions (Klein et al.)
 count: 0 value: 14.32 threshold: 0.0
 PERIPHERAL Likelihood = 14.32
 modified ALOM score: -3.36
 Score for OM-PP discrimination: -32.29
 Rule: outer membrane or periplasmic protein
 Score for OM-PP discrimination: -32.29
 Rule: outer membrane or periplasmic protein

*** Reasoning Step: 2

Periplasmic space? Score: 3.22889
 Periplasmic space? Score: 3.22889

----- Final Results -----

bacterial periplasmic space --- Certainty= 0.933(Affirmative) < succ>
 bacterial outer membrane --- Certainty= 0.253(Affirmative) < succ>
 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>
 bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

The protein has homology to the following sequences in the databases:

^ **gsa_AAY75310 Neisseria gonorrhoeae ORF 649 protein sequence SEQ ID
 NO:2094 |WO9957280-A2|21-MAR-2000
 Length = 103

Score = 35.4 bits (80), Expect = 0.32
 Identities = 25/85 (29%), Positives = 38/85 (44%), Gaps = 5/85 (5%)

Query: 7 ILTGILLATALPASAHGMHKS KPLAMDELPPICQQYFKRAETCYNKAGNKADFARN-NTK 65
 + T T+ PA H H SK L P C++Y +R Y GN + N +
 Sbjct: 13 VSTTAAAGTSEPAHRHTKHISKA-NKQMLHPECRKYLERRAAWYRSQGNVQELRENKKAR 71

Query: 66 FLFQALPAADLGQRKQMCQIAMDSF 90
 F+ LP A ++K C+ A ++F
 Sbjct: 72 KAFRTLPHYA---EQKIQCRAYEAF 93

5

The protein was expressed in *E.coli* as a soluble 9.35kDa His-fusion product and then purified.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 149

- 10 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 297> which encodes amino acid sequence <SEQ ID 298; NGS152>. Analysis of this protein sequence reveals the following:

GvH Examining signal sequence (von Heijne)

Signal Score (-7.5): -5.46

Possible cleavage site: 18

15

>>> Seems to have an uncleavable N-term signal seq

Amino Acid Composition of Predicted Mature Form:

calculated from 1

ALOM: Finding transmembrane regions (Klein et al.)

count: 1 value: -3.19 threshold: 0.0

20

INTEGRAL Likelihood = -3.19 Transmembrane 368 - 384 (367 - 384)

PERIPHERAL Likelihood = 0.53

modified ALOM score: 1.14

Rule: cytoplasmic membrane protein

25

*** Reasoning Step: 2

----- Final Results -----

30

bacterial inner membrane --- Certainty= 0.227(Affirmative) < succ>

bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>

bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>

bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

- 35 The protein has homology to the following sequences in the databases:

^ **gsa_AAY81609 Streptococcus pneumoniae type 4 protein sequence #109

|WO200006737-A2|24-MAY-2000

Length = 1237

40

Score = 48.1 bits (113), Expect = 4e-04

Identities = 80/312 (25%), Positives = 142/312 (44%), Gaps = 59/312 (18%)

Query: 57 RRQARIRVGNLITDSLEHIRVKALLPLPL----KLPVKRI---NLPRNLPALFVRLRXTI 109
 RRQ R + ++ L+H RV L P+ ++PV+++ +PR A RL++ +

45

Sbjct: 941 RRQVR-QPQQVLVHQLQHQRVHRLRRQPVHQSQQQVPRQLPHQQVPRLQQAPVRRLOQVL 999

Query: 110 SPRQIGDALPILKLQRI--RLTLHLKPLPLHPQLGLLHIKRPVRIPLRHLAVQRTLVRNL 167
 +P+ P+ + Q++ RL H + PL L +P R + L QR VRLN

50

Sbjct: 1000 APQF--QPQVPRQPQQVSQRLNRHQVRPLQQVLA----PQPQRQQVHRL--QRQVRVLN 1051

Query: 168 RRIKPPLLQHRLTVRRILRRSRQPFPAPQFPDRRIFIMFRHNPARRIKLCRRQLTVQGPR 227
 R + LQ L A P R+ +H +R++ ++ L Q R

Sbjct: 1052 RHQVRPLQQVL-----APQPQRQQVHRLQH---QRVPRPLQQVLAPQPQR 1093

55

Query: 228 IRRSRPLIKLPLLRQRIRPGRHQRTLVRVKITHRLAAPIHIPVKSQRRRRPSARIRRARI 287
 + R L+RQR+R +HQ R + + H+L +H PV+ Q + R + +++ +

Sbjct: 1094 QQVHR-----LQRQVRVLSQHQRVRQPQQAHL-LNLHQFVR-QPQHRQAPQLQQVPV 1144

60

Query: 288 APREIRPGPRIGGKRLIAARKP-QTGIRTPFESTRPAQPPRPI-LNIVTAQIHIPITRR 345
 + R R+ + + R+P Q +R P R + P+P+ LN H P+ R+

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Sbjct: 1145 RQPQRRQVRRRL---QOVFVRQPQOVFVRQP--QRRQVRRPQFVHLN-----RHQPV-RQ 1192

Query: 346 PGLIIRNGTPHR 357

P ++ + H+

5 Sbjct: 1193 PQQVLVHQLQHQ 1204

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 150

10 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 299> which encodes amino acid sequence <SEQ ID 300; NGS153>. Analysis of this protein sequence reveals the following:

GvH Examining signal sequence (von Heijne)

Signal Score (-7.5): -5.48

Possible cleavage site: 13

15 >>> Seems to have no N-terminal signal seq.

Amino Acid Composition of Predicted Mature Form:

calculated from 1

ALOM: Finding transmembrane regions (Klein et al.)

count: 0 value: 6.31 threshold: 0.0

20 PERIPHERAL Likelihood = 6.31

modified ALOM score: -1.76

Rule: cytoplasmic protein

*** Reasoning Step: 2

25

----- Final Results -----

bacterial cytoplasm --- Certainty= 0.150(Affirmative) < succ>

bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>

30 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>

bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

The protein has homology to the following sequences in the databases:

35 ^ **gbp_15832758 gi|15832758|ref|NP_311531.1| \ (NC_002695) hypothetical
protein [Escherichia coli O157:H7]
dbj|BAB36927.1| (AP002562) hypothetical protein [Escherichia coli O157:H7]
Length = 188

40 Score = 73.9 bits (180), Expect = 3e-12

Identities = 54/169 (31%), Positives = 79/169 (45%), Gaps = 15/169 (8%)

Query: 12 LTQEV LKELLRYDDNTGKLYWAERPRKYFNSGLHYKSWNTGFSGKEVFLYKGR LGYLK LK 71
LT + + ELL +D +TG W + + S F GY +

45 Sbjct: 16 LTVKRIFELLSFDKSTGVFRWKVPTQ----GRIALNSVAGAFDSN-----GYSMIM 62

Query: 72 IFKKQYNAHRLIWL FVY GKH-ASSIGHINRDKTDNRISNLRDVTHAENMKNRGKFKNN TS 130

I ++Y H L++ + + A I H+N +TDNR NLR+ EN +N KN+ S

Sbjct: 63 IDGRRYKTHVLV FYITHNRWPAGQIDHVGIRTDNRPENLRECLPIENSRNIRIRKNSKS 122

50 Query: 131 GHTGVYFHKPSKKWQARIMVNRKNKILGLFEHIEDAA-KAREAASKDFG 178

G GV +HK KKW R+ + K+K G F+ +E A A EA K +G

Sbjct: 123 GCRGVTWHKRQKKWNVRLGFHGKSKHFGCFDDLELAVLVAEEARDKY YG 171

55 Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

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Example 151

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 301> which encodes amino acid sequence <SEQ ID 302; NGS154>. Analysis of this protein sequence reveals the following:

```

5  GvH Examining signal sequence (von Heijne)
    Signal Score (-7.5): -6.98
    Possible cleavage site: 28
    >>> Seems to have no N-terminal signal seq.
    Amino Acid Composition of Predicted Mature Form:
    calculated from 1
10  ALOM: Finding transmembrane regions (Klein et al.)
    count: 0 value: 8.12 threshold: 0.0
    PERIPHERAL Likelihood = 8.12
    modified ALOM score: -2.12
15  Rule: cytoplasmic protein

    *** Reasoning Step: 2

    ----- Final Results -----
20      bacterial cytoplasm --- Certainty= 0.423(Affirmative) < succ>
    bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
    bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
25  bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

```

The protein has homology to the following sequences in the databases:

```

30  ^ **gbp_15830449 gi|15830449|ref|NP_309222.1| \ (NC_002695) hypothetical
    protein [Escherichia coli O157:H7]
    dbj|BAA94132.1| (AP000422) hypothetical protein [Escherichia coli O157:H7]
    dbj|BAB34618.1| (AP002554) hypothetical protein [Escherichia coli O157:H7]
    Length = 148

    Score = 42.7 bits (99), Expect = 0.003
    Identities = 27/99 (27%), Positives = 49/99 (49%), Gaps = 10/99 (10%)
35  Query: 37  IRPRKSKRSVEQNRRLLWFLYREISEKVFIDGRRFSQDVWHE-----FLKRRKFIGCIEMP 91
    + ++ KRS QN R+W + ++S +V G+R + + W + +LK K + +P
    Sbjct: 33  VHVKEPKRSKAQNDRMWPMNDVSRQVLWHGQRLAPEDWKDLFTALWLKTKKLEQRSVPG 92

40  Query: 92  GQ----LMGISTTKLSVREMSEYQEKIISWASMEHGVLW 126
    ++G+ T+K+ M+E E I+ W E V W
    Sbjct: 93  IDGGVVMLGVRTSKMRKASMTPELIE-IMFWFGSERNVRW 130

```

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be
45 useful antigens for vaccines or diagnostics.

Example 152

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 303> which encodes amino acid sequence <SEQ ID 304; NGS155>. Analysis of this protein sequence reveals the following:

```

50  GvH Examining signal sequence (von Heijne)
    Signal Score (-7.5): -4
    Possible cleavage site: 27
    >>> Seems to have an uncleavable N-term signal seq.
    Amino Acid Composition of Predicted Mature Form:
    calculated from 1
55  ALOM: Finding transmembrane regions (Klein et al.)
    count: 0 value: 4.98 threshold: 0.0
    PERIPHERAL Likelihood = 4.98
    modified ALOM score: -1.50

```


*** Reasoning Step: 2

5 ----- Final Results -----

10 bacterial inner membrane --- Certainty= 0.046(Affirmative) < succ>
bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

The protein has homology to the following sequences in the databases:

15 ^ **gbp_15801502 gi|15801502|ref|NP_287519.1| \ (NC_002655) putative
endonuclease of prophage CP-9330 [Escherichia coli
0157:H7 EDL933]
ref|NP_309804.1| (NC_002695) endonuclease [Escherichia coli O157:H7]
gb|AAG56131.1|AE005344_7 (AE005344) putative endonuclease of prophage CP-9330
[Escherichia coli O157:H7 EDL933]
dbj|BAB35200.1| (AP002556) endonuclease [Escherichia coli O157:H7]
20 Length = 119

Score = 47.4 bits (111), Expect = 2e-04
Identities = 38/122 (31%), Positives = 54/122 (44%), Gaps = 8/122 (6%)

25 Query: 71 LILPYPVSANRYWRIWRNRRAVSAAEAAAYKETVRRRIA-QGAGAMPSEGAVAVYVRLIPKA 129
L+LPYP + N YWR + S Y+ V I Q + G +A+ + P
Sbjct: 5 LVLFPYPPTVNTYWRRRGSTYFVSKAGERYRAVVLIVRQQRLKLSLSGRLAIKIIAEP-- 62

30 Query: 130 NKDGGANKTVIDLDNALKVTLDALQGVAYHNDRQVRRIAAEYGGEPVTTGGGLAVEVGELE 189
+K DLDN LR LDAL D + G+PV+GG L V++ ++E
Sbjct: 63 -----PDKRRRLDNLKAPLDALTHAGVLMDDDEQFDEINIVRGQPVSGGRLGVKIYKIE 117

Query: 190 ME 191
E

35 Sbjct: 118 SE 119

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 153

40 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 305> which encodes amino acid sequence <SEQ ID 306; NGS156>. Analysis of this protein sequence reveals the following:

GvH Examining signal sequence (von Heijne)
Signal Score (-7.5): -2.61
Possible cleavage site: 49
45 >>> Seems to have no N-terminal signal seq.
Amino Acid Composition of Predicted Mature Form:
calculated from 1
ALOM: Finding transmembrane regions (Klein et al.)
count: 0 value: 7.96 threshold: 0.0
50 PERIPHERAL Likelihood = 7.96
modified ALOM score: -2.09
Rule: cytoplasmic protein

*** Reasoning Step: 2

55

----- Final Results -----

60 bacterial cytoplasm --- Certainty= 0.307(Affirmative) < succ>
bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>

bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

The protein has homology to the following sequences in the databases:

5 ^ **gsa_AAG90098 C glutamicum protein fragment SEQ ID NO: 3852
 |EP1108790-A2|26-SEP-2001
 Length = 148

10 Score = 102 bits (253), Expect = 7e-21
 Identities = 60/147 (40%), Positives = 88/147 (59%), Gaps = 18/147 (12%)

Query: 3 NAYDVADFFLSPFEEEDGEQISNLKQLKLLYYAQGYALAILNRPLFAENIEHWQHGFPVVP 62
 +A ++A++F++ +E D E +S LKQLKLLYY+QG +A R LF++ I WQHGFPV P
 Sbjct: 5 SAREIAEFVWAGDELDAAE-VSPLKQLKLLYSSQGEHIAATGRKLFSDKILAWQHGFPVTP 63

15 Query: 63 CIYRTYKKGGSPLPAAHIEPDKYADEEL-----VVLNRVRKEQGCTAWALRNRT 113
 +Y K YG +P I+PD++ +E L V ++ G Y+AWALR KT
 Sbjct: 64 GVYSDTKSYGRNP-----IDPDEFVSDEFNWDDYSDVDELVTWVRKYGIYSAWALREKT 118

20 Query: 114 HQEAPWIQT-RQGEVIGI--ALMGEYF 137
 H E+PW+ QG+ I I A + ++F
 Sbjct: 119 HSESPWLDWAQGGONIEITDAALKDFF 145

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

25 Example 154

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 307> which encodes amino acid sequence <SEQ ID 308; NGS157>. Analysis of this protein sequence reveals the following:

30 GVH Examining signal sequence (von Heijne)
 Signal Score (-7.5): -5.65
 Possible cleavage site: 42
 >>> Seems to have no N-terminal signal seq.
 Amino Acid Composition of Predicted Mature Form:
 calculated from 1

35 ALOM: Finding transmembrane regions (Klein et al.)
 count: 0 value: 3.98 threshold: 0.0
 PERIPHERAL Likelihood = 3.98
 modified ALOM score: -1.30
 Rule: cytoplasmic protein

40 *** Reasoning Step: 2

 ----- Final Results -----

45 bacterial cytoplasm --- Certainty= 0.291(Affirmative) < succ>
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

50 The protein has homology to the following sequences in the databases:

 ^ **gbp_6274533 gi|6274533|gb|AAF06681.1|AF163663_6 \ (AF058689) Toul
 [Neisseria meningitidis]
 Length = 272

55 Score = 546 bits (1408), Expect = e-154
 Identities = 267/272 (98%), Positives = 271/272 (99%)

Query: 19 MKGMDKLRVQRDFLNIRPIFTAGEQEYLTELSDRLPLSVLTDSVRNIEEIGIDFVYSPAK 78
 MKGMDKLRVQ+DFLNIRPIFTAGEQEYLTELSDRLPLSVLTDSVRNIEEIGIDFVYS AK
 60 Sbjct: 1 MKGMDKLRVQQDFLNIRPIFTAGEQEYLTELSDRLPLSVLTDSVRNIEEIGIDFVYSSAK 60

Query: 79 LEGNTYNQYDTQALLKLGQTAGGKLYSDAVMLINLRESYRHLLSGLDSPKPFDWLDFLKT 138
 LEGNTYNQYDTQALLKLGQTAGGKLYSDAVMLINLRESYRHLLSGLDSP+PFDWLDLFLKT
 5 Sbjct: 61 LEGNTYNQYDTQALLKLGQTAGGKLYSDAVMLINLRESYRHLLSGLDSPEPFDWLDLFLKT 120
 Query: 139 THSLISENLLKGGSGGVVRRDSVTISGTDYTPLSNPQSLDTELKWLLQEAPKIENPFDR 198
 THSLISENLLKGGSGGVVRRDSVTISGTDYTPLSNPQSLDTELKWLLQEAPKIENPFDR
 10 Sbjct: 121 THSLISENLLKGGSGGVVRRDSVTISGTDYTPLSNPQSLDTELKWLLQEAPKIENPFDR 180
 Query: 199 VYLHNNLAYLRYFKDCNKRTARNCMTSLMRSGFFPCVFPSPDYPAYAEAVVAYYETGDY 258
 VYLHNNLAYL+YFKDCNKRTARNCMTSLMRSGFFPCVFPSPDYPAYAEAVVAYYETGDY
 15 Sbjct: 181 VYLHNNLAYLQYFKDCNKRTARNCMTSLMRSGFFPCVFPSPDYPAYAEAVVAYYETGDY 240
 Query: 259 GLFKKYFISAYENTVNKYGPQPDVDIFRNFSI 290
 GLFKKYFISAYENTVNKYGPQPDVDIFRNFS+
 15 Sbjct: 241 GLFKKYFISAYENTVNKYGPQPDVDIFRNFS 272

A homolog was found in serogroup A *N.meningitidis* but not in serogroup B, so NGS157 protein and nucleic acid are useful for distinguishing between gonococcus and serogroup B *N.meningitidis*.

20 Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 155

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 309> which encodes amino acid sequence <SEQ ID 310; NGS158>. Analysis of this protein sequence reveals the following:

25 GvH Examining signal sequence (von Heijne)
 Signal Score (-7.5): -6.98
 Possible cleavage site: 18
 >>> Seems to have no N-terminal signal seq.
 Amino Acid Composition of Predicted Mature Form:
 30 calculated from 1
 ALOM: Finding transmembrane regions (Klein et al.)
 count: 0 value: 0.16 threshold: 0.0
 PERIPHERAL Likelihood = 0.16
 modified ALOM score: -0.53
 35 Rule: cytoplasmic protein
 *** Reasoning Step: 2
 40 ----- Final Results -----
 bacterial cytoplasm --- Certainty= 0.185(Affirmative) < succ>
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
 45 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

The protein has homology to the following sequences in the databases:

> ^^ **gbp_15791833 gi|15791833|ref|NP_281656.1| \ (NC_002163) amino-acid
 ABC transporter ATP-binding protein [Campylobacter jejuni]
 50 pir|H81391 amino-acid ABC transporter ATP-binding protein Cj0469 [imported] -
 Campylobacter jejuni (strain NCTC 11168)
 emb|CAB75107.1| (AL139075) amino-acid ABC transporter ATP-binding protein
 [Campylobacter jejuni]
 Length = 253
 55 Score = 301 bits (772), Expect = 6e-81
 Identities = 153/244 (62%), Positives = 195/244 (79%), Gaps = 2/244 (0%)
 Query: 1 MALLSIRKLHKQYGSVTAIQSLDLDEKGEVIVLLGPSGCGKSTLLRCVNGLEPHQGQSI 60

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M++L I L K YGS A++ ++L+++ EV+V+LGPSGCGKSTLLRC+NGLE G+I
 Sbjct: 1 MSILKIENLQKYGSHHALKDINLEVKAKEVVILGPSGCGKSTLLRCINGLEEIASGNI 60
 Query: 61 VMDGVGEFGKDVS-WQATARQKVGVMVFQSYELFAHMTVIENILLGPVKVQNRDRAEAEQA 119
 +D + KD W RQKVGVMVFQSYELF H++V ENILLGP+KVQ R + E +A
 Sbjct: 61 YIDNE-KIDKDFKEWPRMRQKVGVMVFQSYELFEHL SVEENILLGPMKVQKRKKDEVLEA 119
 Query: 120 GKLLERVGLLDKKNAYPRELGGQKQRIATVRALCLNPEVILLDEITAALDPEMVREVL 179
 LE+VGLL + +AYPRELGGQKQRIATVR+LC+NPE++L DE+TAALDPE+VREVL
 Sbjct: 120 KIWLEKVGLLHKIHAYPRELGGQKQRIATVRSLCMNPELMLFDEVTAALDPEIVREVL 179
 Query: 180 VVLELAREGMSMLIVTHEMGFARKVADRIVFMKGGIVESSDPETFFSAPKSERARQFLA 239
 V+L LA+EGM+MLIVTHEMGFA+ VAD+I+FMK+G I+E +DP++FF PKSERA++FL
 Sbjct: 180 VMLNLAKEGMTMLIVTHEMGFAKAVADKIIIFMDEGKIIIEENDPKSFFKNPKSERAKKFLN 239
 Query: 240 GMDY 243
 DY
 Sbjct: 240 LFDY 243

20 Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 156

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 311> which encodes amino acid sequence <SEQ ID 312; NGS159>. Analysis of this protein sequence reveals the following:

25 GvH Examining signal sequence (von Heijne)
 Signal Score (-7.5): -4.16
 Possible cleavage site: 13
 >>> Seems to have no N-terminal signal seq.
 Amino Acid Composition of Predicted Mature Form:
 30 calculated from 1
 ALOM: Finding transmembrane regions (Klein et al.)
 count: 0 value: 6.47 threshold: 0.0
 PERIPHERAL Likelihood = 6.47
 modified ALOM score: -1.79
 35 Rule: cytoplasmic protein
 *** Reasoning Step: 2
 40 ----- Final Results -----
 bacterial cytoplasm --- Certainty= 0.312(Affirmative) < succ>
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
 45 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

The protein has homology to the following sequences in the databases:

> ^, **gbp_15794799 gi|15794799|ref|NP_284621.1| \ (NC_003116) hypothetical
 protein [Neisseria meningitidis Z2491]
 50 pir||B81819 hypothetical protein NMA1914 [imported] - Neisseria meningitidis
 (group A strain Z2491)
 emb|CAB85135.1| (AL162757) hypothetical protein [Neisseria meningitidis Z2491]
 Length = 206
 55 Score = 265 bits (678), Expect = 8e-70
 Identities = 131/146 (89%), Positives = 138/146 (93%)
 Query: 1 MTKLYAQIAKTEAQDDGTVKVWGYASSEAVDS DGEVVAEAMKAAIPDYMKFGAVREMHG 60
 MTKLYA+IAK E QDDGTVKVWGYASSE +DSDGEV+AA AMKAAIPDYMKFGA REMHG
 60 Sbjct: 1 MTKLYAEIAKMETQDDGTVKVWGYASSEIDSDGEVIAAAAMKAAIPDYMKFGAGREMHG 60

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Query: 61 SNAAGTAIEINVEDDGRITFFGAHIVDPVAVTKVKTGVYKGFSSIGGSVTARNDLNKSQITG 120
 SNAAGTAIEINVEDDG TFFGAHI+DPV V+KVKTG VYKGFSSIGGSVTAR+DLNKSQITG
 Sbjct: 61 SNAAGTAIEINVEDDGITFFGAHIIDPVVSVKVTGVYKGFSSIGGSVTARDLNLKSQITG 120

5 Query: 121 LKLTEISLVDRPANPDVFTCFKADK 146
 LKLTEISL+DRPANPDV TCFKADK
 Sbjct: 121 LKLTEISLIDRPANPDVSTCFKADK 146

10 A homolog was found in serogroup A *N.meningitidis* but not in serogroup B, so NGS159 protein and nucleic acid are useful for distinguishing between gonococcus and serogroup B *N.meningitidis*.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 157

15 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 313> which encodes amino acid sequence <SEQ ID 314; NGS160>. Analysis of this protein sequence reveals the following:

GvH Examining signal sequence (von Heijne)
 Signal Score (-7.5): -8.3
 Possible cleavage site: 33
 >>> Seems to have no N-terminal signal seq.
 20 Amino Acid Composition of Predicted Mature Form:
 calculated from 1
 ALOM: Finding transmembrane regions (Klein et al.)
 count: 0 value: 7.85 threshold: 0.0
 PERIPHERAL Likelihood = 7.85
 25 modified ALOM score: -2.07
 Rule: cytoplasmic protein
 *** Reasoning Step: 2

30 ----- Final Results -----

bacterial cytoplasm --- Certainty= 0.407(Affirmative) < succ>
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
 35 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

The protein has homology to the following sequences in the databases:

40 > ^^ **gbp_2126352 gi|2126352|pir||JC5218 type I site-specific
 deoxyribonuclease (EC 3.1.21.3) Hsd chain S [validated]
 - Pasteurella haemolytica
 gb|AAC44667.1| (U46781) HSDS [Mannheimia haemolytica]
 Length = 442

45 Score = 97.1 bits (240), Expect = 3e-19
 Identities = 55/149 (36%), Positives = 81/149 (53%), Gaps = 3/149 (2%)

Query: 26 EVAEYSKNRICSDKLNHNHYVGVDNLLQNREGKKLSGYVPSEGMTEYIVNDILIGNIRP 85
 ++ E +I L + NY+ DN+L N G L+ +P+ + DIL NIR
 50 Sbjct: 10 DIVELISEKIKIKDLKENYISTDNMLPNFGGITLAENLPNSASCNRFKKDILFSNIRT 69

Query: 86 YLKKIWQADCTGGTNGDVLVIRV--TDEKVNPKYLYQVLADDKFFAFNMKHKAGAKMPRG 143
 Y KK+W A+ +GG + DVLV+R TD +N +YL+ ++ D F F + A GAKMPRG
 Sbjct: 70 YFKKRWLAEFSGGCSFDVLMVRSKNTDILLN-EYLFLLIRSDDFINFTVISANGAKMPRG 128

55 Query: 144 SKAAIMQYKIPIPLPEQEKIVAILGKFD 172
 K A+ + IP + Q+K +A FD
 Sbjct: 129 DKNAMKGFIFNIPSIEYQKKCIANYFAFD 157

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 158

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 315> which encodes amino acid sequence
5 <SEQ ID 316; NGS161>. Analysis of this protein sequence reveals the following:

```

    GvH Examining signal sequence (von Heijne)
      Signal Score (-7.5): -5.08
      Possible cleavage site: 36
    >>> Seems to have no N-terminal signal seq.
  10 Amino Acid Composition of Predicted Mature Form:
      calculated from 1
    ALOM: Finding transmembrane regions (Klein et al.)
      count: 1 value: -1.59 threshold: 0.0
    15 INTEGRAL Likelihood = -1.59 Transmembrane 302 - 318 ( 302 - 318)
      PERIPHERAL Likelihood = 3.76
      modified ALOM score: 0.82
    Rule: cytoplasmic membrane protein

    *** Reasoning Step: 2

  20 ----- Final Results -----

      bacterial inner membrane --- Certainty= 0.164(Affirmative) < succ>
  25 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
      bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
      bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

```

The protein has homology to the following sequences in the databases:

```

  30 pir||E81921 probable DNA-invertase NMA0772 [imported] - Neisseria meningitidis
      (group A strain 22491)
      emb|CAB84055.1| (AL162754) putative DNA-invertase [Neisseria meningitidis 22491]
      Length = 321

  35 Score = 295 bits (755), Expect = 9e-79
      Identities = 151/322 (46%), Positives = 216/322 (66%), Gaps = 3/322 (0%)

    Query: 14 LRNAVGLDISKLTFDATAIVGNAEYSAKFDNDSKGLDQFSDRLKSLGCQNLHICMEATGN 73
      +RNAVGLDIS TFD I+ KF ND +G + + + +++++CMEATGN
  40 Sbjct: 1 MRNAVGLDISAKTFDVVTIINGETDYRKPSNDEQGCKNLKEWISAKREKDIYVCMETGN 60

    Query: 74 YYEEVADYFAQYYSVYVNVNPLKISKYAESRFKRTKTDKQDAKLIAQYCRSAQSESLVKRQ 133
      YYE+ AD A+ Y V V+NPLKI YA+ RF R K DKQDAKLIA++C++A EL KR+
  45 Sbjct: 61 YYEQAADCLAEEYHVSVINPLKIKAYAQRFSRVKNDKQDAKLIAEFCQTALIERLPKRE 120

    Query: 134 KPTDEQYRLSRMTAAYAQIRSECAAMKNRHHAAKDEEAAKAYAEI IKAMNEQLEVLKEKI 193
      KPT++QY L R+ + +Q+ + + KNR AAKD K + + +K + L +K+KI
  50 Sbjct: 121 KPTEQQYSLKRLLSLSQSLLEQQTSQKNRIKAAKDSFVQKIHEKQLKELENHNAVKKKI 180

    Query: 194 KEQTEKPN--CKEGVKRLETIPAIGRMATAAVLFHHLTSSKFETSNKFPAAGLSPQOKES 251
      +QT K + KE KRLETIP++G+ TA L +L +S FE + +F A+AGL+P Q S
  55 Sbjct: 181 -DQTIKSDKKMKELTKRLETIPSVGKTTAISLSYLNSTFENAKQFTAYAGLNPQNIS 239

    Query: 252 GTSVRGKGLTKFGNRKLRAVLFMPAMVAYRIRAPPDFIKRLEEKKKPKKVIIAALMRKL 311
      GTSV K K+TK+GNR++R LFM A+VA++ PP F RL++ KKKK +II ALMRK+
  60 Sbjct: 240 GTSVNKKSKMTKYGNRRIRGSLFMAALVAFKNNYFFAFTNRLKRAKKPKMLIIGALMRKI 299

    Query: 312 AVIAYHVHKKGGDYDPSRYKSA 333
      V+A++++K D+D +RY++A
  Sbjct: 300 LVVAFNLYKTETDFDKTRYQTA 321

```


A homolog was found in serogroup A *N.meningitidis* but not in serogroup B, so NGS161 protein and nucleic acid are useful for distinguishing between gonococcus and serogroup B *N.meningitidis*.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

5 Example 159

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 983> which encodes amino acid sequence <SEQ ID 984; NGS162>. Analysis of this protein sequence reveals the following:

```

10  GvH: Examining signal sequence (von Heijne)
      Signal Score (-7.5): -0.86
      Possible cleavage site: 33
      >>> Seems to have no N-terminal signal seq.
      Amino Acid Composition of Predicted Mature Form:
            calculated from 1
15  ALOM: Finding transmembrane regions (Klein et al.)
      count: 0 value: 4.08 threshold: 0.0
      PERIPHERAL Likelihood = 4.08
      modified ALOM score: -1.32
      Rule: cytoplasmic protein

20  *** Reasoning Step: 2

      ----- Final Results -----

25      bacterial cytoplasm --- Certainty= 0.032(Affirmative) < succ>
      bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
      bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
      bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

30  The protein has homology to the following sequences in the databases:

      ref|NP_312507.1| (NC_002695) hypothetical protein [Escherichia coli O157:H7]
      gb|AAG58749.1|AE005587_7 (AE005587) putative adhesin [Escherichia coli O157:H7]
      EBL933]
      dbj|BAB37903.1| (AP002566) hypothetical protein [Escherichia coli O157:H7]
35      Length = 1588

      Score = 120 bits (302), Expect = 4e-26
      Identities = 109/359 (30%), Positives = 170/359 (46%), Gaps = 65/359 (18%)

40  Query: 22  AVALGSSSTASGEYSYASGYNSVASGNKSYAAGYASVASAEGSVVIGDSRQVKPEADQGV 81
      + A+G + A G+YS A G + A G S A G +++++ + S+ +G S + +
      Sbjct: 93  STAVGYDAIAEGQYSSAIGSKTHAIGGASMAFGVSAISEGDRSIALGASSYSLGQYSMAL 152

      Query: 82  AVGSKATVKNKAKQRVVVGSEAKVNAERGIAIGKEAKAGGKT'TNTLLDGPAYYADAI AVG 141
      SKA K + +G +K IA+G KA T + +IA+G
45  Sbjct: 153  GRYSKAL----GKLSIAMGDSSKAEGANAIALGNATKA----TEIM-----SIALG 195

      Query: 142  YQAEAGKGGALALGKQAKATKQNGMALGVESEAAGDFSTAVGNESKAKGQGG----- 193
      A A K ++ALG + A+++N +A+G E+EAA + +TA+GN +KAKG
50  Sbjct: 196  DTANASKAYSMALGASSVASEENAI AIGAETEA-ENATAIGNNAKAKGTNSMAMGFGSL 254

      Query: 194  -----VGLGNQSKAEADFAVAV--GNKAEATKE-----NSLVIGRYARANGN 233
      + LGN S+A AD A+A+ GNKA+ N++ +G + A G+
      Sbjct: 255  ADKVNITIALGNQSQAADNAIAIGQGNKADGVDAIALGNQSQRGLNTIALGTASNATGD 314

55  Query: 234  HSVSLGSRSEIKDGVSNVAPGYGVSASENNVVSVAYKETPQSTELSYRKIVGVDDGV-- 291
      S++LGS S +G+ NSVA G S+A +N VSV RKIV V +G
      Sbjct: 315  KSLALGSNSS-ANGI-NSVALGADSIADLDNTVSVGNSSLK-----RKIVNVKNGAIK 365

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Query: 292 -NDFDAVNVRLKAMQGQNMALFSVRSEVRGVAASSAALSALTPLSYDANNPTQFMVG 349
 + +DA+N QL A+ SV + G AA +T +Y+ N ++ VG
 Sbjct: 366 SDSYDAINGSQLYAISD-----SVAKRLGGGAADVDDGTVTAPTYNLKNKSKNNVG 417

5

Score = 86.3 bits (212), Expect = 1e-15
 Identities = 68/253 (26%), Positives = 118/253 (45%), Gaps = 39/253 (15%)

10

Query: 28 SSTASGEYSYASGYNSVASGNKSYAAGYASVASAEGSVVIGDSRQVKPEADQGVAVGSKA 87
 S+ +G + G + A + Y S ++ +G V IG G+KA
 Sbjct: 38 SALVAGGMLSSFGALANAGNDNGQGVYDYGSGSAGDGWVAIGK-----GAKA 83

15

Query: 88 -TVKNKAKQRRVVVGSEAKVNAERGIAIGKEAKAGGKTNTLLDGPAYYADAIYVGYQAEA 146
 T N + VG +A + AIG + A G + +A G A +
 Sbjct: 84 NTFMNTSGSSSTAVGYDAIABGQYSSAIGSKTHAIGGAS-----MAFGVSAIS 130

20

Query: 147 GKGGAIALGKQAKATKQNGMALGVESEAAAGDFSTAVGNESKARGQGGVGLGNQSKAEADF 206
 +IALG + + Q MALG S+A G S A+G+ SKA+G + LGN +KA
 Sbjct: 131 EGDRSIALGASSYSLGQYSMALGRYSKALGKLSIAMGDSSKAEGANAIALGNATKATEIM 190

25

Query: 207 AVAVGNKAEATKENSILVIGRYARANGNHSVSLGSRSEIKDGV-----SNSVAPG 255
 ++A+G+ A A+K S+ +G + A+ +++++G+ +E + +NS+A G
 Sbjct: 191 STALGDTANASKAYSMALGASSVASEENATAIGAETEAENATAIGNNAKARGTNSMAMG 250

Query: 256 YGSVASENNVSV 268
 +GS+A + N +++
 Sbjct: 251 FGSLADKVNTIAL 263

30

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 160

Further open reading frames were identified in gonococcus <SEQ IDs 317/318 to 8621/8622>. These polypeptide and nucleotide sequences are useful for studying gonococcus, for diagnostic purposes, as antibiotic targets, and as vaccine antigens.

35

It will be understood that the invention has been described by way of example only and modifications may be made whilst remaining within the scope and spirit of the invention.

CLAIMS

1. A protein comprising an amino acid sequence selected from the group consisting of SEQ IDs 26, 72, 230, 984, 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314 and 316.
2. A protein having 50% or greater sequence identity to a protein according to claim 1.
3. A protein comprising a fragment of an amino acid sequence selected from the group consisting of 26, 72, 230, 984, 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314 and 316.
4. An antibody which specifically binds to a protein according to any one of claims 1 to 3.
5. A nucleic acid molecule which encodes a protein according to any one of claims 1 to 3.
6. A nucleic acid molecule according to claim 5, comprising a nucleotide sequence selected from the group consisting of SEQ IDs 25, 71, 229, 983, 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313 and 315.
7. A nucleic acid molecule comprising a fragment of a nucleotide sequence selected from the group consisting of SEQ IDs 25, 71, 229, 983, 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313 and 315.
8. A nucleic acid molecule comprising a nucleotide sequence complementary to a nucleic acid molecule according to any one of claims 5 to 7.

9. A nucleic acid molecule comprising a nucleotide sequences having 50% or greater sequence identity to a nucleic acid molecule according to any one of claims 5 to 8.
10. A nucleic acid molecule which can hybridise to a nucleic acid molecule according to any one of claims 5 to 9 under high stringency conditions.
- 5 11. A composition comprising a protein, a nucleic acid molecule, or an antibody according to any preceding claim.
12. A composition according to claim 11 being a vaccine composition or a diagnostic composition.
13. A composition according to claim 11 or claim 12 for use as a pharmaceutical.
14. The use of a composition according to claim 13 in the manufacture of a medicament for the
10 treatment or prevention of infection due to streptococcus bacteria, particularly *N.gonorrhoeae*.
15. A process for distinguishing *N.gonorrhoeae* from *N.meningitidis*, comprising the steps of: (a) contacting a protein, a nucleic acid molecule, or an antibody according to any one of claims 1 to 10 with a biological sample under conditions suitable for the formation of an antibody-antigen complexes; and (b) detecting said complexes.

SEQUENCE LISTING

SEQ ID 1

ATGATTAATCATATTGAAAAATATATAGGCACATTTCTCATGGCTCGAAAAAGCGATTTCGGGAAGTCAGTACAAATTAATATCG
CAGCTATTTCCCTCTTCCCTAACAGGGATTTAAAAACTTATATTACTTTAGGGTTAAGCAAACATGATCTGAATTATAAAGCAG
ATTTGAAATACCTTTTGTATGTTCTTTAAAAATATGATGAAATCAGATTTTCCCATTTTAAAGATGGTTAGCAGAAACCATCATTT
GAGAATAAAAAATCCCTTCTTCGGGGGAGGTTGTTTATTTGCCTAGAAGCATTGTAAATCAACAAAAATGGATGCACTGTATG
TTTCCGCCCATTTTATTTGACGATGATTTCCAAGTCTGTTATGGCGAACACTACAATATGTTTTCCCTTTGCTTGTCCCTTT
GTATAAACAGGAAGCCGAATTGGTGGAAAAAAGGGTTGGAATGCTTTTGAGCAGTTCTTGCTGGATAATGAAGTTGGCAACCTT
TCGGATATGAATCGGAAACCGTTTACTTGG

SEQ ID 2

MINHIEKYIGTISHGSKSDSGSQYKLNIAAIPSSPNRDLKTYITLGLSKHDLNYSRFEILFVCSLKYDENQIFPFLRWLAETII
ENKILLRQGVVYLPISIVNSTKMDALYVSAPFYDDDFQVCYGEHYNIVFPLLVPLYKQEAELVERKGWNAFEQFLLDNEVGNL
SDMNRKPFTH

SEQ ID 3

ATGGACTATAACCAAACTGTTTTATCTCACTTGCAAAAATTTTGAAACATCATGATATTAAAGATTACTTGACTTTAGGAA
GAATTGTTGAAGAACTTCCGATTTCCAAGTTTCCAAGTGATTCTTAATCATGAAGATGAGCCTTGGGTTTATGTCAGCTCTGG
GATAGGTCAATTTTLAGGCAGGAGTTTATCATCAGCCGTTTGAAACACCTGAACATATTGAGACCTTGGCAATGCTGGCA
TCTGCAAGTATGCATTATCTGATCAATTTCAATTAGGGAAAACCGTCAATATCGGTAGACCGTGGGTCGAGCAATCATCTTCC
GGCATTTTCTGATTTCTCTGCTTATCTTATGGGCAAGAGTTGGAATATATGGATAATGTCCGATTTTCTGGTTATTGCCAAT
TACCAGACAGAAAGACTTTTCTTGAATACTCATTGGGTAGAAGAATTGGAAACGAAATTTGATGAAGCGGTATTGATTATTTA
GATATAAATCGTGGAGTACTGTCTGGCAGGCAGGA

SEQ ID 4

MDYNQTVLSHLQKFWKHHDIKFTWTILGRIVEELPDFQVQVPIPNHEDEPWVYVSSGIGQFLGQEFFIISPFPETPEHIETLAML
SASMHYDPQFQLGKTVNIGRPWVEQSSFRHFLISLPYPYQLEBYMDNVRFFWLLPITQTERLFLNTHSVEELETKFDEAGIDYL
DINRASTVWQAG

SEQ ID 5

ATGAACCCCGTTTGGATTATTACCGGCAAGAAGCCCGGACAGCCTGCGTAACCGCTGGGTGCTTGCCGCCGCTCTCTGCTTG
CCGCACTCGCCCTTCTTTGGGTTTCTTCGGCAGCTCGCCACCQGTTCGGTCAAGGTCGATCCGCTGACCGTTACCGTCGTCAG
CCTGTCGAGCCTGTCTATTTTCTGATTCCGCTGATTGCGATGCTGCTTTCTTATGACGCACTGATCGGCGAAATCGAACCGGGT
ACGATGGCGTTGCTGTTGAGTTATCCCATTTGGCGCAACCAATCCTTGCCGGCAAGTTTGTTCGGACACCTCATCATCTCGCCC
TTGCCACCACGGCAGGTTACGGATTGGCAGGCATTACGCTGCAACTTGCCAACGGCGGTTTCGACATCGCCGCTTGGAACCCCTT
TGCGCTGTTGATTGCGCCAGCGTGATTTAGGTGCGGCATTTCGTCTATGGGCTACTTGTATTAGTGCAAAGGTCAAAGAGCGG
GGGACGGCGCGCGGTATTTCCATCGGCGTATGGTTGTTTTCTGCTGCTCATCTTCGATATGGCGCTTTTGGGTATTCTGGTTGCCG
ACTCGAAACAGGTCATCAGCGCGCCCGTCTGTTGAAACGGTGCTGCTGTTCAATCCACCGACATTTACCGCCTGCTCAACCTGAC
CGGTTACGAAATACGGCTATGATGCGGGTATGGCGGGTTTGGAGCGGACAAATCGGCCGTGACCGTCCCCGTTTGTGACCGCG
CAGGTTTTATGGGTTATCATTCGCTTGTTTTGGCAGCCGGAATTTTAGAAAGCGACGAATA

SEQ ID 6

MNPVWIITGKEARDSLRNRWVLAVALLLAALSLGFLGSSPTGSKVDPLTVTVVSLSSLSIFLIPLIAMLLSYDALIGEIERG
TMALLSYPIWRNQILAGKFVGHLLIILALATTAGYGLAGITLQLANGGFDIAAWKPFALLIAASVILGAFLSMGYLISAKVKE
GTAAGISIGVWLFVVFIDMALLGILVADSRQVITAPVVEVTLVFNPTDIYRLNLTGYENTAMYAGMAGLSGQIGLTVFVLLTA
QVLWVIIPVLVLAAGIFRKRRI

SEQ ID 7

ATGTCAGACGAAAAATTAGAACAAAACGGCTTGAGCCGTCGTTCTTCTAGGTACGGCCGCGCTTCCGGTGCAGGTATTGCCG
GTGCGGGCTGTTGGGTTTGGCGGGTTGCTCTAAAGACGGCGAACAGGCTGCCGCTAACGCTTCCGGCGCGGCTCCCGTCGCCAA
GGCGCAAGGGGAATCCAACCCGGCCAACGTCTTCCGAAGTCGGTCCGGGCGAACTCGATCAATATTACGGTTTCTTTCCGGC
GGCCAGTCCGGCGAGATGCGCCTGATCGGTCTGCCTTCTATGCGCGAACTGATCGGTATCCCGGTGTTCAATATGGACAGCGCGA
CCGGTTGGGGACGCACCAATGAGAGCTTGAAAGTCTCAACGGCAATATTACCGAAGAAACCCGTAAATTTTAAAGACAGCGG
CCTGCGCTGCTACCCCAACGGCGACTTGCACCAACCGCACCTGTGCTTTACCGACCAAACTTATGACGGCGGCTATGCCATGCG
AACGACAAGGCAAAACACCGCGTCTGCCGCGTGCCTTTGGATTGATGAAGGCGGCAAAATCATCGACATCCCTAATGATTGAG
AGGCAAACTGGATGATGCGAAAACCTGGAATGCAGTGTACACCGCCATCGACGGCGAAACCATGGAGATCGCATGGCAAGTATTG
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TCTCTCACGGCTGTAACGCAAGCCCTGACGGTAAATACATCATGCCCAACGGTAAACTGCCTCCAACCGTTACCGTATTGGATG
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ACACACTGCATTTCGACGGTCCGCGCAATGCTTATACGACATTGTTTATCGACAGCCAAATGGTGAAATGGAATATTGACGATGCG
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TGGGCGAAACCAAAGAAGCGACGGTCAATGGTGGTGTCTTGAACAAATTTCTCAAAGACCGCTTCTTGAATGCCGGTCTCTTT
GAAACCCGAGTGCACCAATTGATCGGCATCTCCGGCGACGAAATGCGTCTGGTACACGACAACCGGACTTTTCCGAACCGCAC
GACTTGTGTTGGTTGCCGCGTCCAACCTGAACCCGGGCAAACTTGGGACCGCAAGACCCGTGGTTC

SEQ ID 8

MSDEKLEQNGLSRRSFLGTAAASGAGIAGAGLLGLAGCSKDGEQAAANASGAAPVAKAQGESKPGQLSSEVGPGLDQVYGFSLG
GQSGEMRLIGLPSMRELMRIPVFNMDSATGWGRTNESLKVNLNGNITEETRFKFLKDSGLRCYPNGDLHHPHLSFTDQTYDGRYAYA
NDRKANNRVCRVRLDVMKADKIIDI PNDSGIHGLRPQRYPKTYVFANGEHITFVSGVGKLDAAKTWNNAVYTAIDGETMEIAWQVL
VDGNLDNGDADYQKYSFATCYNSEALTVQGASSNEQDWCVVFLDKAIEEGIKAGDFKEVNGVKMLDGRAEAKSKYTRYIPVFN
SPHGCNASPDGKYIMPNGKLPPTVTVLVDVSKLDDLFAKIKERDVVVAEPQLGLGPLHTAFDGRGNAYTTLFIDSQMVKNWIDDA

IKAYKGEKIDPIKQKLDVHYQPGHNHTTMGETKEADGQWLVS LNKF SKDRFLNAGPLKPEC DQLIGISGDEMRLVHDNPTFAEPH
DLCLVAASKLNPGKTTWDRKDPWF

SEQ ID 9

ATGAAACTAAATACTCTCACATGGGCTTTTGATGACCGTTTTTTCCGTTGCGCCATCTTGGGCAGAACAAACCGGCAAAATCTGAAG
AAATACAACCCGTCAAAACCTTCTCCCGCCCAAACCGATTGCAACCGACCGCCGACAAAGGCTATTTCGCCGAAAACCAATTCTGA
CCGCTCCGACCGCAGCGATTATTACTTTGTTACCGAAACATAGACCAAGCCTTCGCTCCGCTGAAGGCAACACGACGATTTTAC
GGCAAAAGCTTTTACAACCTCCGTTACCGCGCAAGCATCGGGCGAAGGTATACGGCGTAGCCAACTCAATCGCGACCAAGGCAAA
ACGGCTCAAGAATGGCGGTGGGCGACACCTGATTGGAATAACAGCCGCTTCAATCAGGCTTTGGTACTCGGTTTCGTGCCGTC
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ACCGAACGCCACATCTCCAAACTCAACGTGCGTTGGGGCAATGCCGATTGTGAGCAATACGGTCAGCGCGGAAGCAGGCGCTATCA
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GAACGCAACACCCACACTGCCATGTGCGGATTTCTTCAACGCGTACCGTTTCGCCGATGTGCACATCGACCGCTGGTGCATTGCCG
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TACGGCACAGCCTGAAAACCCAATAAAACCCGGTTTCCCTTCGCCTCATCACAACTCTGGAAACCCATTACGGCTACGAC
TTCAACGGCAAAAGTCGCGCGTCATGCTTTGTCAAGCGAACTCAAATACGATTTCTACGCGCTCTGAAACGCAAAAATACAGCGTTT
CCCTCGGCAATTTGAAACGATCGGCGACAAACCGAAGCTTCAACTCGTCTGCTGCCATCGTGCAAAACCGTATGAGCGGCAT
CGTGATGACCAAAAATCCAGCCGCCCGCATTGCAGGCAATCCCCCTGCTGAAAAAC

SEQ ID 10

MKLNTLTWALMTVF SVAPSWAEQPANTEEIQPVKTFSPPKPIAPTAAQGYFPENQFORSDRSDYYFVTENIDQAFRLKANSSFY
 GKSFYNSVTAQALGAKVYGVANLNRKTANGYKDGGRDRTDWKYSRFNQALVLGFPVSENQEQYRLTYLHDDINNDRQPQVVNDALD
 TERHISKLNVRWGNADLSNTVSAEAGVYKLRHADNYSLRPNTQQQVFVELDRKVYDFSLKHDAADFQKFHNTAAVSYRNDSONG
 ERNTHTAMCDLFGELYRFDVHDIRWCIADTLSPYKFFDDRHLGLGLSYELNEADIRKNTAQPENPIKPGFFPASSQQIWKTHYGYD
 FNGKVRMRHDLSGELKYDFTPSQETQKYSVSLAHLERIGDNTERFNSLAAITVQNRMSGMLMNQNPAAIAGNPAPAE

SEQ ID 11

TTGCAAGCAATCCCCCTGCTGAAAACTGAAAAACACAACCGCATCAGGCTCACCGCCGACAGCCGCAACGACTACTACAACGGCT
ACATGAACCTCGCTCGCAGCGCGCGGGCTGGAACCTGGGCGGCACGCTTGTGGCGGACAAAGTCAAAGACCTGATTATTTTACCGC
CGCACACGGACAAAGCGGCACAGCTTCCAAAGCAGCGCGGCATCATACACGCAACGTGGACGACGATTGTTTACCGCGCAGGCC
TACGCGCGTTTACAACCTTCAATCCGCATTTAGGCGCGCAGGCATCAAAGCCGCTTACAACCTACGCACACAACGAAACCGCAGCGCAGGC
CGCCCTATCAAATCCGTCGCTTTGAAGCCGCCGTCCAAGCCGACTACAAAACTACTTTGCCACGGCAGCTACAACATCGGCGC
GGCAACACGCTTTGTGCGCAACAACCGCGCGGTGATTTTGATATGGCAAGCGGTCTGGGCATAGACAACCGCAAGCCGCCAA
GGCTTTACCGTTGCCGACGTGTACGACGGCGTAAACATCAAAGACAAATACGGCTTGGCCTTGGGCGTGAAACAACGTATTCAACA
AAAAATACGTCGAATACATACAGCGCGACACGTCCTCGCCCTATCCCCAGCGTAGTGATGCACCGGCAGGACATATTGGTT
GAGTTTGATCGCGGCATTT

SEQ ID 12

LQAIPLLKTEKHNRIRLTADSRNDYYNGYMNSLAGAGWNVGGTLVADKVKDLIIFDRAHQSGTASKDGGIITRNVDARLFTAQA
YARYNFNPFWAAGIKAAAYNYGHNETDGRPPYQIRPFEAAVQADYKNYFAHGSYNIGAATRFVAKQTRGDFDMASGLGIDKREAAK
GFTVADVYAGVNIKDKYGLRLGVNNVFNKKYVEYISGDHVLALSPSVVYAPGRTYWLSLHAAF

SEQ ID 13

ATGGATATGAAAAGACGCGATTTCCTTAAAAATGACCGCCGCGCTGGCAGCCGAGGCGTTTCGCCCTTCTCTGCTTGCTGCCGGTA
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GGCGGACGTGTTCGCTGAAAAATCTGGCGTTTCGCCCGACCAACTGCGCGCGGGCGTGGCAAGCGGGCAATTTAAAGTGATGATGAGT
CCGAGCAATGTCGGCGCTAAACCTGCGCAACCAAGGCGAGAAATCGGCATGTGTAATATTTTGACCAACGGCATCACGCAAGTTGG
TCTGCAAAGGCAGCGCATTTGCCTCGCGCAGGATTTGGTGGCGCAAAAAAATCCTCTGCGCGTTTAAAAACGATATGTCGCCGACAT
CGTGCTCGCAAGCCTTGTGTGAAAAAACTGAAAAATCGACGCACACAAAGTCAGCATTACCTACGCTGCCACACCGCCCGAAGCAGTC
GGACTATTTCCAAGTAAAGGTTACCATGCCGTCATCTTGCCCGAACCGATGGCAACCGCCAGCCTACTGAAAGGCAAAACCATAG
GTATAAACGTCGTGCACGGTTTGTGATTTGGTGAAAGCATGGGGCAGGCGTTTGACACCAAACCGCTGATTCCGATGGCAGGTAT
CATCGCCAAACGAAGAATATTTCCACGCACACAAGGCGCAGTTTCGACATCTTCCATCAAGATTTGAAAAACGCGCTCAACTGGATA
TTGGCCAAACCGCAAAACGCGCGGAAAACTCGGCAAAAAAATACCTACCCGCCCCGAACCCGCCCTAGTCATGGGCTTGGACGGCG
CAGCGCTGACGGTAAGCAACGGCAGCGAAGTGAAAAACGAGATTTTGAAGTTTACGAAATCCTGATGCAGTTCAACCCGGAACCT
TTTGGGCGCGCAAGCTGCCCGATAACGGGTTCCTCTTGGCT

SEQ ID 14

MDMKRRDFLKMTAALAAAGVSPSLAAGKEQFTVYGAPAMPSTVIAVAALQGKLAKQADVSLKIWRSPDQLRAGVASGQFKVMS
PSNVGVNLRNQGQKVGVMNLTNGITQLVCKGSAIASPDQLVGKKILVPPKNDMPDIVLQALLKKLKIDAHKVSITYAATPPEAV
GLFPSKGYHAVILPEPMATASLLKGKTIGINVHGFDLVKAWGQAFDTKPLIPMAGIIANEYFYHAHKAQFDIFHQDLKNALNWI
LANRONAAKIGKNYLPAPEPALVMGLDGARLTVSKGSEVKNEILKFYEILMOFNPELLGKLPDNGFFLA

SEQ ID 15

ATGCGCATGGTGGCGTTGTGGGCGTGGGGCAGCGCCGTGTTTCGGCGAGTTTATGCTGCCCTGCGCCGGTAGAGGTGTTTCAAAAAT
CTTTGGATTATTATTAACATTTTCAGGAAAATGAAATCGGGATTTCGCTGTGGCGGTTCGGTAGTGGGTATTTCGGTTGCTTTGAT
AGCAGGATTGGCGGCGGGGCTGGTGGCGGGGCTGGTGGCGGCAGTTTTAGACGGCGATGGCGTTGCTTAAGCCGTGTGATTACG
ATTTTGTAGCAATGCCGCCGATTATTGGGTGGTGATGGCGTTGTTTTGGTTTCGGGTTTCGGCAATCCGAGCGTGTGTGTTACCA
TCATTGTGTGGTTGCGCCGCTGACGTTTGCGAGTGCGGCGGTTCGGAATGGCGAGCGTGAACAAGCAGCATGAGGAGTTGTTTGA
CGCTTATAAATTAGGCCGCTCTGAAAAAATCCGCTATCTGTATATCCCGCATCTGACGGGCTATGTGATTTCCAGCGTCGGCGTG
CGCGTGGCAATGGGGGTGAAGGCGGTGATCATGGCGGAACCTTTAGGCGCCAGCAAGGCGTGGGCGCGCGGATTCCGGACGCGCA
GGCGCAATGCTG

SEQ ID 16

MAMVALWAWGSAVFGEFMLPAPVEVFQKSLDLLKHFOENEIGISLWRSVVGISVALIAGLAAGLVAGLVAGSFKTAMALLKFVIT
ILLAMPPIIWVVMALFWFGFNPVLFITIIIVLAPLTFASAAGVMAVSVNKQHEELFDAYKLGRLLKIRYLYIPHLTGYVISSVGV
AVAMGVKAVIMAEELGASKGVGARIADARAML

SEQ ID 17

GTGAAAGCCTTGTTCCGGCCGAGCGGCTGTGGCAAGACGACGGTTTTACGGCTGATTGCGGGCTTGAAACGCCGAAATCGGGCA
CGATACGTAATACTTTCCACAAAACGGGTTTTCTGTTTCAGGAAAACCGCCTGCCGGAACCTGACCGCATGCAGAAATATCGC
GATTTTTATGGACAACCCAGACGAAGCGGAAATCGTCGCGCTGGCGGCGAAAGTCGGGCTGACTGCGGGCGATTTGAACAAATAT
CCGACCGAATTGTCCGGCGGCATGGCGAAACGGGTGGCGTTTTTGCGCCTGCTGCTGTGCGGCTGCGACCTAGCCTTGCTGGACG
AACCGTTTTGTCGGTTTTGGACCGCGATTTGCGCGATATTTGGTTGCTATGCTGGTGGAAAAATCGAGCGGCAGGGCATGCGCTG
TATACTGGTAACGCACGACCGCTTCGAAGCCGCGCGCTGAGCCATGAAATTATGCTGCTTTCCGCTAAGGGCATGAACGTGCAA
AACGTGATAACCTGCCACGCCGCTGTCCGAACCGGATTCGGCTTTTGAAGAAGTCGTGGTGGCAAGGGAGTTTCAGGGGATTC
ATTATTATGAG

SEQ ID 18

VKALFGPSGCGKTTVLRLIAGLETPKSGTIRNTFHKTGFLFQENRLPENLTAMQNIATFMDNPDEGETIVALAAKVGLTAGDLNKY
PTELSGGMKRVAFRLRLLLCGDLALLDEPFVGLDRDLRDILVAMLVKIERQGMACILVTHDRFPAARLSHEIMLLSAGMNVQ
NVITLPTPLSERDSAFEEVVVAREFQGIHYE

SEQ ID 19

TTGGGGTTGAGGCAAAAGCTCAGGGGGATAATACCAAACCTTAGCAACCTCAATCGGCACATCTGCCGAAGCAAATGCACCCGGG
CATTGGCTTTAGGGGGAAGTTCTGAAGCATCGAAAAAATTTAGTATAGCAGAAGGCTATCTGGCATCTAGTGATGGCTATGGTGC
AATAGCGATTGGTTCTGCCGCCAAGATAAAGCAATTCGAAAAAGGCACAAATAATCATATTGTGGGAAACGATAATAAAGGTCTT
TATGTCGATGCAGACGGCAATGTAAACAAAGATAACCGTAAGGACTGAGTCGGAAGAGATATTTCTCTCAAGATACGGTCAAACCTT
ACGGTGCCTGGCGCATTAGGTTTAGATCTTCTTACATAATCTTTTGGCAGTTTATTGGAGCGTTTTCTACAGCCACAGCTAT
TGAAAGCTTGGCAGTCGGCGACAGCAGCAATCAACGGGCTACCGCAGTGTACTTTTGGCAGTCACAGCAGGGCTTTGGCAGAA
GAAAGTTTGGCATTAGGTTATGAAACTCGGGCAAATGCTTATGGTTCTGTTGCTTTAGGTGCAGAACTCTGTGGCGAATGAAGAAA
ATACCGTATCAGTGAGTTCGATACATTGAAACGGAAATCGTTAATGTCCCGATGGCACGGAAGATTGA

SEQ ID 20

LGLRQKLRIIPNLATSIGTSAEANAAPGALALGGSSEASKKFSIABGYLASSDGYGAIAIGSAAKIKQLEKGTINHIVGNDNKG
YVDADGNVTKITVRTESEKDILSRYGQTYGAVALGFRSSSHNLFASFAGFSTATAIESLAVGDSSQSTGYRSATFGSHSRALAE
ESLALGYETRANAYGSVALGAESVANEENTVSVSSDTLKRKIVNVADGTEDL

SEQ ID 21

ATGTCGCCGATGGCACGGAAGATTTATGATGCAGTAAATGTCCGCCAGTTGAACCGCTTAAGCAAACGTACAAACCGCGTCGGCG
CAAGTGCTGCGCGCTTTGGCTTCGTTAAAACCTGCACAATTAGGCAAAAACGACAAATTCGCCCTTTCTTTGGGCTTTTGAAGCTA
TAAAAATGCCAAGCGGTGGCAATGGGGCGGTGTTTAAAGCCGCTGAAATGTGTTGCTTAATGTGGCGGGCAGTTTGGCCGGA
CCGGACCGGGCTTTCCGGCGCGGGGTTTTTTGGAAATTCGGCGGCAAACCGACACCTGCGGTTGCCGCACAAAACCGCGCGCATC
CTGCAAAAGTTTTCGAATTGCGGCGAGGAAGTGGCGCGTTGCGCGCCCGGCAGGCAGAAACCGACCGCAAACCTGCACAAACAGGC
CGAAATGGAAACGAGCTGCAACAGTTGCGCGCGCGCTTGTCCGAATTGAAAAAACAT

SEQ ID 22

MSPMARKIYDAVNVRQLNRLSKRTNRVGASAAALASLKPAQLGKNDKFAFSLGFGSYKNAQAVAMGAVFKPAENVLLNVAGSFAG
PDRAPGAGVFWKFGGKPTPAVAAQNAHPAKVLQLRQEVAAALRARQAETDRKLHKQAEEMENELQQLRRALSELKHH

SEQ ID 23

ATGACGGAGGGGAACGGCGCACGGACATTTGCCGGAATCTTTTATGTTTCCATTATCATACTCTTTTCAATGCGCTATTCCAGGA
AAAAGAAAATAGCTTGTGACGGCTGCTTTTTGTTTTTCAGACGACCTGTAAATTAACGGCTGCTTATCCAATCTGCTTTTCAAACCT
ACCTGCAACCGCAAAATCTGCTGCAACCGCTCCCTCCCTGTGGGGGAGGGTTTGGGAGAGGGCATTTTTCAAGTTGCGGCAAT
TCCCCCCCCCGCTCAAAAAATTCCTTAACCGCCCCAATACAAGCCTTTCGGCTTACTGCCCTCTCTCTAACTCTCTCCACGGG
GAGAGAGGACTATGATGCCCGCCGGCGGCTTGTATTAGGAATATCTGAATCGTCATTCACGAAAGTGGGAATCTAGAAACCC
CAACGCAGCGAGATCTATCGGAGAAACCGAAACCGACAGACCCGATTCGCCCTGAGCGGGAATGACGAGGGGAACCGGCGC
ACGGACATTTGCCGGAATCTTTTATGTTTCCATTATCATACTCTTTTCAATGCGCTATTCCAGGAAAAAGAAAATAGCTTGTGCA
GGCTGCTTTTGTTTTTTTCAGACGACCTGTAAT

SEQ ID 24

MTEGNGARTFAGIFYVSIILFSMRYSRKKIACAGCFLFFRRPVINGCLSNLLFKLPATAKSAATRSPLCGGGFGRGHFSSCGN
SPPPLKKFPNRPNTSLAAYCPLNSLPRGERTMMPAGLILLGISESSFPKRWESRNPNAARIYRRNRNPTDPSRLSGNDGGERR
TDICRNLLCFHYHTLFNALFQEKENSLCRLLFVFQPTCN

SEQ ID 25

TTGCTTATAGTTGTACGGTTTGACATATGCACGGAAGGAAACGCCATGACTTTCTTCAAACCTCTACCGTCGTGCTGACCGCAT
CCGCACTCGCGCTTTCCGGCTGCGTTGCCGACCCGTAACCGGACAGCAGTCCCAAACAAATCCGCCATGTACGGTTTGGGTGG
CGCGGCAGTGTGCGGCATCGTCGCGCACTGACCCACAGCGGCAAGGCGCACGCAATTCGCGCTTGCTGCGGCGCAATCGGC
GCAGGCGTGGGCGGTATATGACTACCAAGAGCAGCGTTTGGCGCAAAACCTTGCCGGCACGAAATCGAAATCCAACGCCAAG
GCAACCAATCAGGCTGGTGATGCCGAAAGCGTTACCTTCCGACCGGCAGCGCGCGCTTGGCGGCAAGTGGCAATACGCCCT
GAACACTGCCGCACAGACGCTGGTGAGTATCCGACACGACGCTGACCATCAACGGGCACACCGACAACACAGGTTCCGATGCA
GTCAACAATCCGCTTTCGCAACACCGCGCCCAAGCGGTTGCTACTATCTGCAGACGCGCGCGTGGCGGCTTCGCGCTGACCG
TTTACGGCTACGGTTTCGCATATGCCGCTCGCTCCAACGCTACGGTTGAAGGCCGCGCGCAAAACCGCGCGCTGCAATCCTCAT
CAACCCCGACCAACGCGCGCTCAACCGCGCACGGCACATG

SEQ ID 26

MTFFKPSTVVLTAALALSGCVADPVTGQQSPNKSAMYGGLGAAVCGIVGALTHSGKGARNSALACGAIGAGVGGYMDYQEBRLR
QNLAGTQIEIQRQGNQIRLVMPESVTFATGSAALGGSQAQYALNTAAQTLVQYPTTLTINGHTDNTGSDAVNNPLSQHRAQAVAY
YLQTRGVAASRLTVYGYGSHMPVASNATVEGRAQNRREILINPDQRAVNAARM

SEQ ID 27

ATGAAATCGAAACTTACTGTCGTCTATTACGATTGGAAGCAATATTGCAGAAGAAATACTGTCAGGAAACATAATGCCGTGATG
GAAATTTTCTTATTCAAGAGATTCTCTTTTCGACCCGAATTTGGCTTTAAACGACATTGTTGCCATAGAACGTGAGGATAAGAT
GCTGTTTTTCGACCACTTGATAAAGCTTCAGGAAATACCAGATAAACATCGTTGTTTTGGATCATTTCCCAAAGGATTTATTG
GCAGCCATAGAAGAACACAGTGGTAAATCAGAAAAATGGAGAGAAATATTATTATCGGTTAATTTTCCGCCCAAAAAATATAATT
CTGATTTAAAGGAATTTTAAATAGATATGAGGAAGCAATATCTCAGCTACAGGGAAGCTTGTTTGGGCTTCTCT

SEQ ID 28

MKSKLTVVYYDLESNIAEELSNGNIMP DGNFLIQEIP LFAPNLALNDIVA IEREDKMLFFDHLIKASGNTTINI VVLDHFPKDLL
AAIEHSGKIRKNGENYLSVNFPPKKYNSDLKGLNRYERANILSYREACLGFS

SEQ ID 29

ATGGTGCAATGGCAACAATAACCAAGCGGCGCAATCTTCCGGCGAAACAGTATATCGGGTTACGGGTACGGGTACGGCAAGAAAG
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AGCCGGCCCGAAGCTGCTTTTCAAGCGCGGCAAGGTCAAGATGATGACGCTGTCCGAAGCTATGCGGAAGTATCTTAAACGAAACG
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GGTCTGATTTCCGGAACACAGTTATGCAGAGCGCGCGGAATCCCCGAACCTGGACATTGCGCCAATCCGGGCTTCTACGGCAT
GCAGGAGCTGCAATATATCCGTTCCGTGCTAAACACCGCTTTTATGTGTGGGGCTTGAAATAGGCTGGCAGGAATTTGGATTTT
GCGGCAACCGGCTGAAACGCTCGAATATGGTTGCGAAATCTGCAATCAGGGACAGATTGCGGACCACGGAAGAACTGCAAAACCC
TGACAACTTATTTCTGCGGCAATGGCAAAGCAGGAAATCTTCCATACCGATGCACCTGATTTATGTGGCTGGCGATTATATACCTC
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TCAGGAAGCGTATGCTTGCACAAAGGCATGCGCGACAGCCTTGATACCGTGCACCGGAAATCGGTTTCCGCGGCTTGGACGAG
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ACGATTCGCAATGCAACGGGTAAACGCTGCATGACGTTTGAACAGCCTGCAGAGGTATGTGAGCGTACGCAACGCTCGACGC
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SEQ ID 30

MVQMATITKRRNPSETVYRVQVRVGGKGYPAFNESTF SKKALAVEWGGKREAEIEAGPELLEFKRGKVMITLSEAMRKYLNET
LGAGRSKRMGLRFLMEFFIGGIGIDKLKRSDFAEHVMQRRRGIPELDIAPIAASTALQELQYIRSVLKHAFFYVWGLEIGWQELDF
AANGLKRNNMVAKSATRDRLPTTEELQTLTYFLRQWQSRKSSIPMHLIMWLAIYTSRRQDEICRLLFDDWHKNDCTRPVRDLKN
PNGSTGNKFEFDILPMALPVIDELPEESVRKRMLANKGLADSLVPCNGKSVSAAWTRACKVLGIDKLRFDHDLRHEAATRMAEDGF
TIPQMQRVTLHDGWNLSLQRYVSVRKRSTRLDKFEAMMQAQSDIKSGK

SEQ ID 31

TTGCGACAACGGCGCGGCTTTCAGCTGCTTCAACTGGACCGAACATTTCAAACGGACGGCAAACCTGATCAGCCTCATGCACAGG
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CGGCACGGCTGCGGCGCGGCGGAACAAGCGTTTTTCAGCGCGGCGAAGACGGCAAACCGCAGCGCTCAGCGCATCCGCAAC
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AAAGCCTTGTTGCAAACTACCTGCGGCAAAGTATACACAAACAGCTTTTCTTTATACCGACGGCGAACCGCAAGACTGCA
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AACAGACACCTGCTTGGCGCGACACTTGGCAAATCGAACCGGACTTGTGGCAAACCGTGCAAGAACCTGACGCGGAATGAGAA
AAGGAAGACCTGCTTCTTGGAAACACGAATGCCGTGACGCGCGGCAAGCGGATTGCCCGGGAATTGAGGTTTCAGCAAAATGG
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AAAAAACACTACTTCCCGTGACGCTGCCACTTTTTCGGAGGGCGCGCGC

SEQ ID 32

LRQRRRLQLQLDRTFQTDGKPDQPHAQSGGMRTHIRTCVYHDSGTGKSNTASGISGTAAGAEQAFSSAAKTANRSASAASAN
APPHDPKPKNGRKPMTFQGHNNRKKAGGYAEYITGSLRLVAAKVRRYCGEHPGVFDGAAGSGQLEQYIEPSDFRAVEIQAEAC
KALLQNYPAKVYNTSLFLYTDGEPQDCTVMNPPFSIKLKDLSSEDEKSRIAQEPYWKKSQVADIEFVLKLENARRFGFFILFP
IAYRKSEQRFREIIGNRLAELNRIQAFEDTPIEVLLLVLDKDTDGGCIRELYDCKTDTLAADTWQIEPDLWQTVQEPAPPKE
KEDPVLLEHECRDAAAKRIARELRFKRMVNEIEGWPHAEFDGFCDRLCNLIAQEKYGGKHYPFCSLPLFGGAAG

SEQ ID 33

ATGCAACAGTAGCAACAAAACCGACGGCAAAACAGATGCTTCCGCCAAACCGCGCGGCGAAGGAATCAACCGCGCAGGAACCGG
CCGTCAAACCGCGGACGGTACAGAAACGTTGACCGGAACCGGCTGTCCGCCCGGTCAAAGCGCAAAAAGAAAACATCGCCCG
GATGTTGCTTGGCGCAAGGATATCGGAAGACGAAGCCCTGACGTGCGGCATCATGATGCGGCTGTCCCTGCAGGATATGCGCTAT
GCCGTGAATCAGGAATTAATCAACTTCGCCGAACATATCGTCAAACAGGTGCAACGCTTGGGCTGTACTGCAACACTGACGACC
CCGCGAACGGGGAAGCGTACTGTTGCTTCCGCGAAGCATCGCAGGCGCTCGCTCAATGGACTAAAGATTTTGACAATTTAAG
CCGAATCAGCGCAACTCGTGCTGCGTCCGCTGTCAAATCTCTTCGCCGCGTACGAAGAATTTCTGAAAGACGCGCTGCACGG
CTGATAGCCGAAGTATCGGCATACCTATGGCCGTGCGGGTTGCCAAGAAAGCCATGCGCTTTTATAGAGCTTGACGGCGGTTTGA
TTTCGGCGGTTGGCAAAGTCGTCAACGGCGCGGATTGCGCGCGGGAAGCCCGCTTAAAGTCCCGTACGCGGAATTTACAGG
CCGGATCTACAGCCGCGAACCTGCTTACGATGTGGGACTTTCAGGCGGACAAGGAGCTTTCGGCGATGTACGGCAAGCCGCTG
AATCCCGTGCAGCCCGGACGGAAGACGTCGCGCGCGGCGATGATGAAATGCTTGTGCGGACAAAGCGCGCGCTTGGTCC
GGGCGTAAAGACTCGGAAGACGTCATCCGGCATTGGCACAACGGCGCGGCTTCAGCTGCTTCAACTGGACCGAACATTTCAA
ACGGACGGCAACCTGATCAGCCTCATGCACAGGAAGCGCGCGCA

SEQ ID 34

MQTVATKPTAKQMLAAKRAAKESTRQERAVKRAGTVRNVDRNLSARSKAQKENIARMLSGAKVSEDEALTCGIMMRLSLQDMRY
ACNQELINFAEHIVKQVQRLGLYCNTDDPANGESVLFACREASQAVAWTKDFDNLSPNQRLVLRPLSNLFAAYEEFLKDPAR

LIAEVSAYSILAVRVAKKAMAFLELDGGLISAVGKVVNGADSRABARRLKMPYAEFTGRILHAANLLYDVGIOADKELSAMYGKPL
NPVRRPRRISDVRRPMMKMLVADKGGALVRAVKDSEVDIRHCDNAGFSCFNWTEHFRTANLISLMHREAA

SEQ ID 35

ATGTACGGAAATGTGCCGGATTTAGATTGCCTGCTTTACAGGAAACCGCATATAATCAAAAGTATGAAACCGCACACGATACCA
TTTTCCAAGAGCCAAAGGCTGCCAAGCGCGCGCTTCTCTGCTGTACAAGGCAAACGGCAGGCTTGAAGTACTGAAGCTGATGAA
GCTGATGTACTTGAAGCTGAACGTGAGTCTTTTTTACGCTTCGGAGAAGGCTTACAGGTGACGCGTTGGTTTCAATGCCGCGATGGT
CCGGTACTCTCCATGACCTTGGATTTCATTAACGGCGGACATGAGTCCGTTCCGAACGGATGGGCAACGTGGGTAGCGACCCGG
AAAACAGGATGCTTGCCTTACCGGATCCAAGTATGATTCCGACGCGCGGCAAGACTTATCGGCATTATCCGAAGCTGATTGGA
AGTACTGGAATCGGTTTGGGAGAATTACGGCCATTATTCGCGATGGGATCTGCGCAACATGACCCACAACGGGTTATGCCCGGAA
TGGGAAGACCTCAGCGCTCAAGCCGCCGATTCCCATCAAAAACTGTTGTCTGTGCTTGGTTATGATGACGAACAAGCCGCTAG
CGATTGTAGAAAGGCTGGAAGAACAGGCTTACATCAATCGCGCTTTCGGG

SEQ ID 36

MYGNVPDLDCILLYRPHIISKMPKPHNDTIFQEPKAAQAAFLLYKANRLEVLKLMKMLYLAERESFLRPFGEGLTGDALVSMFPG
PVLSTMLDFINGGHESVPNGWATWVSDRENRLALRDPMSMIRTPQDLSALSEADLEVLESVWENYGHYSANDLRNMTNHLCPB
WEDPHGSSRPPIPKLLSVLGYDDEQAVAIIVERLEEQAYINRAFG

SEQ ID 37

ATGTTTATCCCTGCCCGCCTGCACAAAGACGAACATTCCGCATATGGCGTAACCATCCCCGACCTTCCCGGCTGTTTCTCTTGCG
GCGACACCGTTGAAGAAGCCGTCGCCAAGCCCGTTCTGCCGCTATATGCATATTGACGGTATGATTGAGGACGGAGGGTTCAA
AAACCTTGCCGTAAGCAGCATTGCCGATTGAGCCAAGAACCTGATTATCATGGGGCAACATGGGTAATGATTGAAATCAGCCCT
GCAAAATCAGTCGGCAGCAAATCCGATTCAACGTCAGCTGGCCGCAATACCTTCTTGATAGAGTGGATGAATATACATCCGCAA
ATCATGAAACCCGTAGCGGTTTTTAGCCAAAGCCGCTTACCATGAATCAGGCA

SEQ ID 38

MFIPAALHKDEHSAYGVTIPDLPGCFSCGDTVEEAVANARSAAYMHIDGMIEDGGFKNLAVSSADLSQEPDYHGATWVMIEIDP
AKISRQQRIRFNVSWPQYLLDRVDEYTSANHETRSGLAKAALLTMNQ

SEQ ID 39

ATGAACCGATATGCCATGCGTTTTCGCGTCATACGGTTTATGCCCTATGTCCAAACGCGCGAATTGCCCAACATCGGCATCATCA
TAACCCACCCGCAAAGCGGCTGCTTCGACTTTAAATCGAACATCGCTACAGCAGATTGAGCCGTTTTCGCGCGCTTCGATCC
GCGCGCTATAAAGCGCGGACCCGTGCCCTTTGAAAAGAAATTACAGCGGATTAGAAACCTGGCGGCACACTCCGCGCCCGATCAG
ATACGCGCCATGCGCCGACCATCTGACCCGCCCGCGCGAAGCCCTGATTATGGCCGCCCAACCGGGCGTAACCTCGCCCCGACA
GGGGCAGGAATGAACCGCTGTTGATTATTTGTGCGCCGCGAGCTTCGCCAAAAACCAACCGAAGCAGAACTTACCCGACA
AATACAGGCAATGTTAAAGCCGCTTCAGACGGCATAACCCCTCAAAGAAAGCACAATCGCGCAGCCGTGAGCTTTACGCGCTCC
ATCCCTTGGTGCAAAAGCGGAAACCGCGAAATACGGAATCATCAAGCCTATCTATTTCGGACGGAAGACCCCTGCCGACA
TCTATTACAAGTCTGATAAGCGGATTGCCGCGCATAAAACGGTTGCGGCGCGCGGATACATCGACCGCTCTGAAATATTGTTGCG
CTACGAACCCGCGGAGCGTCCCGACAAGGCACAAGAAAGGCATTGCTTGACGTATCGGGCGACCTGGAGGAACAGGGCATAACAG
CTTGCCGATAACCGAAGCGAAGGCAAAATCATCAGAACTTTGCCCTGCGG

SEQ ID 40

MNRYAMRFVIRFMPYVQTRFANIGIIITHPQSGCFDFKIEHRYSLSRFRFRFPAYKAATRAFEKELQIRINLAHSAAPDQ
IRAMPDHLTRPREALIMAAQPGVTLAPDRGQELNRLFDYFVARSAFNQPEALTRQIQAMLKPLQTAYPFKESTIGDPSGFHAS
IPLVQKAENGEIRKLIKPIYFGRKDPADIYYKSKRIAGIKRLRRGGYIDRSEILFAYEPPERPDKAQEKALLDVSGDLBEGQIQ
LADNRSEGKIIRNFACG

SEQ ID 41

ATGAAAAAAGAGAATTAAATGAAATTGAGACGGCTGAATGTGCCGAATAAAAGAAATTTTAACTCAAAAAAGAAGAACTTA
AGCTAACCAATACAGCTGGCAGAAGCTGTAGGAGTTACTCAAAGCGCGGTGAACCATATTAAATGGCACCAACGCCTTAAA
CGCTCCATTGCAAGCCAGTTTGCCAAATCTTGCAAATCTGTTTTCGGATTTCAGCTCCGACTTGCCGAAGAAATAAGCAGT
ATGTCCATCGGCATGTGATGGAGATAAATGTCTGGCACTGCAAGCAGACATCTCGACACCAACACCATCACCTCAACCTATACG
ACGTATCAGCCAGTTGCGGTGATGGGGTAGTCAACCCGACTATCCGCAACTGCTACGCTCGATTGAGATTCCCAATGACGCGCT
ATTTCGAGCTTTTGGGGACAAACAATCTGACAAACGTGCGAGCTTATGCCCGCGGACGGCAGCAGCATGGAGCCGACCATTCACAG
AAATCGATAACTTTAATCAAAACAGAGCTTAGCAAGTTTCAGACCGCGCGGATCTACCTGTTTACCTTTGACGGTTATACCTACA
TCAAACGCCGTGTCAGAGGCAAAGCGCGCGGATACACGCTACCAGCGACAACAGGCATTACGCCAAGTCGGATTTTCTGATAAA
CCCTGAAGAAGCCGACAAATTCACATTACCGGCAAAATTTGGAAGTTTTCGCGCTGATTTTTACGCTT

SEQ ID 42

MKKRELNEIETAECAELKRIFNSKKEELKLTYQYKLAEAVGVTQSAVNHYLNGTNALNASIASQFAKILQIPVSDFSLRLAEIIS
MSIGIDGDKLLALQADNLDNTITLNLVDVSACGHGVNPNPDYQPLLRSIEIPNDALFELLGTNNLTVNQLMPPDGDMSMEPTIPQ
KSITLIKTDVSKFQTGGIYLFDFDGYTYIKRLSRGKGGAIHATSDNRHYAKSDFLINPREADKFHIGKFWKVLPLDFLDL

SEQ ID 43

ATGAGTGCAGGCTGATGGGGATGGCTTTCAAAACGGGTATCCCGAGGGGGCAGCGTTTTGTTTGGTAAAGTTGTGCGACTGCG
CCAACGACGATGGCTTGTGTTATCCGTCGCAAGAACGCTGGCGGAAGATACGGGCTTCGCCGAAACGCCGTCAGGCGATAT
CAAGTGGCTGAAGGATAACAATTTCAATCAAGTCCGCCCGCGCGGAGAGGGGGCGGAGAGGAAGTCCGACATCTACCGCATCAAC
GTCGCCCTGCTTGAAAAATGCTATGCGGAGGCGGCAAAACGGAAGCGCGCGGAGGCAAAATGTGGGAAGAACCATTGGATT
ACGAACCTTCGGATTTTGAACCGTTCGATTACGAACCTTCGGATTTTGAACCGTTCGGATTACGAACCTTCGGATTTTACGCTTAA
GAACCATCAGATTTTGAAGCATGAACCATCAGATTTTGGCTAAGAACCATCAGATTTTGGCGTAAGAACCATCAGATTTTGAAGC
GGCGAACCATCAGATTTTGGCTAAGAACCATCAGATTT

SEQ ID 44

MSARLMGMAFKTGIPRGQRFVLVKLCDANDDGLCYPSQETLAEDTGFAETAVRQHIKWLKDNFIFKSARRQRGRERKSDIYRIN
VALLEKCYAEAAKRAARQAKMWEEPLDYEPSDFEPSDYEPSDFEPSDYEPSDFDAKNHQILSDEPSDFALRTIRFCAKNHQILS
GEPSDFALRTIRF

SEQ ID 45

ATGGCTTTGAGGAACGCGTCTGATTTCTTGGGGGCTTACGGCGCGCGCGTGCAGCGGAGGCAATGCGCGGAACACGGCG
GATACGCGCGGAAAGCGTTTTCGCGCGCGTGTGGACGGGCTGCCCGGCTGCCGGAAGCTGGAGGCGCGGACGAAATGGCGGC
ATACCGGAAACGCTGCGCGCGGGGCGATGCGCGACGCGTGGAAAAACGCATCGGGCGTTGGGCGATCGCCCCCGGGTTTCA
AACTGCCGGATTGAAAACTACGCGCTCAGCGATTTCGATCCCGGGGATGGCGAGGGCGAAGCGCGCCCGCCGAGTATGCGGCAA
ACTTCGCGGATGTGTGACAGCGGGGCGGAGCATGATTTTTCGGGCGAGGAGGGGACGGGCAAAACCACTTGCTGCGGCAT
CGCCCCGGAAGTCAATCGCGCGCGGCAAAAGCGCGCTGGTCATCAGGTGGGCGATATGCTGCGGACGGTCAAGGACAGTTTCGGC
GGCGCGCGGAGGCGGGGGCGGTCGGGATTTCGTGAAGCCCCGATTGCTGGTGTGCTGGACGAGTTTCGGCGCGGGCAGTCTGTCTGG
AAACGGACGGGCGGATTTCGTTTTCGCTCGTCAACGCCCGGTACGAGCGGCTGATGCCGATGCTGGTGTGCTGACCAACCTGACGGC
GGAAGCCTTCGCGGAAAAACCCGACGCGCGGATCAGGGACAGGCTGCGGGACGCGCGGCAAGCTGATTCCGTTGACTGGGAG
AGCTACCGTGCG

SEQ ID 46

MALRNASDFLGAYGGVVRERRQCAEHGGYAAKSVLRGVWTCGPACRKLAADEMAAAYAEILRRGAMRDALEKIRIGRSIAPRFR
NCRIENYAVSDSIPGMARAKAAAEYAANFADVLQTRSMIFSGRRGTGKNHLACGIAREVIAAGKSALVITVGDMLRITVKDSFG
GGGEAGAVGIFVKPDLVLDEFAGSLSETDGRILFSVNARYERLMPMLVLNLTAFAFRENTDARIRDRIRDGGGKLIIPFDWE
SYRA

SEQ ID 47

ATGAATATAAAGAATTTATGTCTAACTATACCAACCATCCCGTTCTCTTTATTGGAACAGGTATGAGTTTGAGATACTTAGATA
ATTCATATACTTGGGATGGTTTATATCTAAATTCGAATAGATTATTTGGAGATGATAGGGAATATTTGAACATCAAAATCAGC
GTACTGTGAAGATGGTAGATTCCAATATGAAGAGATTGCGAGGAATTACAAAGTAAATTTGATAAAGTTTGAAGAAATGACCCCT
GATGGTAGATTTAAAGAAATAATGATAAGTTCTTTGAAAATATGAGGCGGGAAACACCTTGAGCAGGTTTAAAGATTTATATAT
CCACCCGTCTCTCACAATTTGAATTATAAAGATAATTCTAATACAGAATTATCTGAATTAATAAAGCGAGAAAAAATGTAGGGTC
AATCATTACCAACAAATTTATGATAAATAGCCCAAGATATTTTGAATTTAACCCTAATTTGGTAATGATATCTTTTAAGCAAC
CCTTATGGCTCAGTATACAAATACATGGTTGTGTGGACGATCCATCAAAATTTATTATTACCAAAAGGATTATGAGAAATTTA
AAGAAAAATGAACTTATTAGAGCCCAACTATTATCGTTATTATTCACAATCCAATCATATTTCTTGGATATAATGTTGGTGA
CGAAAAATATCAAGAAATTTTAAAAACAATCTTTACTTATGTAGAACAACAACTCTCCTTCAGCTAATAAATTCGTAGGAATTTT
TTACTCGTAGAATATGAACCTGAGTCTAACAATGAAGATATTTGTTGAACATGATATAGATATAGATATAGATATAGATATAGATAT
TTAATAAAATCAAAACAGATAAATCTCTCAAAATTTATAAGCTCTTGCAGAACTAACACTACCAATCTCAGCTATGGATGTACG
TAAATTTCAATCTATAGCAAAGGAGATTTTACTGGCGGTAACTATAAGTTAGCTTTACGGAAGATATGGACAATTTAAATAAT
AGCGATAAAGTGGTTGCTATTGGTTCAACTAAAATATCAGCTACAATTTCAAAACAACATCAGAGATGATGTCAAATTTATTTCA
AAATAATTGAAGAGGAAAAATTCACAATCTTCAAAATTAATAGATAAACATAGTATAGCATCTACGCAATATTTTCTATTATG
ATTTAGTAGGATATGTTCTGATATACATAAAGAAGCTGTACTAAAACGCCAACAAGAAAGAAATTTAGATCATTTTATTGAAGAA
ATAAATAGGCGTTGTAAAAATAATCATTTCAATCCATCCAATCAATTTTAGATGATGAAATATTTTCAAGACATATAAAACGATG
CGATTGCTTGGGGAATATGGAATAACCAACTTTTCAAGATGAGGTTGAAATTTTAAAAAATTTTGTGAATAAAAAAATAC
GCACTATAAAGACTACTATGTATGTTGATTATAAAAAATATCGGATACCTGTC

SEQ ID 48

MNIKEFMSNYTNHPVLFITGMSLRYLDSYTWDLGLSKIAIDLFGDDREYLNKISRYCEDGRFQYEBIAEELQSKFDKVLENDP
DGRFKEINDKFFENMRAGNTLSRFKIYISTLLSQLNYKDNSNTLSELKKARKNVGSIITNYDKLAQDIFEFNPLIGNDILLSN
PYGSVYKGVDDPSKIIITKDYEFKEKYELIRALLSLFIHNPFIIFLGVNVDENIKEILKTIITYVEQNSPSANKIRNF
LLVEYEPESNNEDIVEHDIDITGFSTIRINKIKTDFNSQIYKALAEITLPISAMDVRRKPSIAKEIYTGNNIKVSFTEDMDNLNN
SDKVVAIGSTKTIISYNFQTTSEMSNYFKIIEEENSQLLKIDKHSIASTQYFFIYGFSRICSDIHKAVLKRQOKEKLDHFIEE
INRRCKNNHSSIQSILDDENISDTYKNDALAWGIWNNQLSEDEVENYLKNFVNKNTHYKRLLCMFYDKKYADTV

SEQ ID 49

ATGCTCTTCAAACCTCCGTTACCTCGCATCAGTATTGGCATTGTCTTCACTGTTGGCGGCATGCGGCGGTTCAGGAAAGTCTGCGG
CAGGCGATGCTTCTCCTGCTTCCGAGACCGAAGCGGCTTCCCAAGTACAGGCTCGGAAGCGGTCTCTTCCGCTTCATCGGCCTC
GCCCGAAGACCAAGACCTTTTGAACCGCGCGCAAGGTGTATTCCAACCTTTGCGGACTGTGGAAGAAATGAGAAATCCGTCCG
TTTACCGAAGAACAGGTCAAACCTCGGACACCAACTCTGGTATGAACCAAGCCTTTCCAAAGGCAATACCGTAAGCTGCAACTCTT
GCCACAACCTTGTCTCCGCGCGGTGTGGACAATATGCCGACAGTCAGGGGACAAAGGGCAGTTTCGGCGGACGCAACTCGCCTAC
CGCATTTGAATGCTGCGCTGCTGGGCAGCCAGTTTGGGACGCGAGCTGCGCGCGGATGTTGAAGAACAGGCTGCGCGGCTTTGGTG
AATCCGGTGGAAATGGCGAATGATTTCGCAAGAGGCGGCTGCGAGCCAAATCGCCAAAGTTCCCGAATATCAAGAAATGTTTAAAA
AAGCTTTTCTGTAAGACGCGCGGCTTCTGTTTAAAAACATCACTACCGCATTTGGTGGCTTTGAGCGTACCCTGCTGACGCGGAC
CAAATGGGACGAATACCTCAAAGGCAACGTCACGCGCTGAGCGAACAGGAACGAAAGGCGTGCAGCGCGTTCATGGACAACGGC
TGTATTGCTTGCACAAACGCTGTCAACCTTGGAGGCACGACCTTCCAGAAATTCGGTCTGCTTCAAGGGCCGTATTGGAATTTCA
TTGAAGATCCGAAACGCGACAAAGGCCGTGCTGACGTAAACAAAAAACGGAAGACGAATTTTCTTCCGTGTTCCGGGGTTGCG
TAACGTGGCTAAACCTTATCCGTATTTCCACAACGCGAGCGTGTGGGAGTTCGGATAAGGCGATTACCATATGGGTAAGGCGCAA
TTGGGTAAAGACATTCGAAAGAAGATGTGGATAACATCGTCTGATTCTCTGAATGCACTTTCCGCAATGTTTCCGAATCAGCGC
GCACGATGCCGGAACCTGCCCTGACCGCACCGATGGAATCTAAGCCGGAACAAAA

SEQ ID 50

MSFKRLRYLASVLLSSLLAACGGQEKSAAGDASPASETEAASQVQASEAVPSASSASPEDQDLLKRAQGVFQPLPTVEEMQKIRP
FTBQVQLGHQLWYEPRLSKGNTVSCNSCHNLASAGVDNMPTSQGHKGQFGGRNSPTALNALLGSQFWDGRAADVEEQAGGFLV
NPVEMANDSQEAAAKIAKVPEYQEMFKAFPEDGAVSFKNITLALGAFERTLLTPTKWDEYLGKGNVNLSEQRKGVRAFMNG
CIACHNGVNLGGTTFQKFLVQGPYKWFIEDPKRDKGRADVTKTTEDEFRRVPGLRNVAKTYPYFHNGSVWELDKAVTIMGRAQ
LGKDIKREDVDNIVVFLNALSGNVSESARTMPPELPLTAPMESKPDNK

SEQ ID 51

ATGACCGCCCTCACACTCTACCGGTGCGCGGCAGACGTACAGGCGGCGCTGGATTACTACTTTGACAGCGAAACCGAGCGCGGAAG
ACACGCTGGAAGCCGTATCGGGCAGTTTCGAGGTCAAAGCCCAATCCGTTATCGCTTATATTAATAAACAAGAAATCACGGAATA
AATGCTTGAAGGGCACATCAGGCAGATGACCGGGAAGCTCAAGGCGGCAAAAGCGCGGAATCAAAGCCTGAAAGACTACTTGGCG
CGCAATATGACAGGCGCGGGCATTACCGAAATCAAAGCGGATGACGCGCACTTTTAAAGCCTCGTTCCGCAATCCGAAGCCGTCG

TGATCTTAGACGAAGCACAAATCCCGCCGAATTTATGCGTGAGGCCGTCAAACCGAACCGGACAAAACCGCCATCAGAAAAGC
GATTGAAAGCGGTTCGGCAAGTAGCAGGCGCGAAGATTGAAGGGCGGAAGAATTTGCAGATTAGA

SEQ ID 52

MTALTLRCAADVQALDYFDSETEREDTLEAVIGQFEVKAQSVIAYIKNQEITEKMLEGHIHQMTGKLLKAAKARNQSLKDYLA
RNMQAAGITEIKADDGTFKASFRKSEAVVILDEAQIPAEFMREAVKTEPDRTAIRKAIESGRQVAGAKIEGRKNLQIR

SEQ ID 53

GTGCAGGCGGATTTAGCCTACGCCGCCGAACGCATTACCCACGATTATCCGGAACCAACCGCTCCAGGCAAAAACAAAATAAGCA
CGGTAAGCGGATTATTTAGAAACATCCGTACGCATTCCATCCACCCAGGCTGTCGGTCCGCTACGACTTCGGCGGCTGGAGGAT
AGCGGCAGATTATGCCCGTTACAGAAAGTGAACGACAATAAATATTTCCGTCGACATAAAAGAGTTGGAAAACAAAGAATCAGAAT
AAGAGAGACCTGAAGACGGAATAATCAGGAAAACGGCAGCTTCCACGCCGTTTCTTCTCTCGGCTTATCAGCCGTTTACGATTTCA
AACTCAACGACAAATTCAAACCTTATATCGGTGCGCGCGTACGGACACGTCAGACACAGCATCGATTGACTAAAAAAAT
AACAGGTACTCTTACCGCCTACCTTAGTGATGCTGACGACGAGTTACGGTTTATCCTGACGGACATCCGCAAAAAACACCTTAT
CAAAAAAGCAACAGCAGCCGCCGCTTGGGCTTTCGGCGCGATGGCGGGCGTGGGCATAGACGTCGCGCCCGGCTGACCTTGGAGC
CCGGCTACCGCTACCAAACTGGGGACGCTTGGAAAACACCGCTTCAAACCCACGAAGCCTCATTTGGGCATGCGCTACCGCTT
C

SEQ ID 54

VQADLAYAAERITHDYPEPTAPGKNKISTVSDYFRNIRTHSIHPRVSVGYDFGGWRIAADYARYRKWNDNKYSVDIKELKNQN
KRDLTENQENGSHFVAVSSGLSAVYDFKLNDFKFPYIGARVAYGHVRHSIDSTKKITGTLTAYPSDADAAVTVYPDGHPQKNFY
QKSNSSRRLGFGAMAGVGDVAPGLTLDAGYRYHNWGRLENTFRFKTHEASLGMRYRF

SEQ ID 55

ATGGACGGCGTTGCGGCGGTAGGCGGCATTGTTGACCGCGCGCCACCCTTTCGCGTTTCGGCACAAACCGCGCAAACTGCCAG
CCGCCGAACACGGTTGCCGAGCCGCCAACCGCTTGCAGCGACACATAAAGCCCGTCTGCCAACCGTCGTTGCGTTCCGCC
GGCTTGTTCGCGGTAGCGTTGGCGGTAAACGTTCCAGCGACACCGAAAGCTGCGACCGGCGGCTCAGCGGTAAGATGCGCCAA
CTGCACACCCGCCCGTGCAGCATATACGGCGCAAGCGCGGTCGGCAGGCGGTTTCGTTTTCGCATCAAAGCCGTGCGTA
CCCGACAATTGCGCCTGATAAAACGGCAAAACCCCAACGCTGTCGCGCGCATTTTATACTGCCAGCCCAAAATAAGCCCTGCCGA
AAGCATCGTCATAAGCCGATTGCGGCTGAAATAATAGCTTGTGCCCGGACATTGGCGCGGAACAGCAGATAATGGTTGTCCGC
CAGCGCAGTCAGCTTTCCGCCCGGCTCATAATCCAACCTGCGCGACGACAGGTCCGGTAACGCTGCATATCCGGCTGCCG
CCGCCCTGCAGCAGTATTGCGCGCGGCAATTGTTGGCGTTTGTTCACAGAAGGGCTGATGCCGCCGAAAAATGCCAGCCCG
TCAGCCCTCCGCTTTTTCGGAACCGCCCATTTTCCAAAACCGCGCGCGCAATCCAATTTTGGCGCCTCCGCAAAATG
CAGCCCTGCCGACTTCAGCCGGAATCGTCAAACCTCCGCCCGCGCAATCCAGCAAAACCGCTCGTCTGCCGCTATTCCTG
TGCAACGCCCGATAGCGCGCCACCGCTCCGCCCGGCTTCCGCCAATTTCGCCAGCAAGCCCGCGCCTGCCGTACAAACCG
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GTGTTCCAACTGCGGCGCGACAGCAGGAAATCCCGCTCGATTACGCGCAACCGCGTTTGGCGGCAATCCCTTCCGGC
GGCATTTCCCGCCCAACCTCCGCGCGCACGCTGGGCGCGCAACCGCGCGCATCGTCCCGAACGTCGGGCAAGCCGGCGGCAT
ACGCGCGCACCGCACCCCAACACACAGCGCGGCACAGCCGCGCATACCGGATACACACTATCCTTCAATTTGCGCTTCTTAAA
AAACACCGCGCGGCGCGCGCAGAAACCGCGCAAGCCCAACGCGCGCGGACGCGGCGCATCATATAGTGGAT

SEQ ID 56

MDGVAVGGIVDRAAHRFAFRHKPRKLPAAEHGCRQAQPPCQRHIKPVLPVFAFRPALFAVALAVTFQRHRKLRPAQAQVRMRQ
LHTRPVQRHRRKPAVGRFRFRKAVATRQLRLIKRQNPRLPRIFILPAQISPAESIVISRFAAEILACAPDIGAEQQIMVVR
QRSQFRPGLIIQPCRTDRSGNAAYPAAALQAVLRRGIVGVFVHRRADAARKMPARQPLRFFPETPHIFQNRRLQIQFCRLRKM
QPCRLQPEIVKLRRRQIQONPLVCRIIPVQRPIARHRLRRPSRQFRQSPRPAVQHRIRIIRQLGIQIRQRSDQIRLIVERVAQN
VFQQLRARQQEIPVDYARTAVCGRIIPFRHSRPTLRSLTGAQRRRIVPNVQAGGIRADRTPTNQTQPAYPIHTILQFAFLK
KHRTAAAEPTQAPRAADAHHIVD

SEQ ID 57

ATGAACATTACCATAGCCGCCCTACTGCTCGCTGCCGTCCGAACCGCATTTCAACCGCTTTTGGTATCTGGCAGAACTATTGT
CGCAATCGCACGACGTGTGCTGATTACCAGCAACTTCAAGCACTACGACAAATCTTTCAGACGGCCGAAGATGCTAAGGCCGC
CTCACAAGGCCGTCTGAAAGTCATGCTGTGGAAGAAAGCGGATACAGCAAAACGTTGCTTTAGGACGCGTGACCAGCCATCAC
CGCTTCGTCAAACATTTTGAATAATGGTTGGAACCTGCCGTCCGGGCGAACAAGACGTCGTCTATTCCGCTATCCGCTGATG
CCACCAACCTGCTGTTGGGCAACACAAAGCGGTTGGGTTACAACTGATGTCGATGTCAGGACGTCATGGCCGAGTCTTT
CTCCTCTGTCTGCGCTTTTGAATAAATCCCGCAACCTACTACCTTTGCTTACGCGCCCAACCGGCGCTACCGCTACGCC
GACCGCTTGGTTCGCGTATCGCAGACCTATCTCGACCGCGCAAGAAGCCATCCGAACGTACCGCGCAAGTCTGCTATATCG
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CTATGACGTGGAACCGTGTGCAAGGCGTTCGCAAGCTGTGAGACGACGGGGAACGTCGAATTGCACATTATGGGCGGCGG
CCCGATTGAGACAGGCTCAAACAATATGCTGCGACGGCATCAAGTTTACGGCTACATCCCTTACGCGGAAATGATGTCGGTCC
CCAAAGGCTGCGACATTGCGGTCAACGCCATCCACTTACGCCCATCGAGTCGATTACCAACAACTCTCCGACTATATGGCTTT
GCAAAAACCGATTCTGAACAGCGAGGTCACGACGAAGTTGCGGAAGTCTTACCCTGCTGCCGCGACGAAACTACCGTTCCGGC
GATGTGGACGGTTTCTGTCGAAGCGCCAAAGATATTTGAAGCGCAAAACGACCTGTTAGTCCGACGAAATCGTCCGCCGCT
TCAGGCACGACATTTCTATCGGAAATCGTCAACCTGATTGAAGATTGGCAATGAG

SEQ ID 58

MNITIAAPYCSLPSEPHFRFWYLAELLSQSHDVLITSNFKHYDKSFRRPEDAKAASQGRLLKVMILLESGYSKNVSLGRVTS
RFVKHFEKWLNCRPGEQDVVYSAYPLIATNLLGKHKARLGYKLIVDVQDVWPEFSFSSVVPPLKKIPHNLLFPASRANRAYRYA
DALVAVSQTYLDRANEANPNVGEVVIYIGADFAALAPPFRFSKTVRFYLGTLSSYNDVETVCKGVRLKLLDDGENVELHIMGGG
PDLDRKQYACDGIKFYGYIPYAEMMSVAKGCDIAVNAHSYAMQSITNKLSDYMALQKPILNSQVHDEVAEVLTLPHENYRSG
DVDGFVQAADKILKRKNDFVQSDIVRRFRHDI SYRKIVNLIERLANE

SEQ ID 59

ATGGGCGGCATATCTGGCAGGCTGCATCCTGCGCCACCGGAAAAATTTGCACAACTGTTTTCATTATTTGAAAAACAAAGGTTTC
CCATTATGAAATCATCTGACTACTTCTATGTCGGGCTGGGCGGCACAGAAACCGCCACCGTCCGCTCCGGCGGCTGCTCAA
ACGCGACGGGCACGACATCATCTCGCCTCTCGGACGGCCCTTTGTCGGAGAGGCGCAAGCATCGGGCATCCGTTGGCAGCCG

GTTGATTTTTACCGGGGCGGGCTTGCCGGCTACCTTAAAGACACCTTTGCCTACGCCCGGATGCTGCGCCGGAACAACCGACA
TCATCGACTGCCAAATGGCGCGCGTTCGCCGGCTTGCCTTACCGCAAAATCGTTTACCGAAAACCAAAATCATCTGCCA
CTCGCACGGTTTGGACGCGGCAACCTACCCAAAACCGCAAACTCTTCGACAAGCTGGGCGGTACATCATCGGCAACTGCAAA
CAGCAACCGGAAAAGCTCATCCGCCACGGCTTCCCGCGCGCGGATTGCCTACGCTACAACACCCCCCGGAATTTTCATTTC
GGAAAACCGGAAAAGAAATGCGCGGTACTCGGCACACTTTCCCGTTTGGACACCGTCCGTGCGGTGCATCTGATGTTGGATATTTT
GAAGAAAATGGTTGGCCGCAATATACCCGTACGCTGAACATGGCGGGCATAGGAGAAGAAATGGACAACCTCAAAGCCCAAGCC
AAACGTTTGGGTATTGAAGACAAAGTGACCTTCCTCGGCGCGTCCGCGATTGACCGGCTACTTCAAAGAAGTCGATATTTAG
TGAACACGCGCATTCGCTAGGTGACCACGGCGCAGGTGTCGCAACAATATTTTGAAGCCGCGCTTACGACACGCGCTGCTGT
GACCTACAACATGGCGGGCATTTCCGAAATGGTCATTACCGGCCAAACCGGCTACTGCATTCTTTCGGCGATGACGAAGCGTTT
ATCGAAGCCGTCGATACACTCATCAAGCATCCAGAGTTGCGCAGCCAAATGGGCAAGCCCTGCACAAACATGTCGAAACCTTAT
GCTCCGACGACGAAATCTACCGACCAACCATGGCTGCGTACGAAATG

SEQ ID 60

MKIIILTTSMGLGGTETATVRLGRLLKRHGHDIILASSDGPVFGAQAAGSIRWQPVDFYRGGLAGYKSTFAYARMLRREQPDII
DCQMARVVPACALAAKIVSPKTKIICHSHGLDAATYFKTAKLFDKLGAYIIGNCKHEREKLIIRHGFAGRIAYAYNTPPEFHF
TEKECAVLGTLRLDTRAVHMLDLILKMMVGRNI PVRLNMGIGEEMDNLKAQAKRLGIEDKVTFLGGVRDLTGYPKEVDILVN
TPHCVDHAGVGNINILEAGLYDTPVVTYNMAGISEMVTGQGYCIPFGDDEAFIEAVDTLIKHPRLRSQMGKALHKHVTCLCS
DDEIYRTTMAAYEM

SEQ ID 61

TTGAAAACCGTGCGGCGTTTTCGTGGGGCAGCCGCTATACCGAGTTTGATTTCACCGATAAAATTTTCAGACGGCCCCGGCACGG
TTTACCAAGTCCGCCCGCGCGTGTTCGACAAAATCCTGATTGAAGAAGCCGCAACAAGCGGTTGAAGTACGTTTCGGGCACGG
CGTAACCGCGTTCGACAACAGCGCGGATTTCGCCGCTTGAACATCGAAACCGACACCGCGAGAGCTATGAAGTACCGCGAAA
TTCGTCTTGGACGCAAGCGGTACGGACGCGTGTCTCGCGCGCTGCTAAACTTGGAACCGCCCTCGCACCTGCGCGCGCGCAAA
CGCATTTACGCAACATCGACGACAAACATTACCCACCGGAAATTCGACCGCAACAAATCCTGATTACACCCATCCGCAACACCG
CGACGTGTGGATTGGCTGATTCCCTTCGGCGACAACCGTTGTTCCGTGCGCGTGGTTCGGCACACCCGCAAACTTGCCGGCGAA
TCGGAACCGGTGTGAAAAAATTTGTTTACGAATGCCCGATGTTGAGCGAAATTTTGGAACAAGCCGTTTGGGAAAACGATTTC
CGTTCGCTCCATCAAGGCTATTTCGCCAACGTCAATCACTGCACGGCAGGCTTTCGCGCTGTTGGGCAATGCGCGCGAGTT
CCTCGACCCCGTGTCTCGTGGCGGTAACCATCGCGCTGCACCTCCGCCAACTTGCTGCCGATCTGCTGACAAAACAACCTCAA
CGCGAAGCCCGCGGATTGGCAAACCGAAATTTGCGGAACCCCTGATGATCGCGGTAGACGCGTTCGCGACCTATGTGGACGCGTGT
ATGATTTCCGCTTCCAAAACGTGCTGTACGCGCCGACCGCAGCCGGAATACCGCGTATGCTTTCTTCGATTTTGGCAGGCTA
CGCGTGGGATACCGAAAACCGGTTTCGTGGCGAAATCCGAACAACGCTGACTGCCTTGTGAGAATGGGTGCGTCAGTTGGAAAGC
GAA

SEQ ID 62

LKNGAASFWSGSRYTEFDFTDKFSDGPGTVYQVRRVDFDKILIEBAKQGVFVRFGHGVTAFDNSGDFARLNIEITDGTESYELTAK
FVLDAAGYGRVLPRLNLETPSHLPPROTHTHIDNITHPKFDRNKILITTHPQHRDVWIWLIIPFGDNRCVGVVGTGPKLAGE
SETVLKKFVYECPLSEILDKAVWENDFPFRSIQGYSANVKSILHGRHFALLGNAEFLDPVFPSSGVTIALHSAELAADLLTKQLK
GEAADWQTEFAEPLMIGVDAFRTYVDGWYDFRFQNVVYAPDRSPEISRLSSILAGYAWDTENPFVAKSEQRILTALSEWVGQLES
E

SEQ ID 63

ATGTTTTTCAGCGCAACAGTTAGGACAAGCAATATCAGAAGCGATTAAGAGAAAAATGTCAGTCAAAAGGAGGTTCGCCGATCATT
TTGGGGTGAAACAGCCAAGCGTTTCAGGTTGGATAAAAAATGGACGAATAGATAAAAAACATCTAGATAAAATTAATTGATTATTT
CTCAGACGTAGTAACGCCAAGCCATTTCGGCATTGAAACATTAGAGTCTTAAATCGAATGAACAAAGTAGCATACGTTTCCCC
CGCTTAAATGCCGAAGCGACCTGCGGCGCAGGCACGATTAAACGACACTATATCGAGGTTGTGGATTATGTAACCGTCGCTGCCG
CATGGGCGCGGGAGAACTGGGCGGAAACCTCAACAAAATCCAAGTCAATACAGCCCGTGGCGACAGCATGGAGCCACCATCGA
AAACGGCGACGTAATGTTGATACCGCGCTCGAAGCTTCAGTGGCGACGCGCTCTACCTGCTTTGGTATATAGACGGCCTT
AAGGCCAAGCGGCTGCAATCCACCGCGCGGCTGATGATCATCAGCGACAACAGCTCATACCGAACCAGAACCGTTCGCGG
GCGAAGATTTAAACGCCGTACGCATCATCGACGCATACGCGCGCATGGCGTTTGAGCCAGTTC

SEQ ID 64

MFSGEQLGQAISEAIKRKNVSQKEVADHFGVKQPSVSGWIKNGRIDKKHLDKLIDYFSDVVTPSHFGLIETFRVLKSNEQSSIRFP
RLNAEATCGAGTINDHYIEVVYVTVAAAWAREKLGGNLNKIQVITARGDSMEPTIENGDMFVDTAVEAFDGDGLYLLWYIDGL
KAKRLQSTVGGGLMIISDNSSYRTETVRGEDLNAVRIIGRIRGAWRLSQF

SEQ ID 65

TTGATGATGAAGCCGCTCTGAAAGTTTGAGAGCGGCAGGCAGGCCAATCGCGTATTACCCGAAATTTGGCAAAGCCTTTGGGCGGTG
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ACCGAAAAATGCGAATGTTTCGCGCGCGCGCAAAACCCACGGCGTACCGCTTCAGGAAATCGCGGATTGTTACAACGAAGTTTTC
GGCGGCGGTTGCCAAGCGTCCAAGTGTGAACGACACGGCGCAAAACGGCGATTGCAAAACGGCTGGTGGCGGATGCTGGGAACGG
CGCGGCCAAACGGCAAGGTGAGGTTTCGGGGACAAGGAAACCTTTGGCCTGGTTTCGCGGTTTCTTCGCGAAAGTGGCGATGAA
CCCGTTTTCGGAATGGGCGAAAACCAACAGGTTTTCGGGTGCGCTTCGATTGGAATTTTCAAGCGGGCAATTCGTCAAATCCTT
GAATGCATCCGCTAAACGAACAGCGCGCAAGGGGAAGGGCA

SEQ ID 66

LMMKPSESLRAAGRPIAYYPKLAKPLGGVNAAILFGHFFYWNDKTQYESGIYRTABEIEIETGLSVQEQRTARAKLRERGVLIET
EKRIEHRITYKLNLDLDAFDDMLQHSGGGESTAPKCNINSPQLQNHSGGGESTAPKCNINSPQLQNHSGGGESTAVIRTEDLTE
DLAVYTPLPPNAGNGKGLNADAFVSADAETCGRETGBEPTSPKAESDSNNGGLSGKPKNANVPRRRKTHGVPLQEIADLYNEVL

GGRLPSVQVLNDTRKRAIANRWCEMLGTAAPNGKVRFGDKETGLAWFAGFFRKVAMNPFWMGENQTGFVAVGFDWIFKAGNFVKIL
 BWHPPKTNQAARGRA

SEQ ID 67

ATGGCACTAGGGCAATTTCGACGATGTTGAAACATCAGTAATTCGCAGTTTAAGTTCTGCAAGCCTGTATATGTTTCACGCGCCGGA
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 GGGCGCTGCCTGATGCGAGTTTATCCACGCGAGCTATTTCGCGCGCGTGGCGGTCAATAACTCCGTACAGATTTCGGAACCTGG
 TGCAACACGAAGAGTATCGGGCGATTTCCTGATTTCGCACTGGCAGGCGAAAGCGGCCATCCTGGAACCAACCGCAGGCGG
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 CCGGGAAGAACAGCCCTGACACGCGGATTATCTGATTATGCAACGCTGCACGAGAAAGACTTCGCGGGCTGGCTGCTTGACCGG
 CGGCAACGGCGAAGAGTGGGAACATTTGTGCTGCTGCCATTTCAGGAAGACGGCAGCGCGTTGTGGCTGAAAGCATGATATT
 GAAACATTGCGCCGAATGGAGCAGGCGCGCGCTATGTTTTCGCGGCGAGTATTGCAAAACCTGCGCGCGCTGACGGCGGT
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 CGGTACGGCGCGGACGAGCGGGACGAGATTTACGCAACACGGCGCAAAAGACGGCGTGAACGAAATATCCATCCCGCAAG
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 CGACAAGGTTACACGCGCGGACGTTTCGCGGACAGGTCAACATCGGCAATGTGATGGTGTGGATGACGGCACATGGGACAGG
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 TGCTGGATACCCGACGGCGCATGATTGATTTCCTGCGATCGCAGGTTCGAGGCTGTGAAA

SEQ ID 68

MALQDFDDVETSVIRSLSSALYMFTRRMFYQRRGYVWQRANHHAPICNALERVFNGETKRLIINIIPRYSKTEIAVVNFIWAM
 GRVPDCEFIHASYSALAVNNSVQIRNLVQHEEYRAIFDLALAGESGHHWKTAGGVMYATGAGGTTGFGAGRHREGFGGCI
 IDDPHKADEARSEVRRQNVDFQNTVESRKNSPDTPIILIMORLHEKDLGWLDDGNGEEWEHLCLPAIQEDGTALWPKEHDI
 ETLRRMEQAPYVYFAGQYLQKPAPPDGGTFKPDNLQFVKALPAGNIRWVRWDLASTANGGDYTAGRLGVTEDGRYIIVANVRG
 RYGADERDRILRNTAQKDGVTIKISIPQDPGQAGKSQTLVYLRQLAGFSVSAGPESGDKVTRAGPFQAQVNIIGNVMVLDDGTWDT
 DALIAEMRMFPNGRHDDQIDCLGRAFGELLDTRTGMIDFLRSQVEAVK

SEQ ID 69

ATGAGTAAAAAGACACCTTTATCGCAAGGCTTTATGCCCCGCTTGGCCGCGGCGTCCGTTACGCCTTTACCGGCAACGCGGACG
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 CGGGCATTCAGCGCGCGGAACGTGAAGCGGTAGGCTTTGCGCAATTACGCGCCCTGCGCGCAACTACCATGATTTGCGTTTG
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 CGCAACGGAAGACCGAAGGTGATGAAGCGGTTCGCTTCTCCGTCGCGCGATAAAGAACATACGTGGCGGAGTGGCTGCG
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 GGGGCTGTTGCGCGCAAGCAGTGGATAACCGCAAAAGACGACAAGGTGTCCGATGTCTGCAATGCCAAGCGCGGATGGGCGTA
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 CAGGGGATATGCCTGAATCT

SEQ ID 70

MSKKTPLSQGFARVAAGVRYAFTGNADGWFDAGEPPAPAAQQAEGRRFDYEPFYNVGHSKPREREAVGFAQLRALADNYDVLRL
 VIEARKDQMECLKWTIQRUVESTEDDESQRDKRVDEAVAFRRSPDKEHTWADWLRLLEDLFVIDAPCIYPRKTLGGGLYALE
 VMDGATIKRVLNDTGRMPLPPDTAYQQLHGMMAVDYTADELIRSRNRSYKVYGYSPVEQIIMTVNIALKRQVHALEYTAGS
 VPDALVGPETWSADDIRRFQYEWDLLSGETAQRRKMRFPVPELGSNRFETKQPLKDVYDEWLARVVCFAFSVEPTFFVAQVN
 RSVETSRQQLSDGMSLKNVWALIDDVLARYMDMAAYEFVWKGESLNPKEQAEIYAIYKNAGILTADEIRAEKGKEPLPGQ
 GQPEFDKQDGRKPEEPNQAELKESPMSEDESAALIEAYLLTRIDGLAEQIAALIEGAADVWQAGDLAAELSRAGVAVANG
 LDFGDWSGLSDVVEPIIRVAEDGVAALLRVMPPEAGMVTNIRSAVKWAHERAAEMVGMKRAGGLVRNPAAEWQITEGTRE
 MIRAQVAEAMRNQDSVQELAGRLKESHAFGNARARTIARTETAMADGMGNLIGWEGTGLVAGKQWITAKDDKVSVCNANGMGV
 IGLHEPFSHGALTIPGHPNCRCAVVPVLADMPES

SEQ ID 71

ATGATGTCGGGATTCTCCCCAAACCTAAGACCATTATCTTAAGCCTTGCAGGTGCATTTGGCGCATTTGGCTTTTGCAGACACCC
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 GTATTACAAAACGTCTCCAACGCTACGTCGGCAAAGAATACCTCGAACGCTACCGCGTCCAATCCGCGCGGACGTAACAA

GGCCTAAACGGCGTGTACAAATGAACACCCGACCGCGCGGCCATCACGCCCAACATACGGGTATCACCGGCAAGGGCC
GCATCCCGGTACCATAGACGGCACCAGCAAAACCATCGACGTATGGATGAACAACACTACGGCGTGGGCGACCGCAACTACCTCGA
CCCCGCCCTGTTCCGAGCATCGCGGTGAAAAAAGCCCCGCCCTCACGCGCGCGTGAATCGGGCGTGGCGGTGCGATGTCC
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TGGCGCAGAAAAACGACCTACGCCAATTCCTTAGGCCGCGACTACCGCACCTCTCGCCCATAGGCGCGACGGCGGACGGGGTATC
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TTCTCGGGCGGTAAAGCCACACCAACTTCAAAGACGACAGGCAGCTGATGTTGTCGCGCGCTTCAAACCGACATTACAGACG
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CGGTGCGGATGCTGTTACGACAGTATCTGACAAATCATGGCGGGAAAAAGATATACTCTGCAAACTTTCGCCAGCCTGGTG
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TACAAATCGGCTACGAATGGAAGCCGCAAAACAACAAATGGATGACCTTCAAGCCGATGTGGCGGTGAAGACCGACAGTA
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AAAACCGTCGCGCAACCTGCGGGGGAAAGCTGCGAAAGCGCGATGACGTGGAACGCCTACGGCTCGGCGCAACCCATGAAGAA
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GCTGGATGGGGCATACGGGCGGCTACTACACCATCACGCCCGCCGATAAAATGTGCTGACCGACAGACCAACCAATCGGCAA
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GCGCGGACGCTACCGACGTCGTCGCAACGGTTTCAACCTCAGCAACCGCTCCGCTTTCCGACAAACTCAGCTCACCCTTG
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TGCCAACCAAAAGCGGATGTTGACGCTTTATGATCCCGATAGAGCTGATGGGCGAGTTGCGAATATCAAGACCTTAACCGCGCT
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CGCGGTATATCCAGGATCGCATATCTACATAACACCGGCTCGGTACGCGAAGAAATGGAACGTATGGCAATGAAACCAAA
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CACCCTCTTCCGCGCTATGCGCGCATGAGCGCTTCCCGCTTTACGAACTGACCGCGCCACCGGTAGCGGAGGGCTGT
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GCATTTCCGCAAACTGCGCAAGGCGACCTCCGCTCACCTACTACAGTAATAAAATCAAAACCAATCGATACATCCAAATGAA
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CGAATGCTTGAAGGTGGCTTCGGCTCAGCGCTTCTTCAGTCTTGGCAGCGAAATATTGCTTACCGCTTGGATGTCGGCAGC
CGCTTCTCAACGAAACTGGAATTTGGGATGCGCGCATCCATCACAGCAAGGCGGAGCGGAGAAATTACGACAAGCTGATCG
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GTCCCCGCGCGGCGGAGGACGATTACCTTCGGCATCAAGGGCAGGTTT

SEQ ID 72

MMSGFSPKPKTIILSLAGAFGALAFADTPNNTEQOKELNTIVVHKRSADQKGAADVYKVNVSNAVVGKEYLERYRVQSGDVLK
GLNGVYNNVTRTAGGAIPTNIRGITGKGRIPVTIDGTEQITIDVWMNNYGVGDRNYLDPALFRSIAVEKSPALTRGVKSGVGGAMS
IRTIEPSDIIPEGRNWGIEVKTEFSNGTVAQKNDLRQLRGLRDYRLTSPIGATADGVSGMPDVLGTGVTGKPSPTALLLDEGLADTK
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YKIGYEWKPNKKNWIDLQADMWRVKTDSNRHQSGGFPVVGITSDFDYDLWYWCNIRKPSNLRGESCEASMTWNAYSARTHEE
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HRLFARYARMSRFPSTLYELTAATGSGGLYGSSETVAEYSLKPEKSTNWEVGVNFNFAHPFAKLQGLDLRLTYYSNKIKNQIDTSNE
DGGMIQYDKAVSKGVELQSLDSGRFFASFGGTYYRLKHMVCDKGIAFKFDYLLQVRPECLEGGFGLSRFFQSLQPKYSLTLDVGT
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VPGPRTITFGIKGRF

SEQ ID 73

ATGAAAGCATCACAATTAACCTCGCGTCTCTTCTGGCCGCTGCTTTTCGGCTCTGCTTATGCAAGTAGAAGTTAAAGCGGGGATT
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CCGCGCAAGGCAACAGCAATCAGATTACCAACAGCACTGATTTAAATATGAACGACGGCAACCGCACGGTTGGTTTGTGGGTG
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GAATGAGCTTTAACGGTGTGAAATTACCAATGCTGACGGCTCGTTCAACAGCATCCAGGCCGAATAACGAAGGCATCAAG

GCCAATTCTACGGCAATGGCGGGCAGCCATGGCGGGCTATGCCACTCGCGGAACCGACAACAAAGGCGATGATGTGGCCTTCGG
CGGCGCGAAAAA

SEQ ID 74

MKASQLTLAVLLAAAFGSAYAVEVKGGDSKGLIQAESDFLPFGSGAADIKVSTGNGLSKSINLEAGPAQRIRNKYGNAPING
GNQNTINVNGAANSRYLQPGDINPIAGWFSKTRLAQVWYEKRANNTVEFVSVRQADPLLPAPKFGGMTFAKVPTAATNVFFGEWA
PRKGNNSQITNSTDLNMNDGNRTVWFVGENPTKNTNRNLTAVTYNVVGINKHTPGKNDFTYTGITATFTGTDKRGFMSGELEHTDDG
ELSFNGVEITNADGSFNSIPGRNNEBKGQFYNGNAAAMAGYATRGTDNKGDDVAFGGA

SEQ ID 75

ATGACCCACCGCCTCTGCCTGCTTTTCTGCGGCTCTGTACGGTCTGCCTTGCCTCCGTCCAACGATGCCCGCGACGAAACGCC
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CATGTGCTGATGGAGCGCACCTGCGCGCGCAACGGATTTCGACCTTCTCATCTATAGCGGACCGCGGAAAAAACCGTCCCG
CTCAAAGGGAATCACGGCGTACAGGTGCGCGGTGTACTGTACGGCAACCGCTACACGGAAGAACAAAGATTCGGCGCGCTATGC
CGGATTACGGCTATCGCAACGGTTTCGTGTACGCGGATACGCTATGCCGACGACGCTCCTCTTTTCCCTGCTGCTTATTT
CGAATACGATTTCGCAACCGCCACACCCACTACCGAGCATGGGGTGGCGATGCCGACTGGTGGCGCACACTCTCCCCGACTGG
CGCATTAACACATGCGCGGAGCAAAAAGACCGGATACGCGGACAAAGCAAACTTATTTTGGCGATTCAAAACAAATACGAAC
TCGGCGCGGGGGCGGAATTTCCATCAGCTGAAAAGCGGCGTCTTGTAAATTTTCGATGCCGCGACGAAAGCCTATCCCGAAAA
ATCCTCTTCCAGCAAGAATATACGGCTCGGCTGGCGCGTATAGGCTTTTTCGGGCGGTACTTATTTAAACGCGCGTCTGCTC
TACCGCGCGAGCTGTATGACGCGGCAAGTTTCGTTCAGCGATAACAAACGGCGCGCGACAAGCAATACATCATGATGGCTGCGG
CGGTTTTCGCGCAATGGAATATCAAAGGCGTATATCCGAACTGCGTTTCAGGCGAACAATCGCACACAGCAACGCGGTGTATTA
CCGCTACCGCCAAAACGAATGGCTGTTGGGTTTTAAATATCGGTTT

SEQ ID 76

MTHRLCLLFLPLCTVCLAPSNDAADERRRLLEDESRQTQYRESGWLDTEQARGEVEENDGYISIGGEIYQVGDIAEELESATY
HALNARQWHKVRQFAARYAKLPRHKPALIHLADALQKRDEGDFRAAGNSFQTALEAPDNPRLLLEAGRFYAEQNQKESAAAFE
KVLKTDIPIAETRPIVENYLSLSELGKRRRWGQISLGYGYSNVNQNGINQCVWEIAGMCLMERTLPAPTDSTFSYSATAEKTVP
LKGNHGVQVRGVLGNRYTEKDKDSAAMPDYGYRNGSLYAGYAYADARSSFSLLPYFEYDFRNRHTRHWAGADADWSRTLSPHW
RINSHAGAKTGYGGQSKTYFADFQYELGAGAEFSITLKSGLLVNFDAAARKAYPEKSSSSKEYTARLGAYRLFSGGTLYLNAVLL
YRRSLYDAASFVSDNKRDRDKQYIMMAAGFPQWNKIGVYPELFRRTIAHSNAVYRYRQNEWLLGFKYRF

SEQ ID 77

ATGAACCAAGAGGGATTACCGCTCACGGAATGCCACGATTACCCCTCAAGCGGAAAGAAAAACAATAAAATTACCGTGGAAAAACG
CCGCATACAGCAGCGACGGCATTTTCGACTCTGATTAAACAGAACGGGGCAAGACCCGGAACAAAGGGATGATGAAATAAAATCAT
ACTGGAAGCCGGCGCGGATAATATTTGTTACCATGAAATCCGGCGATGCGGATGCGGATTATGTAAACAATTCCAAAGTATTAACG
GAGACACCATATTATAAAGCAAAACGAGGTTCCAACGGCATTTTTGCTATGCGGACAAATCGCTGGTCAAACCTGATTGGCGAGA
ATAATATCGTTAAGAGTGAAATCAGTGAAAAATCTAAGGCATTAAATGGGGGATTTCGCCATATCGGCATTTATTCTAGGCAAAA
CGCGAAAGTCGAATTGCTGCGAAGAGCGACATATCGTACAAGCGGGAATTGGGGCTTATACTCCAACAACCTCCTCAATTTCC
CTCAAGGGGAAAAATAATGTGATTTCAAACCCGAAATATAATGTTTTGCGCTACAAAAGGCAAGAGTGGATTGACTGTGCAAA
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GGTAAAAAGCACCAAGTGGGTCTGTATTCGCAAGACGGCGGTTCAATCAATGTAGATAGGAAGGATAATATTATTGAAGCGGAC
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ATGCTGAACAAGCTGCAAAAATAGCCATAACCGGCGCAAGCAATACAATTCATGCAAGCAATGCCGCTATTTCGTTTATTAGACAA
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TATAAAGACGATACCGGTATCACAGGGGCAACCGTATCTGATAAGGGTTTGGTAGCCATCAAACTTGAATAACACGAATATTG
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TGAACCGTAAAAAATATATTGACGATACGCACCTTATGGAGGATGCCCTGACTGTGCAATCTCCGCACATAACGGCGATAAAAA
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AGGCGATTGGATAAGGCTGACGCATACCCGTGTGATTCAATCCAATGCGTTTATAGGTTTCAATAACAAGATTGTAATCGGATAT
GACCGATTACGCTCAACGAGCAGGAGAAAAACGCAAAATGGGCTCTGTACAACTACTACCAATACATAGATAAAGAAGGAGACGAAAC
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CACCGCAAGTACAGTTGCAATATCTCTATTTGAGAGGTACCGGCTATCGGATCGATAACGGCATAAACGTCATTTTAAAGCCACGC
AAACAGCCTGATAGGCCGCTTGGGTTTGGATGTCGTGAGAAAATTTGACGGAGGCAAAAAACCTTTCTATATCAAAGGCAATATC
TTTCATGAATTTTGGGCGAGTCTTCTTTAAGGCATTTGAGGGCAAAAGTCATTATGCTCAAAAA

SEQ ID 78

MNQEGITAHGNATITLKAKENNKITVENAAYS SDGISTLINRTGARPGTRDDGNKIILEAGGDNIIVTMKSGDADADYVNNKSVLT
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LKGNVINSNPKYNVFAKKAKVDLTVENKNTLSDAEFGVYALNTSMVNLSSKDNNEVKSTQVGLYSQDGGSSINVDRKDNIIEGD
AVALVGKGGSQNIRASRTNLISSKSLGIHAEQAAKIATGASNTIHASNAAIRSLDKSEVKIDGQITIDSNVANLARQDGSIHNLN
YKDDTRITGATVSDKGLVAIKPLNNTNIVADTIHYKGDVLAVNKGKVELDFTPNILLAGRLDNFSGLTDSKHKNLFENYVANLDS
KSAGEINFNLAKDALWTMTGQSWLDKLEGGQGTIDFNNDAKTSGRALHIGELAGANKFLMHLNKGDIHSDMLYVVKGTSTPQEVVV
KNLSEVLDSMNYGERLRFATVTNSKNEFVNGKKYIDDTHLMEDALTVEYSAHNGDKNNKDDYNKSFNGSEMTAEKAGDDYVNKTY
TDNRQNVYLKQATGNPSRNVKNINDMFDSTAHYAFTLDITYAKREGERAFSTLDKKEGDWIRLTHTRVLIQSNARFHNDFEIGY
DRFSLNEQEKRRKKGWISLDYGHGRTSLWNTFGKDKIRKYELALYNTQYIDKEGDETGIDNVLIKIGLRNVRVIARNHMGQLWGK
GKYSNTLFSISTEYGRKFLDDDKLWRITPQVQLQYSYLRGTGYRIDNGINVLNLSHANSLIGRLGLDVVRKFDGGKKLFYIKGNI
PHEFLGSRSFKAPEGKSHYAQK

SEQ ID 79

ATGCGCTTCCCCCTCCCTATTACCAATGCTGTGCTAAAAATTACAAATGGCGCAATGGAATTCAAATCAGAAGATATTGGAACCA
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GCTAACCCCTATCTAATACAGGTATTTCTTTATCGGGTACAACTTCTGTATTTGAAAAGGAACATTACCAACGGCGGCATCAT
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GCCGTTGTTAAGGTTTTGGGACAAGACAAGGGGGCGGAAACCGGTAAATTAATATCGAAGACGCTAAACATACCTACACAATGC
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ATACTTCTGGAGCTTTAACACGCGCGAATCAAGATAAAACCATCATACGCAAGCGCACCGGCTACGCATCGTTCCACGCTCAA
AATCTTGAATCAGGCTATGCGATGCTGGATACGCTCCACCAACGCGCGTGGCGAAAATCAAACCTTTCTCGGGACAGGCAAGGCA
ATTATCGGCGAGGATGCGGAAGCAACAGACATAAAGGCTACCAAGGCACCGTGGGTG

SEQ ID 80

MRFLPITNAVILKITNGAMEFKSEIDIGTIKLTAKTFHLKDDTSLTTPEGTLLSGGTLTSLNTGISLSGTTSVFEKGTFTNGGII
TLANQSYADKLTIEGNYVGKDGVLKVNTEWNSPGDDQGGNSQSDLEITGDASGKTTVISVGKDGKENDIDSGISIGELSDRYKRS
AVVKVLGQDKGAETGKLNIEDAKHTYTMRDTFSGTAKTTGAGELQLVSHKDEAGATEYFWLTLTPNQDKTIITPSAPAYALVPRQ
NLESGYAMLDLTHQRRGENQTLSDRQGNRYQDAEATDIKATKAPWV

SEQ ID 81

ATGATTCTTGGCTCCCTTGTCCGCTATTACCGCCGTTTGGAACCGGAAACCGATGAAACGGGCAACCCGAAAGTGCCGTCTTATG
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AAGCCTTCAAGCAATACCATCTCGATTTACTGCAAAACAGCGAAGACGAAGGTTTACAAGCCTTATGCCGTTTTCTGCAAAACTG
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CTTATCCATAAAGCGGAAGCCGCGCAAAACCTTGTGGGCGAGGCTGCTGAAAGTGATGAAGCACTCGAAAGCTTATGCCTGATTA
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ACCGCGCTGAATCTCTTGCGCCGCGGAAATAATCACTGCCGTGACCATAGGCGATGCCAGCACGGTCTTTTGGGCGGAAGCGG
ATGATATAGTGGAT

SEQ ID 82

MILASLVRYRRLATETDETNPKVPVSYGFSEEKIGWILVLDKEGRKLTVPVNLADKKPQPKLMSVPRPEKRTSGIKPNFLWDK
TAYALGVEANKNAEAKERPFTPSEKTFEAFKQYHLDDLQNSEDEGLQALCRFLQNWQPAHFAAENLPAEMLDSNTAFSLEKPTA
LIHKREAAQTLWAGCLKSDEALESLCLISGDTAPIARLHPAIGKVFVGGQSSGSIISFNKEAFSSFGKEQGANAPVSEQSAFAYT
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SEQ ID 83

TTGGCGCGCGGACGGAAGAAACAGCCGGATGTTTTCGGGTATCCCGTCCGAGGACGGGGCGGAATTTTGGATACGGGCGGTGATGC
CGGACCGGTTTGGCGCGTCAGTATGCGGACATGGCGGCTAAATACCGGGCCAGCCGTCGGAGGCGGTGGGGATTGATCCGGATGA
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GCCCGCGCGGCGGCAAAACCGCGG
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GGAAGGGCGCGAAGGCACGGGCGATGCGGCGGCTCGGTGCGCCCGCGCGGTGGAAGAGGCGGTGCGGAGCTTTATGCGGCG
CAGCGTACCGGCGGTGGGCGGCGATTGAAAACCGTTACGGCGTGAAGGTGCGCAACGGTTTGAACCGCGCATGTCGCGGCGGT
TGGCGCGTATCGGCGCCCTGTTGCGCGCTGTGCTGCAACGCTTGGCGGGAAGGCGGCGGTGGAAGAGGCGGTGCGGAGCTTTATGCGGCG
TCCGATGCTGGCGGATTTCACGCGGAATGTGAAGGGGCGGCGGATGCGCTTGGGGCGGCAATCATGTCAGTGATGTTTCGCG
CGGCGCAAGACGGTTCGCGGGAACGTTCCAAGTCGGAAGGCTTGAAGAAGTTCGCGCTGCGGAAACCATCCGTATCTCGGGCA
GGGAGGTTCCGGAAGGCGCAATTTGCGCAATATAAGCGCAATGCGCTGGAATACGGCAATCTTTGCGCGGGCTTATGTGAA
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CGCGCATTCGCCGATTGACACGAGGCGGTGCGTTTTCCTGCGGCGAACATCAGAGCCGCAATCGGCGGTATAACGGGTAA
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SEQ ID 84

LARGTEKQPDVSGIPSEDGAFLDTGVMPDGLARQYADMAAKYRAKPSAVGIDPDDGAVSAAALAADSGAAVPSAVSDDMEAR
SVADDAPSGRSADADRGVPSAYGNVRPGGAPRGAASVAPGGSAAASGGIARVAPLPAGQYFDGLDTRGRKALAKEAGLDIKGV
ADFGQIAAFVRRKIEQAYHARIEADYQAASEAKQGYLPPFVRMADAVFVPPKGFVSPADALDKESRRRFDALPEWVRRAQTVAD
YTADGIMRREAGMADMRGHYPEGLAESAGAVRAYRAQHPESADVLDRNLRAVYGYRRNNGWSVPLLREBERLQGVRTALPDDGA
SEAVVGGGRGLTRALPTEDKGLAQDVRQDVRQGLTQGGRLTPDAGADANAAALQGLPGSAVASGNAPARRQNLQVRARAEGAAP
GLSASENLAGTDGKRAPVAGKRPTVLPVLPVQVAESAGRVSPKKRMADAAADFTRRLAADRRRPEKAGVPLGGGEYRFETDR
RHIDALGAVPGRPKGGMPEEFADMGPSNSDGLVSDGRRYLKREABTLRAGGLSEAVPSEPGRDYRPTQEARAPAKVMARFRD
AADGKAPAGRAQPARAKDTPVAGKAAAANKAATEKPSDDKVRNIEAGKSRFDGKGKSAQAATEKPSSEKTKAKPETFAKTA
SDNPPEARRKARVLQGGPVYTVKERQAPQGFALREHAESIKRLAESIGGLAERVDAVAVSETAPDKAQLLSQRVEGWDFGRT
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GASESKSPLSGIDDKRLQLILQDKDAGKGGIADFDEAVRFSRAANIEAAIGRTGKKSILRNALKDRWDASKGIQLQFLGRRI
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ELGEAVGMLDLDPARARLNDTLTQLYLSLPLDTSWAKHGIHRKGVPGFSDDARRAYAQNMGSGANYLAKLRYADRMABQLDVMQ
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ELLRASQIGLRFGEKFTNTIEDSLNGDEKAAFRKAADYGVIDLQAHDLGAVANGDPGLAGSAWQKVMKAAWLFHHAKEFNROV
TFVAAAYRLAKRAGADSEAAFEQAKATYDGHFDYAAQNRPRFMMGNAKVFLFKQYSONILYALGRNAYLAFKGDKEARKTLAG
LLVSHAMASGILGLPFVSTLLAVASMLGSDDDPDWDAEALRNMLADAFGDKAGEVLAKGFSRLTFLDVSGRGLNLQVLPFDIQD
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SEQ ID 85

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CGCAGGGAGTTGGGCGAGGCTTGGGAAAAGGGCGGGGTTGTCGGCGCGGCTGTGCAATGTGTGGGGGAGCTTAAGAAGGACT
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TTGGGCAATACGCTGATGGAATACGCGGGCAGCTGGACAGGGCGGAGAGGCGGGCGGCTCGACCTGCGGACAAGGATGCGG
TGATGGCGTTTATCGGCCGAGGTGCGCGGGTTCGTTGAAAATGCGCGGTTCAAGGGCGGTTGTCGGCGCGCGGATATGGC
GGCGATGAACTTTGGCGCGAGTATTGGAATATGGGCAAGAGGCCGCGGGAAGCGCATTTGGAGAAAATCGGTGTTGCGCGC
GCGGATAAGCGCGGTTGCGGCGCTAAGGGAACGCTGAATTTGCGGCGCTGCGGAAGGAGTCTGCCAAGGGCGGTTTGGGCG
GTGCGGCACGGCACGCGGCGCTTATGCGACGGAATCGGCGGTTGAGTTTTCGGGCGAGTATTGGGTACGGGGCTGGCAACCG
GGAATGGGACGAGAAGGGGCGGCTTTGGAGGCTTCTCTTCTTTGGGCGATTCTGCGGTGGGGTTGCGCGGACGAAGGCTTAT
GCGGCGTAACCTGACCCGCTCAGGCGCGCGCGCGGACGGAAGGCGGGTTCGCGAGGGGGTATCGGGGCAACAGGAAGGCGGGC
AGGCGGCGCGGGAAGGGGCGCAGGCGTTGCGTTCGGCGGCGACAGGCGGCTGCGGACGCGCGCACAGGCGGCTGCGGACGAGGC
GCGGAACAGGGCGCGCGGTTTCGATACGGCGCATCAGCATCAGTCGCGATCGGCTTTGCGGCGAGTTTTCGGGACCGTACGAAGC
AGGAGGAGGCGGGCGGTTTTCAGCGGCCCTGCGGACGCGCAATACGCGCACGCGGAGGAATTGGCGCGCGGACGGAACACA
CGCGGATGTTTCGGGTATCCCGTTCGGAGGACGGGCGGAATTTTGGATACGGGCG

SEQ ID 86

MSDLVRYDPLEHGRVLVGLKEYRGFTQKDARAAADDTALTRGFKNMSRARMGNALTGDKELGRLKAEDMDYRKIQEGRKSQA
RRELGEAWERGGVGGGLSNVWELKDWREKGLDGALEDVEMAGAVLEQAPNALVPIATATAGGILGALAGGNAAVGAYAGAT
LGNITLMEYGGQLDRAAEAGVDPADKDAVMAFIRGAPGALKNAAVKGAUVGAADMAAMKLGGSILNMGKKAAGKAALEKMGVAA
ADKAAVAAKGTPEFAALAKESAKGGLGAARHAAAYTAGESAFAGEYLTGLANGEWDEKGAALBAFSSSLGHSVAGFAGTKAY
AAVTDPLRPPRGTEGGCAGGYRQOEGGQAGPRGAGVACGTTGCGGRHRRLRTEARNRAARVSIRITISIRILCGSLRTRVS
RRRRGGFSAALPTAIRRTRNRWRAGRKNRSMFRVSRRTGRNFWIRA

SEQ ID 87

ATGGGGACGGACGTACCGGAAACAGGCGTATTGCCCGATAAAAACGGCGAACCCTGACTATCGGGGAATACCGGCTGTTTGTCTG
GTGAAATGATGAACCAACCTGCATGGCGTGCCGTTGCCGACAAGGAAATGGACTACGCCGACGGCAGGCGAGCTTGACAACGAGCT
TTTACAGAAACAGCGCGAGTTGGGCTTGCCCCCGCGCTTGAACCTGATTACCCCGACCTGCTGCGGTACAGGATATGAG
GCGACGATACGGACGAGTGGCGCGTACGGCGGACGGCGGCAAAACCGGCGGGCGGACGTCGCGGACGATTTGAATTTCAAATCA
ACCGCGCGAAGCGCAAGCGCTGCCGACAAGGCTTGTTCGGACGCGTTACAGGGGCGAGATAGCCTGCGGCATCGGCTGGGTGGA
GGTTACACGCAACCCCAACCTTTTCGAGTTTCTTATGAGTGGCGGCTCATCCACCGCAACGCCATCCATTGGGATATGAAATCT
TACAAATACGACCTGTCCGATGCCCGCTGGCTGATACGCCCGCGCTGGCTGCTGCCGGAACGCTGGCGCAATTTCTCCCTGAAT
ATGCCGACACTTCAAAGCGATGGGGCGCGGCGGTTCCGATGGCGCATCAGCGGGGAAATGCTTGACGGCGGCGCAATACCGG
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GCGGAAGTATGGTACAGGCGGTGGGTAAACGGCAGACTGCTTCCGCGACAAAAAAGAGGCGCACGTTGAGTTTTCGCGCGCAA
ACCCAAACCATCGGGAGATGGCGGCAACCGCGCGGTTATGTTTTCGGCTTCCGTCGCGGTATGCGCGCGGCTTTGTCTGTGG
GGATTGGTTCGTCGCGACGACGCGACCCGATTCGCGATCAAAAGTTCCCTTACGTCGCGTTTTCGCGATTCCGCGAGGACAAC
ACCGCATCCCCTACGGATATGTCGCGAATATGAAATACGCGCAGGACAACCTCAACAGCACCAACAGCAAATTACGATGGGGTT
TGTCGGCAATACGCACGGTACGCACCAAGGCATAGTCGATGCTCGGACGAACAGTTCCGCGCAATATCGCACGGGTGGACGC
GGACCTCGTCTGCAACAAATAGAGGCGCGCCAGCGCGCGCTTTCGACGTCAGCGCGGATTTGCAATTTGTCGCGCAGCAT
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ATTGTCGCGCGAGTTGCTGCTTTCGATGATTATCGAGGATTTGGGCTCGGACGAGCAACCGTCGTCATAGAAGGGGACGCGCTC
ACGCAAGGGCGGACGCTGTCATCAACAGGCTGAAACCGACCCGTAACCGGCAAGGCTTATTTGTCCAACGACCTGCAAAACA
TACGGCTGAAAGTGGCTTTGGAAGACGTGCCAGCAACTCTACCGCAGCAGCAGCTGGGTGCGATGAGCGAGGCGGTCAA
ATCCCTGCCCGCGCAATATCAGGCGGCGGTGCTGCCGTTATCTGTTGATGGACATCCCGTTTAAAGACAAAGTGATTGAA
AAAATCAAAGAAGTCCGAGTGCAGGAAACGCCGGAACAAATCGAGGCGGCTATCGCGCAGGCGGTGCAGGACGCATTTGGCAAAAT
CCGGCAACGACATCAAACGGCGGGAATTGGCGCTCAAAGAACAACGTACCGCGAGCGAAATCAAGGAATCGAAGCGCGGGCGGT
ACAAATCGGCGGTGAGGCGGCTTACCGCGGCATGACGCGGGCGGGCAGATAGCGCCATGCCGCAATCGCACCCGTTGCCGAC
GCGGTTCATGAGGCGCGGATATATCCGCGCGGCGGGGCGACGATCCCGGCTTCCCGTCCCGGCAATGCCGCTGAAACGC
AAATACCGCGCGAAGGCATCCCTGAAGCCTACGGCGCGGATACCGGCCGATGACGGCGGTGCGGCCAAGAGTGCGAATCACGC
CCAAACAGGCATGGAAACGCCGAGGTTGTCGGAACCTC

SEQ ID 88

MGTDVPETGVLPDKNGEPLTIGYRLFVGEEMNQPAWRAVADKEMDYADGRQLDNELLQKQRELGLPPAVENLITPTLLSVQGYE
ATIRTDWRVTADGETGGRDVADALNFKLNRAERQSRADKACSDAFRQIACGIGWVEVTRNPNPFEPFYECGVIRHNAIHWDMKS
YKYDLSARWLIRRRWLLPERLAQFFPEYAGHFAMGRGGSWIRISGEMLDGGGNTGLADAWGISGRNTVSEEFWFNETTRELAV
AEVWYRVVNTADCLRDKKTGRTEVEFDGANPNHREMAANGAVLFAASVPRMRRFVVGDLVVRDEFTPYPHQKFPYVVPFGFREDN
TGIPYFYRWWMKYLQDNLSNSTNSKLRWGLSAIRTVRTKGVLDMSDEQFRRNLARVDADIVLNKIEAAGPARGFVSRDFELSAQH
WQMLQDSRATIRQISGITPSFMGNRGNATSGRQESIQVEQSNQSLGLVMDNFRQSRSLVGELELLAMIIEDLGSDEQTVVIEGDAV
TQGRTVVINRPETDPVTGKAYLSNDLQNLRLKVALEDVPSNYSRSQLGAMSEAVKSLPPEYQAAVLFPVMSLMDIPFKDKVIE
KIKEVRVQETPEQIEARIAQAVQDALAKSGNDIKRRELALKEQRTASEIKEIEARAVQIGVQAYAAAMQAGQIAAMPQIAPVAD
AVMQGAGYIRPARGDDPGFPVPAMPFETQIPPEGIEPAYGADTGPMTAVPPKSANHAQTGMETPTVSDNL

SEQ ID 89

ATGACGGGAAAGACGGTTGATTGAAATTGCCCGCAAACTGGACGGGCTGTTCAAGCCTTGCCGGGTACAAGGTTATGTACGGCG
GGCGCGCGCGCGGCAAAATCGCACGGCGCGGCATCCGCACTGCTGGCGCTGGGGGCGCAACGCCCTTTGCGTATTTTATGCGCGCG
CGAAATTCAAAAATCGATGCGCGATTCCGTACACCGCTGTTGAAAGACAAAGTGGCGCAGTTGGGTTGGGGCATTTTCTACGAA
ATAACCGACTTCGAGATACGAGGCGCAACCGCACGCTGTTTGTATTTTCGGGCCTGCAGTCGCATACCGTGGACAGCATCAAAAT
CGTTTGAAGGTATCGACATCGTATGGGTTGAGGAAGGGCACGGCGTCAGTAAAAAAGCTGGGACGTGCTCACGCCGACCATACG
CAAAGAAGGTTCCGGAATTTGGATTACCTCAATCCCGATATGGAGACGGACGAAACCTACCGGCGTTTATCGCTATGCCGCTCC
GAAGACACTTGGCTTTGCGAAATCAACTGGCGCGACAATCCGTGGTTTCCCGAAGCATTGAACCGGGAGCGGCTCAAAGCACAGC
GTTTCGATGAATAAAGAGGACTACGGGAATATTGGGAAGGCAGGCCGCGCATGGTATCGGAGGGGGCGGTTTACCGGCATGAAAT
ACAGGACGCTTTTCAATCCGGACGCGTTACGCTCGTCCCTTATGATTCTTCTTGGCCCGTCATACGGTTTGGGATTGGGGCTGG
AACGATGCCATGACCATCGGGCTGGTGCAGCGCATTTGACGAGCGTGCGCATCATAGGCTACATCGAAGACACGCACCGGACGT
TGGACTGGTATGTTGCCGAATTGGAAGAGCTGCCCTACCGGTGGGGGACGGACTTCCTGCCGACGACGGCAGGACGCGCAACTT
CCAAACAGGCAAAAGTACGATGGAGATTTTACCGGACTGGGGCGCAAGTCGGTTTTCGTGCAAAACGCGACCGGTATCGAAGAA
GGCATCAGGGCGCGCGGATGCTGTTTCCAAAGTGTACTTCGATAAAGACAAACAGCGCGGCTTTTGGAAATGCCTGAAACGGT
ACGGCCGCAAAATACATGCGAAACAGGCGTGGCAATGGGGCCGTCGACGACGAATATTCGACGGCGCGGATATGTTCCGCTA
CCTGGCGCAGCGGTTGATTAAATGGATACAGGCAGCAATACGGGATACCGGAACGCCCGTATCGGATTGGAGGCTTTAT

SEQ ID 90

MTGKTVDLKLPALDGLFKPCRYKVMYGGRRGGKSHGAASALLALGAQRPLRLCAREIQKSMRDSVHRLKDKVAQLGLGHFYE
ITDFEIRGANGTLFVFSGLQSHTVDSIKSFEGIDIVWVEEGHGVSKRSWDVLTPTIRKEGSEIWTILNPDMEIDETYRRFLAMPS
EDTWLCEINWRDNPWFPEALNRRLKAQRSMNKEDYGNIEWEGRPRMVSEGAAYRHEIQDAFHSGRVTLVPYDSSLPVHTVWDLGW
NDAMTIGLVQRDLTSVRIIGYIEDTHRTLDWYVAELEKLPYRWGTDPLPHDGRTRNFOTGKSTMBELTGLGRKSVFVQVATGIEE
GTRAARMLFPKVYFDKDKTARLLECLKRYGRQIHAKTGVAMGPLHDEYSHGADMFRYLAQAVDLMDTGSNTGYTETFPVSDWRLY

SEQ ID 91

ATGATGAAGCCGCTGAAAGTTTGAAGACGGCAGGCAGGCCAATCGCGTATTACCCGAAATTGGCAAAGCCTTTGGGCGGTGTAA
ATGCGGCAATATTATTTCGGGCATTTCTTCTACTGGAACGATAAGACGCAGTATGAATCAGGCATTACCGAAGCAGCGGAAGAAAT
TGAAATTGAACCGGGCTGTCCGTTCAGGAACAAGAACGGCACGGGCAAGAGCTGAGGGAACCGCGCGTATTGATTGAGACTGAA
AAACGAATTGAACACCGCATTTACTACAACTGAATTTAGACGCTTTTGATGATTGATGTTGCAACATTTCGGGGGTGGGGAAC
CAACAGCCCCGAAATGCAATATCAACAGCCCCGAACTTCAAAATCAACATTCGGGGGAGTGGGAATCAACAGCCCCGAAATGCAATATCAACAGCCCCGAACTT
TATCAACAGCCCCGAACTTCAAAACCAACATTCGGGGGAGTGGGAATCAACAGCCCCGAAATGCAATATCAACAGCCCCGAACTT
CAAAATCAACATTCGGGGGAGTGGGAATCAACAGCCGTTATAAGAACAGAAGATTTAACAGAAGATTTAGCAGTATATACCCCT
TACCCCAACAGCCGAAACGCGCAAGGCGGTTTGAACGCTGACGCGTTTGTTCGCTGACCGGAAACGTCGGGCGGGGAAC
CGGCGAACCGACTTCGCGCAAGGCGGAAAGCGACAGTAACGGCAACGGCGGCTTTTCGGGAAACCGGAAATGCGAATGTTCCG
CGCCCGCGCAAAACCCACGGCGTACCGCTTCAGGAATTCGCGGATTTGTACAAACGAAGTTTGGGCGCGCGGTTGCCAAGCGTCC
AAGTGCTGAACGACACGCGCAACAGGGCGATTGCAAAACCGCTGGTGGAGATGCTGGGAACGGCGCGCCAAACGCGCAAGGTGAG
GTTCCGGGCAAAAGGAAACCGGTTTGGCCTGGTTTTCGCGGAAAGTGGCGATGAACCGGTTTGGATGGGCGAAAC
CAAACAGGGTTTGGCGTGGCTTCGATTGGATTTTCAAGGCGGGCAATTCGTCAAAACTCTGAATGGCATCCGCTAAACGA
ACCAGCGCGCAAGGGGAAGGCA

SEQ ID 92

MMKPSLSRAAGRP IAYYPKLAKPLGGVNAAILFGHFYWNKDTQYESGIYRTABEIEIETGLSVQEQRTARAKLRERGVLIETE
KRIEHRITYYKLNLDADFDDLMLOHSGGGEPTAPKCNINSPELQNHSGGGEPTAPKCNINSPELQNHSGSGESTAPKCNINSPEL
QNHSGSEESTAVIRTEDLTEDLAVYTPLPNAENGKGLNADAFVSADAETCGRETGEPTSPKAESDSNNGGLSGKPKNANVP
RRRKTGHVPLQEIADLYNEVLGGRLPSVQVLNDTRKRAIANRWCEMLGTAAPNGKVRFGDKETGLAWFAGFFRKVAMNPFWMGEN
QTGFVAVGFDWIFRAGNFVKILEWHPPKTNQAARGRA

SEQ ID 93

ATGAGCAACGGCGCGCGTTGGACGGTTACCAATGATTCAATGCTGAAAGAGTTGGATTGTCGGAAGACCGCGCAGGTCGAATTTA
GCGACAACAATAAATTTCGTCAAAGTGTCCGTGAGCAAGCTCAAGGGCGATGGCGCGTGTTCAAATGTATGGCGACATCGTCAA
AGGAGAATCGGACAAGCTGATTACCCGAAAGGCAGCGAAGGGACGCATCATCGAATATATGGACGATGCCAAGGCAAAAACG
ACGGGAAGGGAATATCTGAACTGGTTCGAAAACAAGGGCAATCAAGAAGACAATAAAGCATCAAATAAAGCATCATACAAATTGA
ATGTCGCTGTACGGAACAGGGAGGGTGGTGTTCCTTGGCTTGGGTGAGTCGGGTGCTTCCAAAAGGTCAATATTTCCACAGACGG
TAAGCGGGACTTCTACCTCTACCCGGATACCTGACGCCGGCGCATCGAGCAGCGTCCCTTCGGCGAGGCGTTGTATCAGTTG
AACCGCGTTTCCGATGAAACGCTGGTGCAGCGTATGGGCGAAATCCACGCCGACGGAATGCCGAGGAAGACAACAGTTTGGGA
TCAAACGCGTCCGCGGAAATTCCTCCGGCAGCGCAGCGATTACCGCGTGGGCGGTTACGGCAACCGCTATTTGGGCTTTGCCG
CGGCTTCAACAGGACGGGGTTCCGGCGATAAATGGATTATTACAAAGGGCTGATGCTCCGCCACCTCCAATCGTCTACGCTTCC
GAAGACTACGTCGGCAGCGGCAAAATCTTACGGCAGGGCGGCGAGGTGTTTATTCGCGCTGGCTCAACCGGGAAAGCAGGGCTTAT
TA

SEQ ID 94

MSNGARWTVTNDMSMLKELDLSEDAQVEFSDNNKFVKVSVSKLKGDDGVFKMYGDIVKGESDKLITRKSGEGTHIIEYMDAKAKT
TGREYLLKLVENKGNQEDNKASNKASYKLNVRCTEQGGWCFALGESGASKVNIISTDGKRDYLYPDTLTPGASSSVLFGEALYQL
NAVSDETLVQRMGEIHADGMPQEDNNVWIKRVGGKFSGSRSDYRVGGYGNRYWGFAGGFNRGTGDKWIHYKGLMLRHLQSSYAS
EDYVGSGLILRQGGRCFLRLAQPQKQGLL

SEQ ID 95

ATGACCGATATTTTCACTCCATCCAAACGTTCTTCTGATGTCAAAAATCCATAGCAAAGAAACCAACCGGAAGTATTGGTAA
GGAAATTTCTTTTTCCCAAGGTTTCCGTTATCGGAAAAACGATAAGCGCTATGACGGCAAAACCGGATATCGTTTTCCTAAATA
TAAACAGTCGTGTTTATACACGGCTGTTTTTGGCACGGGCATTCTTGTAAATAAAGGACATATCCCGAAAAGCAATATGGATTTT
TGGTTGGAAAAATCAAAAAATCGCGAACGTGATATTAATAAGAACCGAGCTGGAAAAGATTGGTTTCAAAGTGATGTGTCG
TTTGGGAGTGCGAATTAATAAAGCTATTGTAGGGAGCGATTAAATCGGTTGGTCGAGGAAATAAAGATGCCGTC

SEQ ID 96

MTDIFTPSKRSFVMSKIHSEKTKPEVLVRKFLPSQGFYRKYRKNDRYAGKPDIVLPKYKTVVF IHGCFWHGHSNKGHI PKSNMDF
WLEKITKNRRERDIKNETELEKIGFKVIVVWECELNKAICRERLNRLVEEIKDAV

SEQ ID 97

GTGAAAGGTGAAAGCGGAGTTGATATCGAAAAATTGAAAAACAAATTGCCAGAAAAGGAAAGAGAACCGGTAGAGTTATTTTGA
ATCGTTTGGAAAGATTTCGGAGCTTACAAATAAAGAACAAAGCGGAGTAATCTCTGCCTTACATAGTATTATTCCAGAATATCCTTA
CTATCATTTGGCGGCATTTCATCAGGATTTCATACCTGCTGTAACGATTTTACAAATGAAAAGAAGGATTATTTAAGTGCTGCA
ATCGAGGCAGTTAAAGTTTTCGAAGATAAGGTTTCAAGCAGACAGGCTTTCATAGCATAGACGGAAGAGAAATTGATTGAAAAAG
CCTTCGGGAGTAAAAAATCTATGCTTCTATTAACGAATAACAAAACGAGGCGGAACAAAATTTAGAAGATGGTCTTTGAACAGCT
TGCATGCGGAACATGGACTGGATTAGAAATCCTGTGCAACATGAGTTAAGAGCAAATTTATCTCCTAGTATTTTAAATGACAAG
GATGCTTTGGATTAAATCAGCTTAGTTTCATATTTATTGAGAAAAGTGAACAAACAAAAAACGAGCTAAACCTACATCGCCT

SEQ ID 98

VKGESGVDIENWKNLPEKEREPEVEILNRLLEDSELTNKEQAEVISALHSIIPEYPYHWRHLHQDLHTACNDFYNEKKOYLSAA
IEAVKVFEDKVQKQTGLHSIDGRELIEKAFSGSKSMLLLTNNKTQAEQNLEDGLEQLACGTWTGFRNFPVQHELRLANLSPSIFNDK
DALDLISLVSYLLRKVEQTKKRAKPTSP

SEQ ID 99

ATGTCCTGAAGAAAAATTGAAATGAGTTTCGAGCCAACCGTAATCGAACATTTGGGTGTAAAGATGTATTTCGCACACTGTTTCCTG
CGATTGCCGAGTTGATAGCGAATGCCTACGATGCATGTGCTACGGAAGTGGAAGTTAGGTTATTTCGATAAACCGGAGCATAAAAT
CGTTATTAAAGATAATGGCATAGGAATGAGCTTCGATGAAATCAATGATTTTATTGAGAATCGGTCGGAACAGAAGGGAAGAA
AAACAAGCCTCCCGTGGCGGAAGAATTCACCGGTAAGGTTCTTGGTAAATTGGCATTATTTCAGGCTTGGCAACAAAATCG
AAATCTCTACTATCCAAGGAACGAACGGGTACTTTACTTTGGATTATGCAGAGATTAAAAAAGTGAGCGTATTTCATCAACC
GGAGTTTCAGAAAGAGTCTGTAAACCCAATACCGAAACGGAACCACTATACTTTAACCGAGCTGACGAAAAACAAAGGATAC
CCGTTAGATAAATTATGTGGGGCATCTTTCCCGTTTATTGATTTTCGGCTCAGGATTTTAAATCAAAGTAAGCTTGAACGGCT
CGGAACCAAGAATCATTGACGGAACCTAAAATATAATCTTGTATACCCACAATTGGAATGGGAATACAGGATCTAGCAACCAA
TATTTTCATCGTTATCTTCAAATTCGAACAGTATGAATACAGCGGATTAATACAAGGTAAGTTTATTACAACGGAACAACTTTA
AAGAATAATATGAAAGGTATTACGTTGTTTGCCAACCGGCAGAAATGGTAAATATGCCCGAGTTTTCCTGATAGCGAATCCAGCC
ATTTT

SEQ ID 100

MSEELKMSFEPTVIEHLGVKMYSHTVPAIAELIANAYDACATEVEVRLFDKPEHKIVIKDNGIGMSFDEINDFYLRIGRNRREE
KQASPCGRIPTGKGLGKLALFRLGNKIEISTIQGNERVFTFLDYAEIKKSERIYQPEFQKESVKPNTENGTTITLTTELTKKQGY
PLDNYVGHLSRLFDPAQDFKIKVSLNGSEPRIIDGNLKYNLVTPQFEWEYQDLATNISSLSKFEQVEYSGLIQGKFITTEKPL
KNNMKGITLFLANGRMVNMPEFTDSESHF

SEQ ID 101

TTGGGAATGGAACCGCTTTCCCAAATATGCGAGGACATCAAGACGAGACGGATTTTATGCATAGTTGTGCGGGATTATCCG
ATATCAATTTGAAACGATTGGCTTTGATACCTAAAAACGGAGGAAACCGTTTGGCTTTTGGCGATATTTCCGAATTACAGCTGGA
ATGTTTATCGGAAAAGACATAGTTTAAAGACAGCTTCGGTAGGCTATGGTGGGATAAGCCCGACCTACCATAACGACCAAA
TTCCTTAGCATTTCCAACGGGCGGTTTGCCCATCTGAAGAAGATAGGGCGTTATCCCTGCGAGAAGGTGCAACATTGCAATCGT
TCCCTCGTAACATAGTCTTTAAAGCGGCGAGTAGGACAAAGATAGCCCGTTTGATTGGTAATGCCGTTCTCTCCGATGTATACGGA
AAAAATAGGCAGGCAATTGTTGATAATATCGAATGT

SEQ ID 102

LGMENGFPKIMAGHQDETDFMHSAGLSIDINLKRLALIPKNGGNRLAFAHIPELQLECFI GKDNSFKDTFGRLLWWDKPAPTITTK
FFSISNGRFAHPEEDRALSLREGATLQSFPRNYVFKAGSRDKIARLIGNAVPPMYTEKIGRAIVDNIEC

SEQ ID 103

TTGCAGCCTGAAACCTTGGAAGAAAGAACTCGGCTTAAAAAGAAATGATGATGATTGATTCTTATAGGTTGTAGTCTTGTCAAT
ATTGGAGTGTTATTCAAACAGACAAAAGAAATCGGAAAAATCCAAGAGTTTGCTTTTGGAGTTTCAGCGGTTTGTAGAATATTT
CAATCCCGGATATGTTGTTGTAGAGAACGTACCGGAATTCTGAGCAGAATGAAAGAAAGCGGGCTTGATAATTTCAATAAGTTA
TTGGAGAAAAAGGATTACCGTCCATTTCGGTATTCACAATACGGCTGATTACGGAATTCCTCAAGCGGTAAAGAGATTACGT
TAATTGCAACAGAAATAACCAAAAAAGCTGGAACCAAGTCAAGTATTCGGGCAACCGGCTTACGGTACCGGATGTTTGGGAATG
GAAACCGGCTTTCCCAAATATGCGAGGACATCAAGACGAGACGGATTTTATGCATAGTTGTGCGGGATTATCCGATATCAATT

SEQ ID 104

LQPETLEKELGLKNDLILIGCSPCQYVSVIQTDRKSEKSKSLLEFQRFVEYFNPGYVVENVPGILSRMKESGLDNFIKL
LEEKGFTVHFGIHNTADYGIPQSRKFTLIANRIKTSWNQSSIRANGLRYAMFWEWKTAFFKLWQDIKTRILCIVVRDYPISI

SEQ ID 105

ATGAATTTACCTTTTCGGGCAATGGTGTCTGATTTAGGTGGCACACTTTTAACACCTGAACATTTAGTGGGTGATCTTACCATTG
ATACTCTGAGAGTATTAGAGCAAAAGCGGTAGATATTATTTTGGCAACAGGACGCAATCATACCGATATGTCATCCATTCTTGG
AAAAATCGGTCGCGAAGCGTTCGGTTATGATTACATCAACCGGTGCTCGTGTACGGGATTACAGGGTAATTTGCTTTATAGCAAT
AGTTTGCCTGAAGAATTAGTTCTCGAGCTTTACAAAACATCATATGTGGGAAATCTTATTACAGACCAAGATTTTGTGCGCCATC
AA

SEQ ID 106

MNLPFRAMVSDLGTTLLTPEHLVGDLTIDTLRVLEQKGVDIILATGRNHTDMSSILGKIGAERAVMITSNGARVRDLQGNLLYSN
SLPEELVLELYKTSYVGNLIQTPFRFRHQ

SEQ ID 107

ATGGAAGAGCAACTTGCCCAAAACGACCGCGCTGAAAAAATTTGTCGGCTGTACGGCGCTTGGGCAGAAGGCGGCGCAGGCG
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AATGCTGAAGAAATGGGCGAAAGCCCGCACGCAAAACGACACGCTGCTCATGCAATCAATCATGCGGGCAACAGCTCGCCT
GCGGTGGTCAATAAAAAACCGCTTGACCGAGCGCGCTGCCGCTGGTGGGCATGAATGGCTTTATCAATCCGCGCGCGCAATTGA
GTGCCGATGAAATCAACGGGCTGATTACGAATTCGTACAACTGCCAAAATTGCCGAACAGGACGGCTTTTCAGGCGTACAAAT
TTACGCCGTACACGGTTATCTCATAGCCAATTCCTCTCGCCGACCAACCGCGCCCAAGACCAATGGGGCGGCGAGTTTGGAA

AACCGTATGCGCTTCCTTTTGGAAACCTACACCGCTATTGCGCGCTGCCGCGGGCAAAGATTTCTTGGTGGGCGTAAACTCAATT
CGGCAGATTTCCAAAAAGGCGGATTGACGAAAGCGAATCGGTGCAGGTGGTGCAAAACTGTTCGGAATGGGCATTGATTTTAT
TGAAGTTTCCGGTGGCAACTACGAAAGCCCGCAATGCTCGCCGCAAAGACAGCACCCGCAACCGGAAGCCTTCTTCATCGAT
TACGCCGAAAAAGCCCGTGAGCCAGCCAAGCCCGCTGATTATCACCGGCGGATTCCGTTCCGAAACCGCCATGGAAGATGCCT
TATCCAGCGGTCACTTTGGATTGGTTCGGCATAGCCCGCCCGTTTCCTTAGTCCCTGATTGGCGAACAAAATGCAAAACAGAAC
TTACCAACCGGTACAAGCAGACCGCATCCAACTGGCGTAGCATTTGTTGATAAAAAAGCGGGTGCAATGTTAGAAATGAACTGG
TATATGACGCAAAATGGATTGATCGGACAAGGAAAAACAGTCCAACCTAAAATTGTCGGCGTGGAAGTATTGCTGAAAACCTTG
CGGAAAAACGG

SEQ ID 108

MEEQLAQNDQPSSEKLVRLYGAWAEGGAGVLVTGNVMAESGKGSINDVLSDDRALEMLKKWAKARTQNDTLLIMQINHAGKQSP
AVVNKTPLAPSAVPLVGMNGFINPPRELSADEINGLIQFVQTAKIAEQAGFSGVQIYAVHGYLISQFLSPHNRRQDQWGSLE
NRMRFLETTYTAIRAAAGKDFLVGVKLSADFPQKGFDESESVQVQKLSEMGIDFIEVSGGNYESPQMLAAKDSTRKREAFFID
YAEKARAASQAPLIITGGFRSQTAMEDALSSGHLDLVGIARPFALVPLANKMQRNTYQTVQADRIQTGVAFVDKKAGAMLEMNW
YMTQMDLIGQKQSNPKIVGVESIAENFAGKR

SEQ ID 109

ATGCCGCAACAAACCATGAATTTAATGCGCGAGTGCATACCCATTTTACCGTATTGAGCGATGAAAACCGCCATCAGATCCTGC
ATGTATTGTGGAAACACGGTAGGATGAATGTGAATGAGCTGACCGAGCATCTGCATCTGTGCGCCCTGCTGTGTCGCACCATTT
AAAAATCATGCTGCAAGCCGGAGCGGTGGCGGTGGAGCAGGTCCGCAAGAGCGGTTTTACAGTATTGCCATGGCGGATGCGGTG
CGGAGATTGAAAACAGCTTGCCGATTGATGGCTCAAAATGCGCCGCTTTCAAAA

SEQ ID 110

MPQQTMMNLMRECIPIFTVLSDENRHQILHVLWKHGRMNVNELTEHLHLSPAVSHHLKIMLQAGAVAVEQVGKRFYSIAMADAV
ARLKLADLMAQNCPLSK

SEQ ID 111

TTGTACAAACCAATATGCGGACTGGAACAGATTATCCTACAATGCGCCAAATTTATGTTGGCAAGGCCGTCCCCAAAGGCTGGCGGC
AAGCAAGAAATCTGATAATGCGCTAAACCAATCAACCGAAGTGTTCACCGGTTGAAAGAACACAGCAGGAGTATTGCCGCTGT
TTCTGATTTAGATCCTTCCGATTTCATGTGCAGATTCTGTTATCTTTGAGGTGCCGCTTCTGACATGATAGGCACAAATCGAAGCT
GCCCTGATTAAATTACACAAACCTCTATGGAACCTCTGTGTGTCGATGTTTCGGAACACAGACCCCGGAAAAGGCCGTTACGAAC
AAGCCAAATCGGATTGGGATGTCTTTCATAGCGGGCGGTTTGGGCAGATAGGCTAAACCGCATACCGAATAGCTATGATCCAT
ACTTGAAAATATCAACACACATTTAGAGATAATAAAGAGAAAA

SEQ ID 112

LYKQYADWNRLSYNAPIYVGKAVPKGWRQARNSDNALNQSTELFHLRKEHSRSIAVSDLDPSDFMCRFVIFEGAGSDMIGTIEA
ALIKLHKPLWNSCVDGFGNHDGPKGRYEQAQSDWDVLHSGRVDADRLNGIPNSYESILENINTHLEIIRK

SEQ ID 113

ATGAAGTCTTTGGAAATTTTTCGGCGCGGGCGGTTGGCAAAAGGCCTTGAACCTTCAGGATTCCAACATGCATCTTTTATTG
AACTCAATAAAGATGCATGAATCTTTAAGAAGCAACTTTAACCCCAAGCTTGTATTATCAGGGAGATGTGGCAGATTTTGATCT
TTCCAGTCAAGAAGGCATAGAAGTCATTGACGGCGGCTCTCTTGCAGCCCTTTTCATTGGGCGGGAACACCTTGCCCATGAA
GACAGAAGGGATATGTTTCTCATGCGGTGAGATATGTGGAGTATTACCGCCCCAAGCTTTTATCTTTGAGAAATGTAAGGAC
TTTTAAGAAATCATTCGCTGATTATTTGAATATATCTTACCTTCGGCTTACTTATCCGAATCTTGGTATTTTCGAGAATGAAGA
TTGGAAAGGCCATCTGACACGCGCTGAAAGAAATGAATTCATTTATATAAAGGAATCAAATATAAGGTTTCATATCAATTTGTTG
AATGCAGCTGATTACGGAGTGCCGCAAAACGCGAAGCGGTGTTATCGTAGGTATCCGGCCGATTGGATTTGATTGGAAAT
TCCCAAAAAGAACACATTCGGAAGACAGGTGAATTTGGGAAAAGTATGTAACGGGGGAATACTGGGAAAAACACAACGAACCCAA
AAGATTCAATAAAGATATTGCTGAAAAGTTACAAAAAAATACGGTATATTGCAACAGAAAAAAACCTTGCGCAACGGTAAGG
GATACCTTGTCGACATCCCGCATCTTTGGGGAATCATAAAATACAGGACATGAATATAGGGATGGCGCAAGAAATTTATCCCG
GACACACAGGAAGCGGATAGACGAACCGTCCAAAACCATTAAGCAGGTGGGCATGGCGTTCGCGGCGGAGAAAAATATGATTCG
TTATGATGATGGAACAGTCAGATACTTTACCAGCTATGAAGCAAACTTCTTCAAACATTCCTGAAAGAAATTTGTCATTCTGGA
GCTTGGGAGAGAAGCAATGCGACAATGGCAATGCGGTCTCTGTCAAATTTAGGCAAAACATCTGATGGGGGTGT
TGTCCGAGAAAAGCAGCCTGCACAAC

SEQ ID 114

MKSLEIFSGAGGLAKGLELAGFQHASFIELNKDACNSLRNPNKLVYQGDVADFLLSSQEGIEVIAGGPPCQPFSLGGKHLAHE
DRRDMPHAVRYVEYYRPKAFIFENVKGLLRKSFADYFEYILLRLTYPNLILQNEWDKHLTRLKEIEFNLYKGIKYKVSQYLL
NAADYGVFPKRRERVIVGIRADLDIDWKFPRKTHSEDRLNWEKYVTGEYWEKHNEPKRFNKDIAEKLQKKYIGFEPEKKPQWTVR
DTLSDIPLHGNHKITGHEYRDGARIYPGHTGSGIDEPSKTIKAGGHGVPGGENMIRYDDGTVRYFTSYEAKLLQTFPEEFVISG
AWGEAMRQIGNAVPVKLSEILGKHLMGVLSEKSSLHN

SEQ ID 115

TTGTCCGACATATCGGCTTCGCGGCTGCCTATATGGATGTGCAAAAACAATATCCCTTTGAAACCGTCGCCGTATGCGTGCTGC
CGAACCATATTCACGCCATTTGGACGCTGCGCCCCGACGATGCGGATTTATCCCTACTCCGCGCGCTGATTAAACCAAATTCCTC
CGCATATTCCTCATATAAACTTAGGGGCTGTACTAGATTATCCC

SEQ ID 116

LSDISASRAAYMDVQRQYFFETVAVCVLPNHIHAIWTLPPDDADYSLRLRLIKTKFSAYSPHTKNLGAULDYP

SEQ ID 117

TTGTTCAATAGGCTTATATTTTGGATTGTTAGAATGAATACTAAAACAGAGTTACAAAACTTTTAGAAGAGGATATATCAACTT
TAAAAGAAACACTAATTCGTGTAGATGCTCTTCCTCCAAGATATGTACSTAGCATTCGAACCTCTATTGTCGCTCGATGGTTAAT
TGACAAACAATTAATATCTCGCAAAAGAAATAGGTTTAACTATAGAATTGCCCATCTTGATACAAGTTTGGTATTTTGAAAAA
TTGTCAACCTTAGAGAATAAAGTTAATTTTATAGTAGATTAACAAAAATCAGGACAAGCGCGGCGAGCCGACAGTACAAATA
GTACGGCAAGGCGAGGCAACGCCGTACCGGTT

SEQ ID 118

LFKWLIFWIVRMNTKTELQKLEEDISTLKETLIRVDALPPRYVRSIATPIVRRWLIDKQLNILAKEIGLTIELPILDTSLVFEK
LSTLENKVNFSRLTKIRTRRAADSTNSTARRGNAPV

SEQ ID 119

ATGGCTGGTGGAGTTTATTTAGGCGGAAAAATTATTAGCCCTATATATCATTCATCACAAGAATTTTCTGGTGAACCAATAATCT
ATGCTGGAACAAATATAATTTTATGCTGCTGAAAAATTTTAACTTTAAACGAGTTTTCATAATGGAAATATTTTAAATAT
GAATCAGATAATTACTTTTATCCAAATAACAAGGGGAGTACGTTTTGATAAAAATTACGATAAATATAAACTTGGCAAGTT
GCTATAGAAAAAGCAGCAAATTTTAAACTCGGTAATCCATATAAT

SEQ ID 120

MAGGVYLGKKIISPIYHSSQEFSGEPIIYAETNIILCPAEKFLTLKRVFHNGNIFNMNQIITFLSNKQGGVRFDKNYDKYKTWQV
AIEKAANFLKLNPNYN

SEQ ID 121

ATGACAGAATTACCGTGGATAGCCGAAGCGAGAGGCACATCGGTTTGAAGAATAATCCCGCGCGGAAACACAATCCGACGATTG
TGCAATGGCTCAAAGAGACGGGCGGCTTCCCGCGCGCGGCAAGTCTTGGTACTTTGAAGACGAAACGCCGTGGTGGCGCTGTT
TGTCGGATACTGCCTGGGCAAAAGCGGACGCGCGGTATCAGGGACTGGTATCGCGCCAAAGCCTGGTCAATGTCGGGTTTGACG
AAACTCGAAGCCCCCGCATACGGCTGCATCGCGGTCAAACCGCGCGCGGGCGGCGGACACGTGTCTTCTGTTGTCGGCAAGACG
CGGAAGGCAGAAATCTTGGGCTTGGGCGGCAATCAGGGCAATATGGTATCCATCATCCCGTTTGACCCTGCGGACATTGACGGCTA
CTTCTGGCCGTCCAAGCTGATTGGCGGCAAGCCGTGCCTTCGTCCCCCGCGAAGGGCGTTACCGGTTGTCTGGACGTTGCCGCC
ACGGCGAAACAGGGCGCGGGCGAGGCC

SEQ ID 122

MTELPWLABARRHIGLKEIPGAHNPTIVQWLKETGGFPGAASWYFEDETFWCGLFVGYCLGKSGRAVIRDWYRAKAWSMSGLT
KLEAPAYGCIADVPRRGGHVFFVVGKDAEGRILGLGNQGNMVSIIIPFDPADIDGYFWPSKLIIGKAVPSSPAEGRYRLSDVAA
TAKQGAEGA

SEQ ID 123

ATGATTGGGGCTTTGCTGAAAAATTGGAAGCCGCTGCTTATTTGTCCGCAATCGCGTTCTTTCGCCGTTTCTTGGCAGCTGGACA
GGGCGGCGCAATACCGTCCGCGATACGGTGCAGCGGTGTCTGGAGGTTTCGGAACGCCCTCAAAGCCGCGCGGTGCAACACGCCGA
ACACGCCCGCAAATCGTCCGCGGTATCAGGCGCAAAAGCGCGCGCGGAGGAAAAAGAAAGGGTCCGCTATGTGCAACGCTT
AAAATCATTGAAAAACCTGTGTACCGCAATGCCTGTTTGTATGCTGACGGCGTGCAGCAACTCAACGCCCGCTTGACGACGGCG
GT

SEQ ID 124

MIGALLKNWKPLLILSALFAFFAVSWQLDRAAQYRRGYGAAVSEVSERLKAAVEHAHARKSSAAYQAQKAAREEKERVRYVQTL
KIIKFPVYRNACFDADGVRELNAVDDGG

SEQ ID 125

GTGCGGCATCGGTTGTTGTCCGGATCGGTACGGCATTTTCATTTCCGCCCATTTATGGTGGCGCTGATAATTTGTATAACGCC
CCTTCGCGCAAAACAAACGGCAAAATTTGCCGCGTCCGCCGATATGTAAAAAATCGGGGGGAATGCCGACACTTCCCCCGATG
CGGCCGCCAACCCGGAACCGACGGTTCGGTTGCAAACTTCCGGTTGACAACCTCAATCCGCGCCCAACGCCGTACCGAGCGCGCG
TGCCCGCGCCCTGCAGTCTGTTATACATACCGGCCCGCTTCAGGGCCACGGCAGCACGTCCGCGCCCGTGTCTCCCTTCAAGGTGCG
GCAGTTTCCGGCAGGGCCGACCAATCGGCGGGCGGCTTAACGCCGCTGTCACAGCGCGCGTTGAGTTCCGCGCACGCCGTGAG
CATCAAAACAGGCATTGCGGTACACAGGTTTTCATGATTTTAAGCGTTTGCACATAGCGCACCTTCTTTTCTTCGCGCGC
CGCCTTTTCCGCTGATACGCGCGGACGATTTGCGGCGGTGTTCCGCGGTGTTGACCGCGCGCGCTTTGAGGCGTTCCGAAACC
TCCGACACCGCGCACCGTATCCGCGACGGTATTGCGCGCCCTGTCCAGCTGCCAAGAAACGGCGAAGAACCGGATTGCGGACA
AAATAAGCAGCGGCTTCAAATTTTTCAGCAAAGCCCAATCATTTACGCCCTCGCCCGCGCCCTGTTTCCGCGTGGCGGCAACGTC
CGACAACCGGTAACGCCCTTCCGCGGGGACGAAGGCACGGCTTTGCGGCCAATCAGCTTGGACGGCCAGAAGTAGCCGTCAATG
TCCGACGGGTCAAACGGGATGATGGATACCATATTGCCCTGATTGCCGCCCAAGCCCAAGATTCTGCCTTCCGCGTCTTTGCCGA
CAACGAAGAACCGTGTCCGCGCGCCCGCGCGGTTTACCGCGATGCAGCGCTATGCGGGGCTTCGAGTTTCGTCAAACCCGA
CAT

SEQ ID 126

VRHRLLSGSVRHFHFRPLLVRLLIILYNAPFAQTKRQKFAASARYVKNRGECHFRPCGRQPGTDGSVANFRLTTQSAPNARTSAP
CRALQSLYIPAAFRAGHSTSAFVFPSCGSGFQGRKTSAGGLTAVVNGGVEFAHAVSIKTGIAVHRFFNDFKRLHIAHPFFFLAR
RLRLIRGRFAGVFGVDRGGFEAFRLNRHRTVSATVLRFPVQLPRNGEERDCGQNKQRLPIFQQSPNHLRLRALFRGGNV
RQPVTFPGGRRHGFANQLGRPEVAVNVRRVKRDDGYHIALIAAQDSAFRVFADNEEHVSAAPARFDRDAVCGGFEFRQTR
H

SEQ ID 127

GTGTATGTTAAACATACACCCTTGCTGAAAAAGCCAACGGGCGGACTTTCCGGACATCTCCGGATGTGCTGTTTCCACGAGCAGT
CGACCAACCTGAAACGTCCGCTACCTCTTCTTGGTGAAGAGAGGCTTTCAAACCTTTCGTGGAGCTTAAATGCAAAACACCAT
TTCTGTATTTTCTTCAAATCTCAAATGTCCGTACTCAAATCTTGGGGGCTGAACCTTGGTTTTCCTTGGCGATGTTGCGGAA
ATTCTTCAAATTCAAAATGCCGTCAGTTGCCATTAAAAGACCAGGCATTCAAAAATCCAGCGTTGCAACAAAAAAGGCAACC
AAGAATTACTTTTCATCAACGAGCCGAATCTCTACCGAGTCATCTCCGTTACGCAAGCCGAAGCCGTCAAATTCGAAGACTG
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TTGCGCGGGCGGTTGCGCGGCTTGTCCGGCGCAACACGCATAGGCTACTCTCCGCGTACAGTATGATACCAACCGTTCAACG
TCGAAGCCGTGGAAGGCATCCCCGCGGACAAACTGCCGGAAGCCGTGCCTACGTCCACGCATTGACACTGCACACGGGTTTGGC
CGGCGAAGTCCCCGACCGCAACCGTTGCCCGCGCGCAACCCGCCCTGCCCATAGCGGCAACGCTTTGGCGGACATTGCCGCT
ATGGTTTATTACGCGACACGGATGATCGAATTGGGCAAGACGTTTTCCGCGCGCTGAAGCAGCTCGGCTGCAACAGGCGGTTA
CGATGTGGACGGTTTGGCACGAAACCGTTCAATCTGAAAAGATCCGTGCGAGCCCTCGAAGTGTGCGGGGATATGCGGACAA
AGACGCCCTCCGCGCGCATAGCCGCATGCTTGAAGGCATTACGGCAAGGCTGCGGCAAGG

SEQ ID 128

VYVKHTPLLKPTGGLSGHLRMCFFHEQSTNLKRPTSSWSKRGFQTFVELKMONTISVFSFKSQNVRTQILGAEPWFCLGDVAE
ILQIQNARQLPLKQGIQKSSVATKKGNOELLF INEPNLYRVIFRSRKAEAVKFQDWIFEVPIQIRKTGGYQITPKTTADDRGT
LRRRAVALVGRKRIGYSSAYSMLHQRFNVEAVEGIPADKLPEAVAVYHALTLHTGLAGEVPDREPLPAPQPALPISGNALADIAA
MYYVGTMIELGKDVSAPLKQLGCKQAVTMWTVWHETRSLIKRSVAALVLRGYADKDAAGRIACLEGTYGKAAAR

SEQ ID 129

GTGTGTACCTTATGCCGGACCTGCATGTTGAAACATAAAGGAAAAATCATGAACCGTCGTCAATTTTGGGCAGCGCCGCTGCC
GTCTCTTTGGCTTCCGCCGCCCTTTTCGCCGCGTGCCGACGACACGCCGACTACCACCATCATCAGATATGCAGCCTGCCGCCG
CATCCGCCCTACACCGCCGTCGCCCAAACCTGCCGCACACTGTCTGGATGCCGGACAGGTTTGCCTGACCCACTGCCTGTCCCTGCT
CACTCAGGGCGACACGTCTATGTCGACTGTGCGGTTCGCCGTGCCGCAGATGCTTGCCTTATGCGGCGCGGTGCACGACCTTGCC
GCACAAAAATCCCCCTCTGACACGCGACGCGGCAAAAGTGTGCCCTCGAAGCGTGCAACAGTGTGCCAAAGCCTG

SEQ ID 130

VCTLCRTCMLKHKGKNHEPSSIFGQRRCLFGFRRLFRACARTRRLPPSSRYAACRRIRLHRRPFPNCRTLSGCRTGLPDPFPVPA
HSGRHVYVRLCGCRAPDACLMRRGARPCRTKFPSTDRRGKSVPRSVQTVCSL

SEQ ID 131

ATGAACCGTCGTCAATTTTGGGCAGCGCCGCTGCCGCTCTCTTTGGCTTCCGCCGCCCTCTTTCCGCGCTGCGCACGGACACGCCG
ACTACCACCATCATCAGATATGCAGCCTGCCGCCGCATCCGCCCTACACCGCCGTCGCCCAAACCTGCCGCACACTGTCTGGATGC
CGGACAGGTTTGCCTGACCCACTGCCTGTCCCTGCTCACTCAGGGCGACAGCTATGTCCGACTGTGCGGTTCGCCGTGCCGCCAG
ATGCTTGCCTTATGCGGCGCGGTGCACGACCTTGCCGCACAAATCCCCCTCTGACACGCGACGCGGCAAAAGTGTCCCTCGAAG
CGTGCAACAGTGTGCCAAAGCCTGTAAAGAACTCCGCCACCCTGCGGAATGCAAAAGCCTGTACAGTCTGCCTCGACTG
TATCAAAGAAATGCGAAAACTCGCCGCC

SEQ ID 132

MNRRQFLGSAAVSLASAAAFARAHGHADYHHHDMQPAASAYTAVRQTAHCLDAGQVCLTHCLSLLTQGDTSMSCDAVAVRQ
MLALCGAVHDLAAQNSPLTRDAAKVCLCACKQCAKACKEHSAHAECKACYESCCLDCIKECEKLA

SEQ ID 133

TTGGAAGTGGCGGGGCAACAAACCGCTTGGGGCGCGGAGCTGGCGGATTTGAAACCGCTTTACAAAGACTTTATGTATTGGGAAC
GCGGTCTGCACATGTATAAGGCAAGTGCCGTCGTGCCGACCGGATATGTACGGGTGGGAATACCGCGCCGCTGTGCCGCCAAGA
CACGCAGCGGTATGCCTCTTTTGGGGCGACGGCTACGACGTGTACCGTCAGTTGAGATGGCGGCAGATACCCGAAAAACAGAGA
AAGGCATTCAAAAAAGCCGCAAAAGCAAAATACCGTGATGTTTGGCGGACGGGAATACGGCATATCCAAACAGAAATTTAGCG
ATGTTTGGGATGATTTTGAAGACGCGATGGAATGAAGGCGTTTCCCTGCCTGTCTTCGCTGTTTCTGACCAAGTGGCATAAAAA
TCTATATGAATATCTGGAGGAATATCCGTTTATCACCCGATTGTGTCTGGAACACCGGTGACACCGTGTGGATTTCAGCAAT
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GCGAAATCAAGGAAACTGCAAGGTCTGTACCGCGGAAAGGGCGCGGCTGATTTTGAAGTGGGCAAAAGCGTTCCCAAAGT
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CTCAAAACCATACGCGCTGTGGGGCAAAACCGGGCAATATCGCCAAATTTTCCGCCGATATCGGGATTGAGGATTGGAAGTGTTC
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CCTGCCCGAAGAGGCGCGGAAGGCAGTGAAGAACTTTATAAGAAACGGAAGGAAGACGGGCTGGACCCGTTGGATAGAAAAAGCC
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GCCGAGCGGTTGGAACGATATTGGACCTGATACCGGATGGGTCTTGTGCCGACAAGGAAAACTGTTTGAATATTGTATAAAA
ACAGGAATTTT

SEQ ID 134

LDWRGNRPLGAAELADLKPLYKDFMYWERGLHMYKASAVVPTGYVRVGNAPLCGEDTQRYASFWDGVDYVRQLRWRQIPEKQR
KAFKKAASKNTVMFAGREYGISKQNLSDVWDDFEDAMELKAFCLSSLFTKWHKNLYEYLEEYPFITRLCLENHGQTVLDFSN
TRITDLSDMTGVEESLYLNEGLDSLNLKGEIKENCKVCTAGKAGLILEVGKSVKVRGLENLTAVNVMGIADFDQNLSETYFK
LKTIRLWKGPNIANFSAVSGFEDLEVFTAVIDLFGFGADDI.PHPDRLPKLHRLWMSLPEBAKAVKLYKKRKEGDLDPWIEKA
RKPEWLAQNFDNPFWDGAEHIPKSHAKAAELYRKTRAGVVKLLGNPPENIGEGLAEAVKAYTGGFNKMDKKHFIDTVEREDI
AALETILDLIPDGSADKEKLEIFDKNRNF

SEQ ID 135

TTGCAAGAGTTTAAATTTATTTTGGACAAGATTTCGGATTGTCTAAAAAAGAGGCTATTTCGGAAAGTGTGAAATGGCTTCCGT
CCCATTTCAAAATTCACACTGATGGTAGCTCAAGGCATTCAGGGTTTTCATCTTAAAGCTGTATTTTGAAGAATGATAAGAATGA
ATATTATGCTTTAATCGGTTCTTCAAAATTTGACTCATGCTGCGTTTAAATAGCAATTATGAAGCAAAATTTTACTAAAAATTTCC
GAGCAGGATTTTATAAAAGTCAAACTCTTGGGCTGATGAAATTGCGATGAAATCTATCCCGGTATCGGAAGATTGGCTTGAGGAGT
ATCAGGAAGCTGAAATTAACATAAGAAATCAACTGTTAGACAATCAGTGTGATAAGTTATTTATGGAGATGCCAAATTATAA
TCAAGAAGTATGCGGCACGGAGAAAGCAGATGAGAAACCATCAAACTGTGTATCAATTAATAAATCTTATTAAGCAATGT
GCAGCAGGAAAAATAGACAATAATGATTTTATGGGGAATTTAATAAATTATGTTCTTGGAAAAAGCGAAAAATAAGGAGAAGGGG
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TTTTGATGCTCCACTTACTGAGAGAGATAATGTGGTTGCCAAGCAAAATGATTGGCTAAAGAAATGTGGGGTTTCCACTCGTGT
TCAGTTTTTTCTGAAATGCTTTGTCAAGAATATCCAGATAGATATCTGTTTTAAATGCTCCCATTAATAAATTTTGAAGAAA
ATAAATTTAAGTCTGCAAAAGGAGCAAGCGAAGGCTCCAAATATATTGATTAAAGTATGAAGTTAAGAGCTTTACTAGCTATGCA
GTCAGAAATAAAGATTGGCTGAATTAGATGTTTAGTACAGGCAGAAATATCGCAATCGTACAGATATTGATTGGGAA

SEQ ID 136

LQEFKFIQDFGLSKKEAIRKVLKWLPSHLKFTLMVAQGIQGFHPKAVFWKNDKNEYALIGSSNLTHAFAFNSNYBANILTKIS
EQDFIKVKSWADEIAMKSI PVSEDWLEEQEABINYKKSIVRQSVMDKLFMEMPNYNQELIAARRKQMRNHQTVCNQLKNLIKQC
AAGKIDNNDYGFENKLWSWKSENKGEVGNRFQDKTWKRTGKSSDFRLCIAIQSVFDAPLTERDNVVAQIDWLKECGVSTRG
SVFSEMLCQEPYDPDRYPVLNAPIKKFLEENKPKSAKASEGSKYIDLSMKLRALLAMQSEIKDLAELDVLVQAEYRNRDIDWE

SEQ ID 137

TTGTCTGAAAAACGGGAAGGGCAATTTGCCGCGACCGCGCGCTCATTTCCCGGAACCTACATTCCGTCATTCCCACGAAAGTGG
GAATCCGGAACGCAAAATCTAAAGAAACCGTTTATCCGATAAGTTTCCGCACCGACAGGTCTGGATTCCCGCTTATGCGGGAAT
GACGGCGCGGGAATCGGCGGATTCGGCGGAGTTGGTGGATTGGCGGGCTGAAGCCCGCCCTGTATATCGGAACCTCCGTTATC
ATAGCGACAAACCGCCCGCGCCGCCACCGCGCCCGCCCAAGGCAGACAACCGTTGCG

SEQ ID 138

LSENGKGNFAAAAVIPANLHSVPTKVGIRNAKSKETVLSDKFPHRQVWIPAYAGMTAAGIGGFGGVGGFGLKPALVYRNFRILATNRPAATRPRQTTVA

SEQ ID 139

ATGAAAAAACTTCTAATGATAACCCCTACCGGTATGCTTGCAGCTTGTTC AACAGGTGTCAATGTCGGCCGGTTGATGGTTGAAATGCCGAGGGAGAACGCCCTGTTGTCGTGCAGGTTCCCGCGACGAAATAACCCGCTTTC CGATGCGGTGGCTGTTCGGAATGATTAA AACATCCGGATCGCCTTCGGCATCAAATATGATTGAAATGCTCGGCGCGGACAATATCAACGTCGGCGTGGCGGGAGGCAGCCAA ATGTTTAATAAGGCGACCGCACTTTATTCCCTTAAACCATGCAAAGAAAGTCGGAATAATGTCAGTGTCTATATGACGGGGCATA CGGAAAGCGACAAGGCCGATTGTGAAAACCGCGCAATGCCAAAAATATTAAATTACATTATTCTTTAACCAAAAA

SEQ ID 140

MKLLMLTLTGMLAACSTGVNVGRLMVEMPQGERFVVVQVPATNNPLSDAVAVGMIKTSGPSASNMIEMLGADNINVGVAGGSQMFNKATALYSLNHAKKVGNNVSVYMTGDSBSDKADLENAANAKNIKLYFFNQK

SEQ ID 141

ATGCGCTATTTTAATAGAAACGGAAGGATGCCTGACAACCTTGATTTTGATTTTCGGTTTTTGGCAAAGCCCTCGCCGACACACGCACGCAAAACCTTGATAGGCGGATATCACATTGCGGCGTTCCAAACCGATTGAGACGACGCATCGACAGGATCGGGCTGATTTGCCGACCTGACCATGGTCAAGCTCGGAAAGCCCTTCCCGCTAAAGGCGGTATTGCAATAGGCTTTGATATCGCCCTATCGGTTGGG GAAAATATTTTCGGTTTTCGGCTGAACATAGGAATAACCGCCTTTCAATTTGCAAACAACCGAAATCGTACCGATTGTTTCAGACA CAGCCAAAAACAAATGCCGTCTGAAACCCGATTGTGAGGCTTCAGACGGCATTMTTGTTCAGGCGGTTGCCGCTTCTCCCCG AACACTTCCCGCCACAATTTC

SEQ ID 142

MRYFNRRNGRMPDNLILISVLAKPSPTHARKTLIGGYHIAAFQTDLDGRIDMRADLPSTMTVKLGKPLPRKGGIRIGFDIALSVGENISVCLNIGITAFQFANNRNRDCSDTAKNKCRLKPLSGFRRHFLFRRLPLPPTLPATIS

SEQ ID 143

ATGACGCACACCGCATCGAAAACACCCAACTCTGGGCGGTTCATTGCCGCCCGCGCATTCATCTGCTGATTACCATCGGCATGAGGATGACGCTCGGACTGTTTCGTCCAACCCGTCGTCAACACCACCGAATTGAACATTGCCCAAGTTTCAGCCTCATCATCACCGTTTT CCAACTGATGTGGGGCGTATTGCAACCATTTGCCGCGCGCTTGCAGCCGTTTCGGCGCGTTTCAGGATTAAGCGGGCGGTGCC CTCCTGCTGCTGTCGCGCTGCCTGATTGCCCTCAACATCCGACTTATTTGGGGGCTGATGATTGCCGTGCGGCTGCTGCTCGCAT TCGGCACCAGGTTCCGGCGGGTTTTCCATCATTTATGGGACAGGTCCGCCGCCAAAGTCCCAACACACAAACGCGCTTGGCATCCGG ACTGGTCAACGCAGGCGGTTCCGGCAGGACAATTCTGTTCGCACCGCTGGTTCAAGGACTCAAGGACTCGTCGCTCTGCCCGAAG TCGGCTGGACGGGTACATTTTACGTTTGGGGCGCAATCGCCCTGC

SEQ ID 144

MHTASKTPKLWAVIAAAAFILLITIGMRMTLGLFVQPVVNTTELNIAQFSLIITVFLMMWGLVQLPSGALADRFGAFRVLSGGA LLLVCACLIASNIPTYWGLMIAVGLLLAFGTGSGGFSIIMGQVAAQVPTHKRGLASGLVNAGGSAGQFLFAPLVQGLKDS SSPK SAGRVHFTFGAQSFC

SEQ ID 145

GTGGGGCGTATTGCAACCATTTGTCCGGCGCGCTTGCAGCCGTTTCGGCGCGTTTCAGGATTAAGCGGGCGGTGCCCTCTGCTC GTCTGCGCTGCTGCTGATTGCTTCAACATCCCGACTTATTTGGGGGCTGATGATTGCCGTGCGGCTGCTGCTCGCATTCGGCACC GTTCCGGCGGGTTTTCCATCATTTATGGGACAGGTCCGCCGCCAAGTCCCAACACACAAACGCGCTTGGCATCCCGACTGGTCAA CGCAGTCGGCTTCGGCAGGACAATTCTGTTCCGACCGCTGGTTCAAGGACTCAAGGACTCGTCGCTGCTGCTGCTGCTGCTGCTGGA CGGGTACATTTTACGTTTGGGGCGCAATCGCCCTGCTGATTCTGCCCGTCTCATGGTGGCTTGGCGGCGGCAACACGGCGGCAA CAACGCGGCCACACCCAAACACACCAAGCCACACACGAGACAAGCCTCGGAGAAGCAGTCAAAACCGCCTTCAAACCCCAAGC TACATCTGCTGCACCTGAGCTTTTTTCGCTGCGGCTTCCATATCGCCTTCTCGTAACCCACCTACCCACGGAAGTCGCCCTGT GCGGACTGCCCGCCACCGTCGCTCGACATCCATCGCCATCATCGGACTGGCAAACATCGCCGGTTGCGTGTTCCTCAGGC

SEQ ID 146

VGRATIIVRRACRPFRRVQGIKRRCPFARLRLPDCLQHPDLLGADDCRRAAARIRHRFRFRVHHYGTGRRRSPHTQTRLGIRITGQ RRRFRGRTIPVRTAGSRTQGLVVLPEVGWGTFTYVWGAIALLLIPVSWWLAGGNNGGNNAHTQHTQATHGQSLGEAVKTAFTPS YILLHLSPFACGFHIAFLVTHLPTEVALCGLPATVASTSIAIIGLANIAGCVFSG

SEQ ID 147

ATGGTGTCTGATTTACATCTTCTACCCAAAACCGACCTCAACTTTTACATTTTTCGCCCGCGCACTCGGATTCACATGGCTCGCCA CCGTCGCCCGGACCGCCGCGTTACCGGCAACTCTTCGGCAGCGCTACCTCGCCACCTGTTTCGGACTGGTGATGCTACCCCA CCAATACCGCGGATTCCTCGGCTCGTACATCGGCGGCTGATTACACAATTTCGGTGACTACGGCTGGATGTGGTACGCCGAT GCCGTACTCGCCGCGACGGCAGCCCTGCTTGTCTGCCGCTCGCGAACCCCGAACCGCCGCA

SEQ ID 148

MVLIYIFSPKTDLNFYIFAAALGFTWLATVAPTAAVTGKLFTRYLATLFGVLMLTHQIGGFLGSYIGGIVITQFDYDGMWYAD AVLAGTAALLVLPVREPRTA

SEQ ID 149

ATGAACATTATCGATGCCATCATCAATTGGCTAACAAACCTGTGTGCGGGGTCAACTCCCATTTCTCAAAGCAACAATCGTGCCA ATCAGGCAGGTGATGCTTTTGAAGAATATGTAAAGACTTGTTCGGGAGTTTCAACCTAAATGAAACCAACGCATAGCCCG ACACGCAAAAGTATTCTCATATTTGGGCAACAACCTCAACCTCTGATGCCATGTTGCGAAACGGGGATGCCATCGAAGTTAAG AAAATTGAAAGTAAAGATTCCGCACTGGCGCTGAATAGCAGCCACCCAAAATCAAAGCTCTCTGTTGATGACAGCATGCTTACAA AAGCTGCAAAGATGCGGAAAAATGGGAAGAGAAAGACATTATCTATAATTGTCGGCGTCGT

SEQ ID 150

MNIIIDAIINLANNPVVGVNHSQSNNRANQAGDALEEVKDLFSGSFNLNETQRIARHAKVFSYLGNNSNPPDAMLRNGDAIEVK KIESKDSALALNSSHPKSLSVDDSMITKACKDAEKWEEKDIIYNRRR

SEQ ID 151

TTGGCAATGGTTTACGGAATCGACTACTGCGCCGATGCCGAATGCTATTTGAAGATAAAAAATCAAATTAAGGAAGGAATCGGCA ACATCGGCGGCATACAGTTTGCAGAAACCAAGAGCTGGGCAAGGTCAACCGCATTGATCCGCTCAACATAACTTATCTGAGAGT ACGGGGTATGTGGGGAATCGAAAATCCATGTTTGTCTTCAACTATATTTACCAACGGAATATGGAAGAAAGTTCAATTTTCATG

GCCATTATCAACGAAGACAAATGGAACAGTTTTTAACAATACAGACAAGCTGCTTGCCATACAGGATTCCAAACCTGGCCATTTCCG
ACATTAATAATAAAAATCCCAACAACCCGGCGCGATTAAAGAAATGCAAAACTCATCACCTACCACCTTA

SEQ ID 152

LAMVYGDYCADAEYLIKIKNIKEGIGNIGGIQFAETKELGRVNRIDPLNITYLVRVGMWGIENPWFVFNYYIQRNMEKSFNFM
AIINEDKWNFSNNTDKLLAIQDSKLAI SDIKIKNPNPARLRNAKLITYHL

SEQ ID 153

ATGCAAAATCATCACCTACCACCTTATAATCCTATGAAAAATCATTAGTTTGTGTTAGCGGTTGCGGCGGTTTGGATTGTTGGTTTCG
AAAAAGCGGGATTGAAATCCCGCCGCCAACGAATACGATAAAACCATTTGGGCAACCTTCAAGGCAACCATCCAAAGACCCA
TTTGATAGAAGGCGATATACGCAAGATTAAAGAAGAAGATTTCCCTGAAGAAATCGACGGGATTATCGGCGGCCACCTGCCAG
TCTTGGTCTGAAGCGGGAGCTTTGCGCGGCATCGACGATGCGCGCGGACAGTTGTTTTTCTGACTACATCCGTATTTTGAAGCA
AACAGCCAAAATTTCTTTTACGCGAAACGTCAGCGGAATGCTGGCAAAACCGCCACAACGGAGCCGTACAAAACCTGCTGAAAAT
GTTTGACGGATGCGGATACGACGTAACCTTGACTATGGCCAAACGCAAGACTACGGTGTAGCACAGGAACGCAAAAGGGTCTTC
TACATCGGTTTCCGTAAAGACTTGGAATAAAATTTCTTTTCCAAAAGGTTGACGCGTGAAGACAAAGACAAGATTACATTGA
AAGACGTTATTGTTGGATTGTCAGGACACAGCCGTACCTTCCGCCCCGCAAAACAAGACCAACCCCGACGCGAGTCAACAACAACGA
ATATTTTACCGGCGAGTTTTCCTTATTTTATGAGCCGGAACCGAGTTAAAGCGTGGGATGAACAGGGTTTACCGTCCAAGCT
TCAGGCGAGGCGAGTCCAACTGCACCCGCAAGCCCCAAAGATGGAAAAGCAGGGGCAAAACGACTACCGTTTGTCTGCCGCGCAAG
AAACACTATATCGGAGGATGACGGTACGCGAAGTTGCAAGAATCCAAGGCTTCCCGACAACCTCAAATTCATCTATCAAAATGT
CAACGACGCATACAAAATGATTGGCAACGCCGTCCCGTCAACCTTGCTTACGAAATGTCAGCGGCAATTAAAAAACCTAGAA
AGG

SEQ ID 154

MONSSPTTYNPMKIIISLFSGCGGLDLGFEKAGFEIPAANEYDKTIWATFKANHPKTHLIEGDIRKIKEEDFPEEIDGIIIGPPCQ
SWSEAGALRGIDDARGQLFFDYIRILKSKQPKFFLAENVSGMLANRHNGAVQNLKMFDDGCGYDVTITMANAKDYGVAQERKRVF
YIGFRKLEIKFSFPKGSTVEDKDKITLKDVIWDLQDTAVPSAPQNKTNPDVNNNEYFTGSGSPIFMSRNRVKAWDEQGFVQA
SGRQCQLHPQAPKMEKHGANDYRFAAGKETLYRRMTVREVARIQGF PDNFKFIYQNVNDAYKMI GNAVPVNLAYEIAAAAIKKTLE
R

SEQ ID 155

TTGAAACGTCAATTTAAAAATAAAGAATCAAGGGTTAGCGTGAATTATAAGGAATGCTGTAGTATTTTTCTGATTTTCTGAAATGG
AACCGTATAAAAAATGCCGTTAGGAAAGACAAAGCAGCTGAATTGTATTATTTGAATTTATCTTTATCAAGAGAACTTTTTCATGT
TGTTTCTATATTGAGATCGTTTAAAGAAACAAAATGATATTGCTTTCCGCGAGGAGTTAAAGACAGAAACCGGTTATATGAT
AGCATACAACCACAAACGAATCCTGCAATTGAAATATCAAGGTTGCTTTTAAAGAAATGTTACGAAAGAACTGCGCGAATTAAATCA
AGGTTGCAATTATCTAAAAATACAAAATAATAGCGGAGGAAAGTTTGACCACAACCAATTGGTTGCGAGGACTAGGATTCGGTTTGTG
GCGGTATCTGTTTGGCGGGAGGAAAGATGCTCAATTTGATGCTGCAGGAAAGATTGATGAAAGTTTTCACAAAAGCCCCAAA
TCTACACCAAGTGTCAATATAACCAAAAATGGATTTTTCGAGAACTTTCCATATTAACAAATTTCCGTAATCGTTTGGCACATC
ACGAACCGATTTGTTTGTAGTTTAAAGGTGCAATAAAAGATACCGGCTACGCTAGAAATATTCACCAATCTATTTTGAACGTCT
TAATTACATGGATGTAGATACGCTTCAGTATTTAGCCATTTTAGCGATCAAGTGATTGCGGCTGCGGATGAAATCGACAAACTG

SEQ ID 156

MERYKNAVRKDKAAELYLLNLSLRELPHVVSIFEIVLRNKIDICFRQEFKDRNRLYDSIQPQTNPAKYQGCFLRNGTKESAEI
IKVALSKIQNNSGGKFDHNQLVAGLGFGFWRYLFAAGKDAQFDAAGKVLKMFVFKPKKSTPSVQYNQKWI FREL SNINNFRNRLA
HHEPICFSFGA IKDTGYARNIHQSIFELLYMDVDTASVFSHFSDQVIAVCDEIDKL

SEQ ID 157

ATGAAACGCTTTATTTCTGCCGCTGCTTTTATCCGCAACAACCGCCCCGGCTTCTCCGATTGTGCGGTACATGGCATTGCATCGGCA
CTGATGAAACCAATTCACAGTGATACAAAGTCAAATATCTTCAGGACGGCAGCTTCCGTGGCGATGCTATACTCAAATCGATGA
TGACGGCAATATCTTGGCATAACCGTGTGTCGGTGCAGGTAAATGGCGTTTTCGGAACAATGCCCTTAACCTCAAAGCCAAATCAAG
TACGGTGAAGTTTACGACAGCACAGCCCCGAAACGCTGGCGTGGTTAGAAAAGTTCGGAGGATGCACGACTCTTGGAAAGCATGA
TGACACCGGATTGTTGCGCGAGATGGACAAACCCGAAAGATGATGTGTATCAACTGGATAAATCAGGCAAATTAGTGTCCGA
AGACGGAACCTCCCGTGAGGCATGTACGAAAGTGGAG

SEQ ID 158

MKRFILPVLISATTAPASPIVGTWHCIGTDENIHSDTKVKYLQDGSFRGDAILKIDDDGNILAYRVVAGKWRFANNALTQSQIK
YGEVSRQHS PETLAWLEKSEDA RLLESMMYTGLVAQMDPKGDVVYQLDKSGKLVS EDDGTSREACTKVE

SEQ ID 159

ATCATCACGCCGAGTAAATTTGTAATTAATGTTGACGGGGCTTTAAATATCCGTTTCGTGTAACCCGCACCCAACTTCAGTCCA
AGACCGCGCTTAATATTTTACCGTACCCAACTTACACCATAACGCCGTGAAGCCTGCTCTTTCTCCACAGTATTATCAAACA
TACCGTTAATACCCCGTACAACCTGCCAAGCCGACATAGCGTAATAGCTGAACGTACCGCTACCCGAAATCGTTTACTGTTGTA
ACGTTTTCGCAAAATATTCGTCTATGTTGTTGCGGCCATACTGGAAAGATTGGGTGCTGCGCCATTTTTCATTAGACGGCGG
CTGTAATCCAACACAATACCCGTATTTGCCGTATAACGGTTATTGCCAGCCGGTTTGTGTTGACAAAGGGCCGGAATCCCCACT
CTAGACGGCTATTCCGATAACGGTAGCCTACTTCGGCATGAAACGCCCTGTTGCTGTAATAATCCCGGCATTCGAATAATGCACACC
GGAACCGCTGATGCCCTAAGCGGGCAAGTGATTGCTGCGCATGTTAAACATCCGATCAACGCCCGAGTTCGTACCTTATCCCGTTG
GCGCGTTTGGGCGAGCTGTCTTCCGATTTTATCCATTTCCGGCCGTTGATGACGATGTCGGTGAAGGGACGCAATTGTTTACAT
TATCTGTTTGTTCATAGTTTCAATTTGAACGAAGGATGCCACGCTGCACGCTTCCGCTGACGGATATATTCGCGTGAAGCTG
CCGCATATCGGGCGGCAACACCTCTCGGCCCGGTGCAACTGAACCAATGCCCTACGATATGTTTGTCTTCAAACAGCATCAGC
CCCAATCAAACGGGATAAACAAGATCGGGCTTTTCCGACAACAACCTACGGTATAGATCGGCGCGCTCGAACAT

SEQ ID 160

MFEAADLYRELLSERPDIVYPRFDLGVMFLFEDKQYREALVQLHRAEEVLPPDMRQLAREYIRQAEAVQAWHPSFNMNYYEQTDNPN
NASLSRDIVINGRKWIKSEDSLPRKANGIRYELGVDRMFNMAGNH FARLGISGSGVHYWNARDFSEQAFHAEVGYRNRNSLEWG
FRPFVKQNRNLGNNRYTANTGIVLDYSRRLNEKWRSTQSFQYGRKQYHDEVLAKRYNSKTI SVSGTFSYYAMS AWQLYGGISGMFD
NTVEKEQASRRYGVSLGTVKILDGGLGLKL GAGYTKRIFKAPATLIYNFTRDD

SEQ ID 161

TTGTCGGATACGGATAAACAGGCTTTTTTGACTTCTGTGAGCTCAAAAGAACAGGTTAAAAAAGTCATTGAACCAAGAAAAGTTA
CGAAGTGCCACATTGCCAATCTACACATTTCGTCAAAAATGGCAAAGATTGTGGCAACCAACGTTTTTGTGTGCTGATTGTAA
AAAGTCTTTTGTTGAGCAGACAGGCACTATTCTCTACAACACGCAAAAAGACATTGAAGTTTGGGAAAAATACATTCAATTGTATG
ATTGAAAAATACCCACTTCGCAAATGTGCTGAAATTTGCAAAATCAATCTTGCTACTGCGTTTACTTTGGCGGCACAAAATTTTGG
ACGCATCTCAAAACATGATGAATGAAGTTGAGTTAGACGGCATTTGTCAGAGCTGATGAAACTATTTCGACGATTTCTTACAAGG
GCACCACAAAAATTTTAATCTGCCACGCTCTGTCAACAACGAGGAACGAGGCAACGAACGTCATTTCCAAAGAACAAAGGT
TGTGTTCCTTGTGGTATCAATTTAGACGGTAAATCTGTTGCTAGAATTAGCAATTTGGGTAAGCCATCTCTAAAAAATATCAAC

SEQ ID 162

LSLSDTKQAFLLTSVSSKEQVKVIEPRKVTKCPHCQSTHFVKNKGKDCGNQRFLLCRDCKKSFEVQTGTILYNTQKDIIEVWEKYIHCMI
IEKYPLRKCAEICKINLATAFTWRHKILDALQNMNEVELDGVQADETYSTISYKGHHKNFNLPRPAHKRGTRATKRGISKEQV
CVPCGINLDGKSVARISNLGKPSLKNIN

SEQ ID 163

ATGTTTGCTCTTGCCGCCAGTAATATGATTTTACGCGGAGACGGTAAAGCCAATTTACACCAAAGCAGTTGTTTCATGACTGATT
TTCAGGATTTAATCAAAAATCCCAACCTGAAACAGGCTTAAACGCCCAATGTTGGCTTTCTCAATCCACCTTACGCCCAATC
CAAAGCGATGCCGAATTGCATGAACTTTATTTTGTCAAAGAAATGTTGGATATGTTGGCAGAAGGTGGCACAGGCATTGCCATT
ATTCCAGTCAGTTGCGTGATTGACCAAGCAAAGCCAAAGCGAAATTTGTGAAATATCATCGCTTAAAGCCGTGATGTCATATGC
CGAGCGAATGTTTACCAGTTGGCACGGTAACGTGCATTGTCTGATTTGAAAGCCCATAAACCGCATTTTTCAGACAGTCTGTGAT
TGACCCGGACACACAAGAAGAAATCAGCACGAAAAAAGCCTGTCGCAAAACGTGGTTTGGCTACTGGCGTGATGACGGTTTTGAA
AAAACCAAACACTTGGGACGCATTGATTTATACGACCGCTGGCAGGGCATTAAAGCGCGCTGGTTGGAACATTATTTAAACAACG
AAGTTCACACAGGAGAATCGGTAACAGCATTGTAACTGATAACGATGAATGGGTGCGGAAGCCATTTTGGAACCTGATTATTC
CAAATTAACCGAGCAGATTTTGAGCAAGTCGTGCGTGAATTTGCTTTATTTCAACTACGCTGGGAGCGGAAGTAGGCCGACTGAA
AATTTGGATAATGAAAGCTATGAAGACGATGACAATAACGACTTCGGAGACGATGAA

SEQ ID 164

MFALAASNMLRGDGKANLHQSSCFMTDFQDLIKNPKPETGLKRPNVGFLNPPYAQSKSDAELHLYFVKEMLDMLAEGGTGIAI
IPVSCVIAPSKAKSEIVKYHRLKAVMSMPSELYFVPGTVTCIVVFEAHKPHFQTVVIDPDTQEEISTKKACRKTWFGYWRDDGFE
KTKHLGRIDLYDRWQGIKARWLEHYLNNEVHTGESVTAFTVDNDEWVAEAYLETDYSKITRADFEQVVRFEALFQLLGAEVGPTE
NLDNESYEDDDNDFGDDE

SEQ ID 165

ATGGTTGAAATTGCAAGAGATTTTGTAGTGTAGTTACGGTTCAA AATTAGATTTGAATAAAATGAGCAGCTTCAATCCAACAATCA
ACTTTGTAGGCAGGT CAGGCAAAAATAATGGTGTACAGCATCTGTGGATTATTGAAAAATACAAAACCTTATCCAGCAGGATT
ATTAAC TGTTGCATTAGGTGGTTCTGTTTTATCTACTTTTTTACAAAACAACCATTTTATACAGCTCAAAATGTTGCTGTTTTTA
AATCCCAAAACAGAAATGACAGAACAACAAAACCTCTTTTATTGTGCTGCTATTTTGGCAATGCCTACCGTTTTCTGCTTGCG
GTACGGAAGCTAACCGACGTTACGACAAGTTTGTGCCATCTTTGATGAGATCCCAAGCTGGGTGAAAGCGTGAATTTAAAT
TCTAGTTCGCGGTGTAAACGGAACCGAAATTAAGGAATCGCTTGATTGGCTGTGGTTCGACAATCAAAACGACTTGATGAAATT
TTTACTATTCAAACGGCATTGCCGCAACCAAATTAAGAATTGAACAACGGCAAAAGACACGGTTGTCTATATCCGTCCTG
CCAGTACGCAAGCAAGAAGCTACGAAGTTATATCGCTCGTGATAGCGTTGATGAAAAACATATTTTTCCATGCCATACGCTTTT
CACTTCTACCAATGGCGAAGGTAGCCATACTTATAGCTATGTTTCAACTTGTGAATTTGTAGCAAATAGTGATGTCGCCGTATTA
ACACCCATAACAGTCCGATAGCAATAGAAAGTAAACTGTATTACGCTAAATGTATTACAGCAAACCGCTATCTGTTTTCTTATG
GACGTAAACCCAAAGCGGCAAAATTAAGAAGCATTATGTTACCGTATTTTGACCAACAAGAAGATTTTGATTATATCTGCGCGTTT
CAGTCACACCTTGCTATTTAGTAACAATTTG

SEQ ID 166

MVELQEIFDVSYGSKLDLNKMSFNFPTINFVGRSGKNNGVTASVDLLKNTKPYAGLLTVALGGSVLSTFLQNKPFYTAQNVAVL
NPKTEMTQQKLFYCAAIFANAYRFSACGREANRTRLQLFVPSLDEIPSWVESVNLNPSAGVTEPKLKESLDLPVVRQSKRLDEI
FTIQNGIAATKLKEFEQRQKDTVVYIRPASTQARTLSYIARDSVDEKHIFPCHTLFTSTNGEGSHTYSYVSTCEFVANSDAVL
TPIOSDMPLEVKLYYAKCITANRYLFYGRKPKGKELKSIMLPYFDOOEDFYICRFIHTLLFSNNL

SEQ ID 167

ATGAAGAAC TGTACTCCAAC TAACGGCACATGGTTC AAAATGGGTGCAACACTCTACTGTTGCCGTGGCCGCTGCACAGTATCAA
CACCTACATCCGCCATCCCCGT TACCCACATAAAATGCCTGCGGATAAACGGGCAGATTAAATGCGTCAAACCGATAAGCCCTAA
CACTACCCCTGCCGCAGAGCATATTGAGCATGTGCGGAAAAATCCGCGCCGCAAAAGCAGCGATTGGACAGGGCGGCAGCAAGAATT
GCCGATAAAATAGCCCTCAAGCAGGCGGGGAAACATTTGTTCAGCTTAAGGATGAAAAAGGGGTTTACCAGCTCCGAATTGGCAA
CCGCGCAGGATTGCCTCAACCTTATCTGTCCGCATCGAAAAACAGCAAAACATCCCTGCAGATTAAGACTGTACAAAAATTGGC
AAACGCATTAGGCGTTTCCCGCTTGAGTTCGCGCAGCGTTCGAACGGCGGTACGAATATATGGAGCAGGCA.

SEQ ID 168

MKNCTPTNGTWFKMGATLLTVAACTVSTPTSAIPVTHIKCLRINGQIKCVKPISPNTTTPAAEHIEHVRKNPRRKAAMDRAAARI
ADKIALKAGGETFVSLRMKGFTQSELATAAGLPOPYLSRIENSKQSLQDKTVOKLANALGVSPLVRAAFERRYEFYMEQA

SEQ ID 169

ATGACGGTCCGAAACACGCAAAACCGAAACCGTCCGGACGGAAGCCGCGCCGCAACAAGGCGGCAATACCAACCCGGGCTATTACA
AAAACCGCGCCTTCGAGTGGTTCGGGTTTGCGCAATACCTCAACTTCAACCTCGGCAACGCCTTCAAATACATCTGGCGGCACAA
GGAAAAAGGCGGGCGCGAAGACTTGGA AAAAGCCCTGCGGTACTTGGAACGCCAACGCGCGGGCGCGCGGAAGTTCAAGAACTC
AAACACCGCCGCTATGAAAAATGTACGCCGGTCTGAAAGATTGCGGGTTCGACGGCGGCAGCGAGCGCGCGCTGCTTGCCGTCA
TCTCCGCGCTTATTACATCCGCAAGCGGCAAGACATTTTCGTCGGGCGGCGCCCTGTGTGCAAGATTGTGTGAAAAAATGCC
GCCGTGAAGCGGCGGGCGGCCACCCTGTAAAGACCGGATGCCCGCTGAAACGCGCGGGCGGAGGCATT

SEQ ID 170

MTVRNTQTETVTRTEAAPQQGGNTNPGYYKNRAFECVGFQAQYLNFLNFGNAFKYIWRHKEKGGREDLEKALRYLERQRAGAPKFKKL
KHRRYEKMYAGLKDCGDFDGGTEAALLAVISAAVYTRDGEDNFAWAAACVEDLLEKMPPEAGRAPHPESEMPPPETAGGGI

SEQ ID 171

ATGAACGTGAACCAACTCACACAAGAACGATTGAACGTGTAAGTCGGCACAAAGCGGCGCGGCGCCTGACAAAGGTTTTTA
CCCAGCCGGCTAGTTTTTACCGCCGGCCTGCAAACTATGACCTTTCCGCGCCGTCTCAAAAACCTTACCCGGTATTGACCCCGTT
CGCAACCGTATCCCGCGCGTGGGCGCGCGCCGACCATCGGCTCGAACTGGAAAGCGGTACGAATATCAACGTCGGCAACCAA
CGCGCCGGTATCGGCGAAGGCAGGCGCGCGCGGTATCAATCAGAAACGGTGAACGCAACGCGCAATTCCGCGCCATCGGCT
TGGAAACCAAGTAACCTTTGAAGCGGATTACGCCGCGCGCGGTTTCGAGGACGTGAAAGCGTTGGCGGTTCGCCAAACCCCTTCA
GGCTACTATGGTTGCGGAAGAAATGATTTTGTCTGGGCGGCAACACCAGCCTGAAGGCAGGCGTTACACCTACACCGACCGCGCTC
GTTTCCGCGGACGCGCGCGGGGAAAATCAGCGTCAGCACCTTGTCTGTAATCTGTGTGGCTTTGGGCTTCAGGCGGTATTGGGACG
TGGCAGGCGCGAACAACGGTGCAACCGGTCAAAGCCCGAACATTAACCTGCCCCAAGTCCCTGCCAAATCACACGCGGAACCG
GGATGGTACAAACCGATACGTTCCGGCGCGGTTCCGCCGAAAATCTGCGCGCGCTTCCGTTTCCGGTATTGAGGCAGGCAAAAA
GTAACCGCGGTGATTCCGGCTGTTCCGCGCGCGGTTGCCTATGCTTGGTACTGGGGTGCAGCGCGGTTCTGAAAACTGGGCGCGG
TTACCACTGCCGCCAAAGTGGAAATTTCCGCTGATGCCGAAGGTACCCAGACCGCGCTTCCCTGCCGTCCGAAGACAATTCAC
TTCTATTTTGGAAATTTGACGGCTGTTGACCCAAATCGCCCTGCCTGATTCCGGCGCGGTTCTGGTTCGGACAACAAAGCGCGCGG
CTGACTTCCGACAACCGCGCGCGGTGTATGAATTTGAAGAGGCGTTTCGCGCATTTCTTTACCCGATACCGCTGTCCCCGATA
CCGCTTACGTCAACGCCCGCGATTTCGGCGCGCTGACCAAGCTGATTATCGGAACAGCGCGCGCGCTTGATTAAGTTGAACGT
TGACGTGAACAATAACGCGAACAATCCGCGCGGTGTCTGTCTGTTTATGAACAAGATCACGGCGCAGGACCTGAACATC
GTGGTACACCCGAACCTGCGCTGCCGTACTTACCTGTTCTACTCAAGCCGCTGCCCGCTACGTTACGGCGCTCGGCAATCTGC
TGCAAGTGCCTACGCGCAAGAGTATTACCAAATCGAATGGCCGCTGCGCACCCGTATGTACGAATACGGCGCTATGCGGACGA
GGTGTCTCAAGGTATGTTTCATGCTGCCTTCGGTATGATTACCAACGTGGGT

SEQ ID 172

MNVNQLTQETIELMKSQAQAGGPPDKGFTQPASFTAGLQTYDL SAPSQKLYPVLTPLENRIPRVGGRTIGSNWKAVTNINVGNQ
RAGIGEGRRGV VINHETVERNAQFRAIGLENQVTFEADYAARGFEDVKALAVAQTLQATMVAEEMILLGGNTSLKAGVTPPTAV
VSADAAGKISVSTLSVICVALGLQAYWDVAGANNGATGQSPNIKTAQVPAKITRRNADGTTDTFGGGSARKSAAASVSGIEAGKK
VTAVIPAVRGAVAYAWYGAAGSEKLGAVTTAAKVEISADAEGTQTAASLPSEDNSTSILEFDGLLTQIALPDGAFWSDNKG
LTS DNAGGVYEFEEAFHFTRYRLSPD TVVNARDLAALTKLIIGNSGAPLIKLVNDVNNTANIRAGVVVGSYMNKITGDDLNI
VVHPNLPAGTYLFYSSRLPAYVQGVGNLLQVRTRQEYVQIEWPLRTRMYEYGVYADEVLQGMFMPAFGMITNVG

SEQ ID 173

ATGGCCGCCCCGGTATCGCTTGAGGAGTTCAAGCAGCGTATCGCGCTTGAACATGACCGCGGGACGATTTCCTTCTCAGCGTCA
TTGACGGCGTGTTCGGCGCGCGCGGAAGCCTATATCGGGCGCAGCCTCTCGCGCGCGATTATGTCGGCGCGGTACGACGGCAACGG
CAAAGACCGCATCGTGTGGACAATTATCCCGTCTGTCTGCGTGTCTCGTCAAAATCAACGGCGCGGATGCCGGCGGCTGGGAG
TTTGACAACCTGGCTGCTGATGCGCCCCGAAGGTTTCGCGCGGGGGCTGAAAAATGTCGAGGTATCGTACCGCGCGGTTATGAGC
GCATGCCCGCGGACATACGCGAAGCGGTGATGATTATCGCGGTGCAGCGCGTGAACGAAATCGAGGGCAAGGGCGTACGGAGCAA
GACGCTTGACGGCGAACCCTGCGCTTTTCTACGTTCCGTAATTCGCGCGGTATGCCCGCGTTCGGCTTTGCGTACTCAATGAG
TACAAACGAAAGGGCGTG

SEQ ID 174

MAAPVSLERFKQRIQVEHRRDDFFLSVIDGVSAARAYIGRSLLAADYVGRYDNGKDRIVLDNYFVLSVSSVKINGADAGGWE
FDNWLLMRPEGFARGLKNVEVSRYRAGYERMPADIREAVMI LAVQRVNEIEGKGVRSKTLAGETVAFSTFGNSGGMPPSAFALINE
YKRRGV

SEQ ID 175

ATGCAGTTGACGTTTGGCAGCGCGCAAGTGTTCGCCCAAATGATTACGGATGCTTACGGCAACCGTGTACAGAACGCAACGCCCG
TGCGGATTATGGGCTTGACAGGAATGTCCGTGATTTGTTCGGCGGAATTGAAAGAGTTCTACGGTCAAACCGTTATCCTTTGGC
TGTGGCGCAAGCAAGGTCAAGGTGTTCGGGCAAAATGAAAGCGCGTGTGATTAAACGGCTGACCCCAATACCTGTTTTCGGT
ACGGAATATGCAACCGGCACGATGAAGGCGCTTTGGGCGGAACTACGGGCAAGTCCTCGATGGCGACAATTATCTTACCTTC
AGGCGAGCGCGCGCGCGCGCGCAAGTTCGTGAGGACGCGCGCGTGTACGGCCAGGACGCGCTTATATCAAAGTAGCATC
CTCCCCGAAACAGGCCAAATATACGGTTTCGGAATTCGGCGGTGATACGCTTTAAACAGCTCGGATAAAGGCAAAACCGTTTATCCG
AGCTTTACCTATACGCAACGATGCCCGCGGCAAGAAATCGAGCTGACCAATATGGCGACGGGCAACACGCCGACGTTTAAAGA
TGAGGTACCTGACGAGTTCAAAGGCAAAAAGCCCTGTTGGAACGTGAAAGCGTAACACGGCGCAAAATGGGCTTGTCTCGAC
TAAAACGACGACTTCTCCGTCCCCGAAATCGACTTTACCGCTCAACCGACGAGGCGGGCTTAAATCGGTACGCTGTGGATT
CAGGAG

SEQ ID 176

MLTFGSGEVFAQMITDAYGNRVQNAFVRIMGLQEMSVDL SAELEKFYQGNRYPLAVAQGVKVS GKMKGAL INGLTLNLTFFG
TEYATGTMKALWAETTGVLDGDNYSYLQAAAPGGGKFAEDAGVMQDGTAYIKVASSPRQGYTVSESGVYAFNSSDKGRTVYP
SFTYTQTMPPAKKIELTNMATGNTPTFKMRYLTQFKGKKALLELESVTSGLGLFSTKNDDFSVPEIDFTASTDEAGFKIGTLWI
QE

SEQ ID 177

ATGGGTGGTAAATCGTCAACCGTTACATCTGCCGAAGAGCGGATTTTATCGTTACAGGTTACGCGGTATCACAGGGCTGACCC
TGCCCGTCATCTACGGCAGGACGCGCGTGGCGGGCAATTTGATTGGGTACGGCGATTTCGTACCATCGAGCATAAGGCCGTGAC
CGGTCAGGGCGGCAAGGGCGCGCGGTGTGAAACAGGTTCGGTATTTCTTATACCTACGAAGCGCGCTCATGCTTGTCTTGTGC
GAGGGCGAGATTACGGGCTGGGGCGGGTTTGGCGGACAAGGAGAAATTCGATTTCGCCGCGCAGTTCCGCTGACGCTTATGC
GCGGCGGCGACGAGCAGCCGTGTGTGACGCACTGCAACAGGCGAAGCACCAGGCCAAGCCTTGAATPATTCGGGCGACGGCTTA
TTTGTGCAGCCCGAACTACGAACTGACGAAATCGCGCGCAATATATCAGCACAAATTCGAGGTATCGGGAAATCGGGCTATTCC
GGCAACATCCCCGATGCAAAACCGCGCGAAATCGTATTGGATTGTCTGACGAAACCAACGCTACGGCTCGGTTTCCCGTCCCAA
ACATCGGCGGATACCGACCGGTACAGCAATTAATGCGCGCGCGGTATTTCTTAAGCCCTGCGCTACACGGAACAGGGGAGGC
GCAACGGAATATTTCCGAACCTGCTGGAGCAGACCAACAGCGCGCGGTATTTTCGCAAGGCCGCTGAAATCATCCCTACGGG
GACGGCAGCCATTTCGGGGAACGGCGCGGTGTACGTTGCCGACAATAAGGCCGCTACGACCTGACCGATGACGATTTCATCGTTT
CGGGCGCGCAAGACCTGTAAAGGCCGGCGCAAAACCAATGCCGATGCGTTTAAATCAGATTAGGTCGAGTACCTTGACAGGGA
CAACGACTACAACGTGCGCATCGCCGAAGCGAAAGACGAGCGAATATCGAGCAGTACGGATTGCGCCCGAAAGACGCGGTACAG
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AGTTTAAGCTGGGTTGGAAATACTGCCTGCTTGAGCCGATGGACATCGTAACCTGACCGACGCGGGGCTCGGCCTGAATAAAAC
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GTGTCCGAATATCCGACGACGCGCTCTTCGGGTTATTTCGGCCGACTACAACGTTTCGCCGGGCAACGCCCATGTGCGCGTAATTT
TCGAAGCGCGGTTGCAACTGACGGGCGGCGAACCGCAATCTGGCTGAGCAACCGCGGGGGCGGTATGTGGCGCGCGCAAGT
GTGGGTATCGGCGGACGCGGACAGCTACACCGCGCTCGGCGCGGTCAACCGCAAGGCGCGTTTCGGCGCGCTGACCGCCGATTG
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TTGTTCAAATACGCCGTTCCGCGCAACTGGATTGGCCGACCGGTTTGGGTCAAACCTGGTTTCGTACAACGTTTCGGCGCGGCA
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CGTTTATAACCATCGCCAAATGCGGCGGCAACCGCTGGAGAAAGGAAGACCTATTACTTGAGGCGCGCGGTTACGACGTTT
CGGCAAGATAACCTGAAAATCAGCGCGACATATCGTTTACCGTTTACGACGTATCGGCAACCGCACTGTGCGAAAGCAGTCTG
AACAAAGGCTTTTCGCGGACAAAATCAACCTGATTGACGGCAACGCGCGGCGGCGAGCTCAACGAGCGCTGAGGCGAGTCCGATCGA
CGGCGGACGCAATGCGGCGGCGGTTGACACACGCGCGGAAGCATCAACGGCTTGGAGGCGCAATACAGGTCAGGTTGATGC
AAACGGCAAAAGTGGCGGGCTTCGGCTTGGCGACTACGCCGAAAACGGCACGCCCGAAAGCAAGTTTATCGTGAATGCCGACCGC
TTCGGCATCGGTGCGGCGCGGAAGGCGGATGTGTTCCCGTTCGTGGTGGACACGAGAAAACCGGTGGGCATCAACGGCGAAT
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AAACCGCCTGAAAGCGGAAGCGTTACGCGCGCGGAAATCGGGCTGCGCGGTTACCGCGGATAAAATCGGGGCAACGCGGTG
ACTGCCGATAAAGATTACGTTGCGGATTGAGCGCGGTATCTTCCAATCTCGGAAGCATACGCGGCGGCGAGCTGAATATCGGCG
GGGTAATTTTACGGTGTCTTACAGCGCATCTGACGGCGGCAATGCGGTAATACGCGGACGAGTTGAGGCGGATTTCGGGTTA
TTTCAACGGCACGGTCAGGCTTCGTCCGTGAGGCGGACGTTTGGAGGCGCACAGGCTGCGTTGGACGAGGGTAACGTTTGG
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TGCAGGCAAAAGTGTCTGTTGAACGGGGTGTGCTTGC CGCGAGGAGTCAAGGAAACCGAGAACTATACCAATTTATTTGGCG
CGGCAAGCTTTTCGGGAGGTACGAAGACCTGCCCGCGGAAAGGGGGGGGGGATTATACCGAACAATCCGGCTCAAGGTAC
AGAACCCGCTTCGAGTACAGATTCAAGTCATCCCGCGGCAACCCGTCAGCTGAAGTTGTGCTCGCTTCCACGAATCGG
TGTTTTTCGCGTTCGTGTGCGTTTCGTATTTCGCGCAATCCGACTACGAATACAAGCAGCTGCTCGGGAGGATGTTTGGCGCAC
CTTTTCGGAAAGTTTCGCGTACGACAGTAAGAAGCAGATTTATTTGGGCGGCGACCGCGGTGTACACGATTACCAAAATCAGATG
TATAAACATTGGAATGCTTACGGCGGCTGCTGCAAGTTCGCGGACGATATCTACGGCATATCGTTTCGAGTACCGCGCTTTTACCA
ATGCCGACTGGAGTACGATGCTTGCCTTTCGCGGTGACCGGTGAGTAAGTTGTAGTGGTTAAGAAATACCGGGGTCTACGCCCCCAACA
GTATCTCTGTTTCAGGAGGAGTTTAACTACTGCGGTTCCGAAATCCAACTGCTGTTTTTGTGGAACACTGGTGGCAGTATATC
GAGCTGCGCAATATCAGGGTGTGATTCCGGAATCGCGGAAACGAGGTTTGGCCCTCCGTC

SEQ ID 178

MGGKSTVTSAEERILSLQVQRSSQGLTLFVIYGRTRVAGNLIWYGFVTIEHKAVTRQGGKGGGVKQVQGISYTYEAAVMALALC
EGEIQVGRVVRDKEKFDSPAQLRLTLMRGGDEQPLWTHLQQAQKHQALNYSGTAYLCSNBYELTKSAQIYQHNFEVICKSGYS
GNIPDANPREIIVLDLLTNQRYCGFPSONIGDTRYSNCRVAVGIFLSPAYTEQGEAQRNISELLEQNTSAAVFSQGRLEKIIFYG
DGSHSGNGAVYVADNKAAYDLTDDDFIVSGAQDPVKAGRKTNAFNFQIQVEYLRDNDYNVAIAEAKDQANIEQYGLRPFDAVR
MHGICDAKVAQKVAQQLLQALYVRNEYEFKLWKYCLLEPMDIVTLTDAGLGLNKTFPVRITELBEDGEVLSVKAEDCPAGVYT
VSEYPTQPSSGYSADYNVSPGNAHVPIFEAPLQLTGGEPIQLWLATAGGGMWGGAEVWVSADGDSYTRVGAVNRKARFGALTADL
PDGAVFDRNTLTGVEISAGQLTGGTEQDSRDLTLCLYVDGEFLAYADAELKGVGRYTLGNLTRGAYGSVNAHAAGSRFARIDEA
LFKYAVPRNWIGRTVWVKLVSYNVFGGQIDLAEPVAYSRTIEGAPLQIQLNRLTSSWAYGKEAVIAWDLKDADGTVDVEITYAG
GSRRLRAVDGIVDINSYTYTQADMKADGGQVRGIVFVKRYGRTAVTGKTGNWAQIAAQNPQLQALQGISIDSLRQAFFTCQKPDDE
DFAGIIVWCENACPAADANKAYDGAETFIITAKCGGKPLEKGTYYLRAAGYDSFGKDNLKISGISISFTVYDVSAITLSESSL
NKALRDKINLIDNGAGSVNERVEAVRSTADGNAAVQTHARSINGLEAQYTVKVDANGKVAGFGLATTPKNGTPESKPIVNAADR
FGIGAAGKADVPFVVDTPQKNRVGINGELVVNGKAVVDKLNAGDIHGKIAADTLNANRLKAGSVTAREIGAAAVTADKIGANAV
TADKIQVADLSAVSSNLGSLITGGSNLNIGGNFTVSSDGLTADNAVIRGRIEADSGYFNGTVRASSVGBDVLRAHLRWTBEGNVW
VLDLKDPLPRVLIPINFYVVSFTFGNNRVQAKLLNLGGVLAAPREVRETYNTNYIWRGRTFGRYEDLPPRARGGGDYTEQSGSRY
RTRLEYQIQVIIPAGKPVSLKLSLASHESVFSFVSYSYLAQSDYEQQLGRMVWRTFAESFRYDSKKQIYLGDRRVHDYQNM
YKHNWYAGLLQLPDDIYGISFEYRPFNTADWSTMLAFDRSDKFVVVKYRGHAPQOYSLFQREFNTAVPKSNLLFFVEHWQYI
ELRNIRVLIPIESRENEVWPSV

SEQ ID 179

ATGAGCGATTTCGAAGCCAAAGTCAGGATAACGGTAGAAAAACCATACGAAGCAGGGTTTTGATTTCGGCCGCGCGCGATGCTGATA
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CAATTTGCACGCGGATGTGAAGCGGGATTGAAGCGGCGGCAATCAGCGCGCAACAGCGCTCTGAAAAGGTTAGGGCCGAAGTG
GGTAAAATCGGCTCAGGCTTATCGGGGCTGACCAAACCTGCTGGCAGGATTAGCAACCGCAGACTTCGCCAAATCGGTGCTTGATA
CCGCCGATGCGATGCACTGATAAACAGCCAAAGTCCGACAAGTCACGTGCTGAAACGGAGTATCTGGCCGTGACGACGAGCT
TCTCGATACGGCAAACCGTACCCGTGCATCGCTTGAATCAACGGCAAACTGTACGTTTCCACAAGCCGCGGCTTGAAGACTAC
GGCTACACCGCAGCAGGAAATTTTAAATTCACCGAGGCGGCAACAACCGCATGACCATCGGCGGCTTGGCGCGCAACAACAGG
CCGCCGCGTGATGCACTTATCGCAGGCTTTGGGCGACGCGGATATGACGGCGATGAATTTAAATCCATTTAAATCCGAAGCCGACC
TATTTTCGATGATACCATTCGCGGAATATATGGGCAAAATCCCGCAGCAAAATCAAAGCTGGGCGAGGAAAGGAAATGACGGCG
GATGTGATTTTCAAAGCCATTTCGGCGCGCTCGGAGAAGTTCGGGGAGCAGGCGGCAAAATGCCCGTGACGATGGGGCAGGCTT
TGACGGTGTCTCGAACAACCTGGCAAAGCATGTTTCAAACCTGCTGAACGACAGCGGCACAATGTGGGGATTCCCGCCGTTAT
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CTGGCTTTGAATCTTCGACTGCTGGCAAACCGCTTCGGGATTATTGCGGTCGCAATCGGCACGGTTGTCGGGCTGATTGCGAAAT

TCGGCGATGAAATCGATGTTTTTCGGCGCGCGCTGGTCAATCTTTCCGATGTGATTCGGGCGGTTTGGCAAATCATCACGGAAAC
CGTCGGGGAAGCGGTGGGAACCGTCAATCGTGGTTTGACGGGCTGACAGGCGGCTGAACGAGGGCGCGGGCGGCTGGCCGTGCG
TTGTTTCGGGCGCGTGTATGAGCGTCATCTCAAGCCCAATCGGCGCGTATGTGAACGTTTATATCAACATATTCGCAACCGGCTGGA
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CGAACGGATGATAACAAAGCGGTAGGCATGATTAACAGCATGATTGACTTTGCCAACAAGCCGCGTTCGATGGCCGGGATATCG
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ACCGCGCGCGCCCAATGGCAATGCCGTTCGCGAACGGGCGCGGATATTCACGAAGCCGATGCCCTCAAGGACCGCGCGCGCGG
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GCGGCCAAAGACCCGATGCGAGGCTTGGGAAGGGGAAATCAAAGCCCGAAAACTCGCACACCGCGAAATGCAGCGCGAAACGCTCG
CACACCAAGAATGGGATTTGGCGCGTGGGCGGAATATTGGCGGGCGAAGCTGGCAACGGTGGACGCCAACGGCAAAACGGGCGT
GAAATCCGCGAAAAATTCCTGATGCTTGAAGACCAATTATCGAAGCAGTCAACCGAAGCCAAATGAATCAGGCGGCGCAATGG
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AGACCCGGCATACAGTCAGGCGGCAATCGGCAAGCTCAAGGCCCAATGGGCGGAATTGGGGCGGGGCGACGAGACGCGAGCGGCG
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CAACGCGCGTTGCTCAGTAGTAATGCTGTTCAAGCGGCTTCAGGCGCGGCGGCTTCCAGGCGCATATCCCATATGTCGCGCGGAT
TCTTGGCGTTGCGGCAATGGCGGCAATGATGTCGGCAGTGTGCGGCTTGGGACATCCCGGCGAGGATCAACCGCTGACCCAACTGCACGAAACGAGATGG
ACGACGCGCATTCCTTCGGCGCGCAGGCGGCTGGGACATCCCGGCGAGGATCAACCGCTGACCCAACTGCACGAAACGAGATGG
TCTTACCGCGAGAACACGCGCCAAACCATCCGTGAAATGGCGGATCAGCAGGAGGCGGCGCAGCAGCGTCATCATCAATTTCACAGG
AGGCGATTTTCATCCATAAAATGACTTGGCGAAGCTCTTGAAGCAGATGAAACGGGACTTTAAATTTGTC

SEQ ID 180

MSDLEAKVRITVENHTKQGFDSAAADADKAAEKMRSSGDNAAKGFKAIDSMEHETMRNLHADVKAGFEAAGNQAQQAASEKVRAEV
GKIGSGLSGLTKLLAGLATADFAKSVLDTADAMQSINSQVRQVTSSETEYLAVQQQLLDTANRTRASLESTANLYVSTSRALKDY
GYTQOEILKFTAAANNAMTIGGVGAQQQAAALMQLSQLGSGVLQDEFKSISEAAPILLDTIAEYMGKSRDEIKKLGSSEKLT
DVIFFKAI SGA SEKFGEQA AKMPVTMGQALTVF SNNWQSMVSKLLNDSGTMSGIAAVIKLIADNLNLVVPVIVAGFAVAVAAVAPT
LALNLALLANPFGIIAIVAIGTVVGLIAKFGDEIDVFGGWSNLSVDIRAVWQIITETVGEAVGTVKS WFDGLTGRNLNEGAGGWPS
LFGVRMSVSSAIGAYVNVYINIFATGWMLIKEAANDMPQFFANLGAIGNVFI SAIERMINKAVGMINS MIDFANKAAS MAGIS
GIGKLNKVRMGRMDGGLGERIHDSLT KDRAGAMANAVREARAADIHEADALKRGGGGHAKTARKKPGANQGGGKGGKSRSGPG
AAKDPMQAWEGEIKARKLAHREMQRRETLAHQEWDLAREAEYWRAKLATVDANGKTGVKIREKILMLEDQLSKQSTEAKMNQAAEW
EKLDKHKLEMEKDAADQALADGRISQLERLDEIEFENRRYRIAYDALQERIALAEQDPAYSQA AIGKLKAQMGE LGRGHERTQA
KNEGKRENQRRKDA PNVMEMLQDGG RNVWQEAQQQMGQAF TAMLARAQNFRQAMNGFFKSMGQTF IQEMVTKPLTGLMRRMVQES
AIYKMI FGTKETLE TAAAKTAATKATET TAVVSSNAVQAASGAASQAHI PYVGPILAVAAMAAMMSAVMGLMGGGGSGVTTTT
TTRIPSAAGWDIPAGINPLTQLHENEMVLP AEHAQTIREMADQGGGSTVI INSTGGDF IHKNDLAKLLKQMKRDFK FV

SEQ ID 181

ATGGCAACCATCACTCAACGTAACGCGCAATGGCGCGTACAAATCCGTATGAAAGGCGTTTCCCGTTCCGCCACATTTGAGCGGG
CATCAGACGCGAAGGCGTGGGCGGCGCAATAGAGTCGCAAAATTATGGACGGCATCCAAGGCAATGCCCGCGGAAATACATATCTT
TGCCGACCTTATCCGGCGGTATTTATCCGAGGTACACCATCAAAGCGGGGCGACGGGAAGAATCATACCGCATTTGGACGCGCA
CTAAAAACACCTTTGGCAAAGGTGCGGCTTGCCGACCTGCGCCCTCAAGACTTCGCGGATTGGCGAGATCAACGGTTGCAGGAGG
TATCCCCCACCAGCGTCGAGCGCAATTAACCACTTTATCCGCGCTGCGCAACACGCCATGAAAGAGTGGGGACTTCTTCGCGA
AAACCTGTACGCAAAATCAGCAAGCGGAAAAAAGCCGGGCAAGGACAAGACGGCAACCGAGCAGGAAATGGCGATATTTGC
GCCGCCCTCCTATACCGGCTTAATGAGAAACGAAAAATGGCGGTGCAACGGGTGCGGCTTGCCTTATTTGCCATCGAAACCG
CCATGCGGGCAGGCGAAATCTGCGGCTAAAATGGGCAGATGTGAATATGCGGCGTCTGATTGCCCACTCCCAATAACTAAAAA
CGGCGACAGCGGTGACGTGCCATTATCTTTCGAGCGCGCGAATAATAGAGCAACTGCGCGGAATTGATGACACATGGGTGTTT
AGCCTGGATGCCAAAGCCTTGATGTATTATTCAGGCGAGCGCGGATAATTGCGGCATACAAGGCTGACATTTTACAGCACCC
GCCGCGAAGCCCTCAGCGCGCTATCAAAAAAGTGCCTGTGGAGGCTTGGCAAAAAATCAGCGGGCATCGGGATTTAAGGATTTT
ACTCAATGTTTACTACCGCCCCGACATGGCGGATATGCAAAATGTTGGAT

SEQ ID 182

MATITQRNGKWRVQIRMKGVSRSATFERASDAKAWAARIESQIMDGIQGNAPRNTIFADLIRRYLSEVTPSKRGAREESYRIGRA
LKTPLAKVRLADLRPDQFADWRDQRLQEVSPSVGRELTTLSAVCEHAMKEWGLLRENVRKISKPKKSRRARTRPTEQEIADIC
AALLYRPNEKPKMAVQRVAVAVLFAIETAMRAGEICGLKWADVNMRRRIALHPITKNGDSRDVPLSLRAAELEQLRGIDDTWVF
SLDAKSLDLVFRARDNCGIQGLHFDTRREALTRL SKKVPVEVLAKISGHRDLRILLNVYRPMADI AKMLD

SEQ ID 183

ATGACATATTTAAAAGTAATAGCAATTAGTATAGTTTATACATTTTATTATTCGAAATTAATCTTAAATGTTAGAAAAAGGA
TTGATTTCTTAGTAGAAAAATATAGATAAATATTACAGCAATATGGATCTTACCCAAATATTTTGATTTTATATCAACTAAAC
TGATTTTACCACGTAATCATATTGTGATTTTGGGATAAAAAATATTCAGGATATGGTAATTGTTACTTCGTAAAGAATGATAAA
GACTATACTATTTTAGTCATGGGTTTCTCATCGAAAAATACTATTTTCATCTCACAATAAAATAAAGAATTCAATTCAAATAAAT
ATGAT

SEQ ID 184

MTYLLKVIAISIVLYILLQLINLKMLEKRIDFLVENIDKYYQYQSYSPNNFDFISTKTDFTTESYCDFWDKNLAGYGNCFVKNDK
DYTILVMGFSSKILFSSHNKIKEFNSNKYD

SEQ ID 185

TTGATGACCCATTACGTTACGTTTATGTCCCAACCCACAACGAAATTCGCGCGTCAAAATCCCCGCGTTTTCGACCTGATGC
GCTTGGGCTATGATTATCTTTTCGCTAAAAAATGCAAAATGGGACAGACAAACCAATATCTTTCCCGAAATCTTTGTAGACAGCCT
CTGCCGATCAATCCGATTTGCGCGCGGATGATGACGCGCGCTGCTTGGCGACATACGCTTAGAGCTGGATAACGAAGATTTG
GGGCAAAATTTTACGAACGCCCTACCAATCAATCCGGCGTAAGAAGCTGATCGATTTCCAAATTTTGACAACAACAGTTTCC

ACGTTGTAAGTGAAGTTGCCTTGTATCAACGGCGACGAAGCATTCCGCCCCGACATTGCCCTGTTGGTAAACGGCATGCCTTTGGT
CTTTATCGAAGTCAAAAAGCCCAACAATAAAGGGCGCATCGGCGAAGAGCGGGAGCGCATGGGCAACCGTGGCAAAAATCCCAAA
TTCCGCCGTTTATCAACATCACCAATTATGATTTTTCCAAACATGGAATACGACGACGGCGCAACCGAGCCGGCAAG
GCGCGTTTACGCCCTCGTCTGCTTGGCGCAAGCCCGTATTCAACTACTTCCCGGAAGAGCATAAATTAAACCTTACCGAATTATT
GGACACGCTTTCAGACGACCTTGAAAACAACGTTCTACAGACCAACCTGCCCGTTATCAACACAGCCCGAATTATCAGC
AATAAATCGCCCGATACGCGACCAACCGCATCTGACTTTCGCTGCTTTGCCCGCAACGCTTTCTTTCTTCTGCAACACGGGC
TGACTTACGTCAAAGCAAGTCAAGGCTTGGTGCAAAAACACATCATGCGGTATCCGCAGCTATTGGCCACCTTGGCAATTGAAA
ACATTTGGCAACGGCGGCAAAAAGGCGTGATTGGCACACCCAGGCTCTGGCAAAACCGCGCTTGCCTATTACAACACCCCG
TACCTGACCCACTATTATGCCAAACAGGGCATCGTGCCGAAATCTATTTCATCGTGGACAGGCTTGATTATTGAAACAGGCGC
AGCGCGAATTACTGCCCGCGATTAGTCTGCTCATACATCGACAGCGCGAAGCCTTTGCTGCCGACATCAAATCCGCCCAAC
TTTGCAACACCGCAGGCAAGCGGAAATCACTGTTGTTAATATCCAAAATTTCAAAGACGACCCCGATGTCGTGCGCCGTAAC
GACTACGACCTCGCCATTACGCGCTTATTCTCGACGAAGTACACCGCAGCTACAACCCCAAGGCTCATTTCTTGCCAACC
TTAATCAGTCCGCTAAACGCGTCAAAATCGGGCTGACCGGCACGCGCTTATCGGCGTAACCGCAGGCAACGTCAACACCCG
CGAATCTTTCGCGACTACATCCACAAATACTATTACAACGCTTCCATTGCCGACGCTACACCTGCGCCTGATACGCGAAGAA
ATCGGCAGCCGATACAAGCGCAATTACAAGAAGCACTGGCGCAACTTGAAATCGAAAAGGCGAGCTTTGACCGCAAGAAATCT
ACGCCCCATCCGCACTTCTGTCACCCGATGCTTGACTACATCTTGGACGACTTCGCCAAATTGAGAAAACCAACCAAGCAGAG
CCTCGGTGCCATGGTCTGTTGCGACAGCGCAGAACAGGCAAGCGGCTTTTGGAGCATTTTCAGACGCGCTCAGACCACAATTT
ACCGCGCGTGTATGTCACGACGTCGCGCACTAAGGAAGAAGCAGCAATGGGTTAAAGATTTCAAAGCGGGCAAAATCGACA
TCTTGTGTTGTGTAACAACATGCTTTTGACCGGCTTTGACGCGCGCGCTGAAAAGCTCTATTGTTGGCAGACTGATAAAGCCCA
TAACCTTTTACAAACCTGACCGCGTCAACCGCACCTACAATCTTACCGCTACGGCTATGTCGTGCTGATTTTGCCGATATCGAA
CGCGAATTGACAAAACCAACCGCGCTTATTGGGACGAATTTCCAACGAATTGGGCGACGAAATCGGAGTTACAGCCAGCTAT
TCAAAACCGCGCAAGAAATCGAACAGGAAATTCAGACATTAATAACCGCCTGTTGATTTCGATACCGAAACCGCGCAAGATT
TTGACGCAAAATTAGCCAAATAGAAGCAAAAAACAGCTTACGCTTAAAAAAGCCCTGCAACCGCCAAAGAGTTGTACAAC
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GCAACTTCGACCAAGACGACCCGCAATACATCAGCTTGGCGAAGAGCTGGAACGCATCTCAAGAAAAGAACCTCGCCGAAG
TCGGGCAAGAAGAAATGACGCAAAATCGCCCACTTCAAAACCGCTATACCAAAATCAAGAGCCGACCGCAACCAACGACCT
CTTGGCGCAAAATACGGCGCGGACGCCAAATACGCAAGCTATCGTACCAAGCGGTTGATGGAACCGCGCCTCTACGGAGACAAA
CTCAAGTCTTTAACCGGCTAAGCGGTGTAAGAACCGATGCGGACCAAAAGTGCTGGATATGGAGCAGATTTTGGACAACCAAA
ATACCTTTGAAAAACCAATGCAAGGCATCGTATTAACGCTTTAGAACGGAACAGCAATTTCTGTTACGCTGACAGATCCA
AGCCATCAACCGCTGTTGGTGGCGGAATATTTAAAGAAAGCGGCGGATT

SEQ ID 186

LMTHYVTFMSQTHNENS RVKIPAVLHLMRLGYDYL SLKNANWDRQTNIFPEIFVDSL CRINPDLPPDDARRLLADIRLELDNEDL
GQKFYERLTQNSGGKLLIDFQNFNNFSFHVTELPCINGDEAFRPDIALLVNGMPLVFIEVKKPNKGGIGEERERMGKRAKNPK
PRRFINITQFMIFSNMYYDDGATEPAQGFYASSACGKPVFNYPFREEHKLNLTELLDLSDDLNNVLQDNNLPVIXHSPFIS
NKSPDPTNIRILTSLLCRERLSFLLQHLTYVKASQGLVQKHIMRYPQLFATLAEKHLANGGKRGVWHTQSGKLTALAYNTR
YLTHYAKQGI VPKFYFIVDRLLDQLQAQREFRTARDLVHTIDSREFAADIKSAQTLHNHAGKAEITVNNIQKFQDDPDDVYVARN
DYDLAIQIRVYFLDEVHRSYNPKGSFLANLNQSDVNAV KIGLTGTP LIGVTAGNVNTRRELFGDYIHKYNNASIDGYNTLRLIREE
IGSRYKAQLQELALQLEIEKGSFDRKEIYAHPHFVHPMLDYILDDFAKFRKTNQDESLGAMVVCDSAEQARQLPEHFQTASDHNH
TAALILHDVGTKEERDQWVKDFKAGKIDILFVYNMLLTGFDAPRLKLYLGRLLKAHNLQTLTRVNRYKSYRYGYVDFADIE
REFDKTNRAYWDEL SNELGDEIGSYSQLFKTAEBIEQEIADIKNALDFDTEAEEFCSQISQIEDKQLLALKKALQTAKELYN
ILRLQGSHEFLAHLDFDLNLLYRETAARLDTLNLAEKLQGDTAHLLEALEDDVYFQVKIGEAELKLADDLKDIMRKVREGLA
GNFDQDDPEYISLREELERIFKKKNLAEVQGEEMQANIALTLQTVYTKIKEPNRQNDLLRHKYGGDAKYARIHKRLMENAALYGDK
LKFVNALSGVKTDADQKVLDMBQILDNQNYFEKMQGIVLKRFRTEQQFPVQPADIQAINRLLVREYLKESGRI

SEQ ID 187

ATGAATCATTTTAAAGAAACAACAATTCAAAATATTGCTGATTTTAAATCCGAGAGAGCAACTAGCCAAGGGAGCATTGGCAAAAA
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CAATGGTGATACCTTATTAGCTAAGATTACCCCGTGTGTTGAAAATGGGAAAACCGCTTTTGTAGATATTTTAGATGATGGAGAA
GTGGCTTTCGGTCTACCGAATTTATCGTGTAAAGAGCAAAAAATGAAACCAATCCCGAATTTCTCTATTATTTTGCATCAGTC
CCGATTTTAGAAAACGAGCGATTGAATGTATGGAAGGAACCTCCGCGCAAGCAACGTGTCAATGAAAATGCATTAAAAACACTGGA
GTTGCCATTTCAGAACCTCAAATCCAACAATCCATCGCCCGCTCTATCCGCTTTGGACAAAAAATCGCCCTGAACAAACAA
ATCAACGCGCGCTGGAAGAGATGGCGAAAACCTGTACGACTACTGGTTTGTGAGTTCGATTTCCCGACGCCAACGGCAAGC
CCTACAAATCCTCAGGCGCGGACATGGTGTGTTGACGAAACCTTGAAACGGGAAATTCCGAAGGGGTGGGGAAGTATAGAATTACA
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AGTCAAGATTTTATTGTTGATTTACCAATGATGAAAATCTATATTAACCACCAAGATGCTCATATTATTTTGGTGATCATA
CAAGAATTGTTAAGTTAGTTAATTTTCAATATGCGCGGGGAGCAGATGGTACACAAGTAATATTAAAGCAATGAACGAATGCC
AAACTATTTGTTTACCAAATCATAAATCAAATAGATTATCAAGTTATGGTTATGCTAGACATTTTAAATCTTAAAGAAATTT
AAAATAATTTTGCTAGTAAAGATATTTCTCAAAAATATAATGAAATAGCAAATACTTTCTTTGTTAAAGTTGCAAAATATCTAA
AACAAAACCCACCTGACCCAACTACGCGATTTCTACTACCCATGCTGATGAACGGGCGAGTATCCGTAAGATGTAGCGGAGC
AAGAGATGGA

SEQ ID 188

MNHFKKQIQNIADFNPREQLARGALAKSVPMAMLKBFQRQITGYEIKAFNGGAKFRNGDTLLAKITPCLENGKTA FVDILDDGE
VAFGSTFIVLRKNETNPEFLYFAISPDRKRAIECMBSGSRQVRNENALKTLELPIPEPQIQQSIAAVLSALDKKIALNKQ
INARLEEMAKTLYDYWFVQDFDPDANGKPYKSSGDMVFDETLKREIPKGWGSIELQSLAKIPNTTKILNKDIDFGKYFVVDQ
SQDFICGPTNDEKSILNPQDAHIIFGDHTRIVKLVNPOYARGADGTQVILSNNERMPNYLFYQIINQIDLSSVGYARHFKFLKEP
KIILPSKDISO KYNEIANTFFVKVRNNLKQNHHLTQLRDFLLPMLMNGQVSVRCSGARDG

SEQ ID 189

ATGGATAAACTATTTAAATATTTATTAATATAAGTAGTACATCTTTGCTGTTATCAATATATTTTATTAATCGCAATATTATA
TATTAGACCTTACTTGGTTTTATCGTGTAAATTTCAATCATTTGGATAGAACCTATTTCTAAGTTAAGTCTACTTTTTTATTTTCT
AATACCATTATCGCAACCGCTACTGCTTTATGGCTAAGCAAATCTTTGGGGAAGGATGAATTCAAGCAAGGAGAGGTGAAAGAA
TTAGAATATGTTAACGATAATTTCTTACCTAGCTATCTTGGTTATTTTTTGTGCTCTAAGCATACCCGATAATAATCTTTTTT
TGCTATTTGTTATGTATGGAATATTTTCTTACTAGTTTCATGCTCTAAGTCATTTTATTTTAACCCGTTTTTTCTTATTTG
CTATCGATTTTATCAAGCAAAACTGAATCAGGGTTATTTAGTCTGATTAGTAAACAGGAATTTAGAACGCCACAAAGTGTA
AGTTCGATTGCTGTATATCGAATTAATAATTTTACTTTCTTAGAAAAA

SEQ ID 190

MDKLFKILLNISSTSLLSIYFIKSQYYILDLTWYFVRVSNHWIEPIKLSLLFYFLIPFIATATVWLWLSKYLKDKRQGEVKE
LEYVNDNLFPSYLGFFVALSIPDNNLFLFVYGIIFLLVSCSKSFYFNPVFFLFYGRFYQAKTESGLLLVLISKQEFRTPOSV
SSIAVYRINNFTFLEK

SEQ ID 191

ATGAATTTTGTGTTTAGCTAAAATTACTTGCAGAAAGATTTAGTAAAAATATTATCTGATGATCATATTTTCCCTGACTTTTCTT
ACGAGAATTTAAATTTTATAACATATAACTATGATTACAATCTTGTATGATGATACTTGGTTTCAAATTTGAAAATTTAAAGAATCA
AGATTTTGTCTTAAGTTTGTGATAACTCAAATTTATTTGATTCAAAAATGTTTAGTGAAATAAAAAAGGAAGAAATAAATATA
GAGAACTAAAGTATTTAGTATCTTGTACTAATGATGCATATTCTTCCAGAAAATCACAAGTTCATTATTACTCAAAAAGAAGC
ACTTGCTAACTATATGCGGAAATGGTGCGAACTATGCGAACCACAAGACTTATTTGGTTATTAAAGATATTCTGATGCTGTTTA
TATAATAAAGGATGATAAATTAATATTAGAACCCTTCTTCTATTTCAAATATATTAAAGGGATTGAAGATTTGTATCGAGAA
GCTACAAATCTGAAGTACAGCAATCTTAGAAAGCGATTATTGATTAAAGAAGATTTTTAAGTGAAAAGTATCTATTTC
CCAATAGGAAAAGATAGCTTTAGTTCAAGATAGATTGAATAATATGACGCTAGATCAAAGACAAGAACTATTAAATTACCTTGC
TGAATATAATAATAATATCTTGAAATTTAACGCAGATGGCTCTCGTGTAGAAAATTTCTACTGATGTACAGCTGAAACATTTGTTA
TATGGTATTGATGAACGTTATTACACAACAGCATTAGGAAAAGAGAAAAGGTTGGCAAATAGTGTCAACCTATT

SEQ ID 192

MNFVLAKITCKKDLVKILSDDHIFPDFSYENLNFITVNYDYNLDDTWFQIENLKNQDFCPKFLDNSNLFDSKMFSEIKKEEINI
EKLKYLVSCTNDALDFQKITSSLLLLKKHLLTICNGAKLCBPQDLLVIKDI PDAVYIIKDDKLIFRTLSSISNIFKGIEDLYRE
ATNTEVQQFLESDFIDLKEDFLSEKVSIPNRKRIALVQDRNLNMTLDQRQELLNLYLAEYNNNLIKFNADGSRVEISTDVQLKHL
YGIDERYTTALGKEKRLANSVQPI

SEQ ID 193

ATGGGAAACAGCCGATTAAGCCAACTCCCGCGCCCGCCGATCGAAGAAACCGACTTTGAGGGCATCTTCGCGCGCAAAAAAG
CCGCCCCACCGCCCTATGTCCCGAAAGCATCCCGCGAAACCGTCGCCCAAACCTCGAATTAGAATCAGAACCCCTAACCATCGA
CCTGCAACAGCAAGCCTATCAAGAGCTGCTCGTCCGCAACCGCATCAACGAAGCCGTCAAAGCCCAACCTTTGGCATACGCACAA
GGCAGCGACCTCGACCACATCGCCGCCCAATACGGACTTTTACGCAAAACCATCCGCGCCGCCGACCCCGACGCGCAACCCGCCG
TTGCCGCCGAATACGAAACCGACGACGATTCCGCGCCCGCTCCAGCCCATCCCGAAAAATACGCCGCCGGCGCCGCGCACCCGC
ATACGAAGCCACGCCATCGACGACCCCCCAAATCACACAGCCCGCGCCGTGCGCCGCCGCCGCCGCGCACGGTGGAGGTTTACA
TCAAAACCCAAAGCGGCACGCCCGACGAAACCATTT

SEQ ID 194

MGNRSLSQLPAPAAIEETDFEGIFARKKAALTALCPESIRETVAQTLELESEPLTIDLQQQAYQELLVRNRINEAVKANLLAYAQ
GSDLHDIAAQYGLSRKTI RAADPDANPPVAAEYETDDAFRVRVQAHPEKYAAGPRTA YEBAHAI DAPPKSHT PAPCAAPPARWRFT
SKPKAARPTKPF

SEQ ID 195

ATGAATCCGCTTTTACCACGAACGAGGATTTCCATAAGAAATATTGGATGGCAATATTCTTGCAACCAACAATAGAGGCG
TAGTCAGCAATGCGGATGGGAGCAATACCCGAAGTTTCAATATAGCCAAGGGGATTGCCGACTTACTGCAATTCGGAACCGTTTC
GGAAGATTACCCGGTCAGACATCGGGAATGCTTTTGAAGCAATATGCAAGTGTGTTGTTCAATCTGCTTTTGAATAATGTCAG
CATATCAGACCCCGGACGGAATGTTAAGCAGGTCGGTTCTCGCAACCGTCTGGAATCGCACGTTATCAGCAATACGCACATC
TGACAGCCTTAGCCAAGGCTGCCGAAGAAAACCCGAATTGGCTGCCGCTTTGGGCAGTGATTACACCATTACTCCCGATATTAT
CGTTACCAGAAATTTGATTGACAGATGCGAAATCAACCGTAATGAATTTTAGTTGATGAAAATATTGCCACATATGCCAGTTTG
CGTGCGGGTAATGGCAATATGCCGCTGCTCCACGCCAGTATCTCTGTAATGAGCAGATTGCGCAGCAGAGGCTCAAAATGCC
GTTCTGAAGGATTGAATTTGGTTAGAAACAGAAAGGCAGACTGCCGCACATTTGTTGCTAAGCGCAGAACCAACGCCAAGCCG
CATTTTCATCTATTGCTTGGGTACAGGGGAAATAGATTGCGTTTACCATTTTGCTTATATGAGCTGGAACAAATTTTACAATCA
TTGAATTATGAAGACGCTTTGGATTGTTTACATCATGGTCAATGGTATACGATTAAAGATATTTCCGACCTTCCCTTAGATT
TGGCATTT

SEQ ID 196

MNPLFTQERRIFHKLLDGNILATNNRGVVSNDGNSNTRSFNIAKGIADLLHSETVSRPLPGQTSNNAFPAICSEFVQSAFEKLQ
HIRPGDWNVKQVGSRRNLEIARYQOYAHLTALAKAAEENPELAALGSDYITTPDIIVTRNLIADEINRNEFLVDENIATYASL
RAGNGNMLLHASISCKWTIRSDRAQNARSEGLNLVRNRKGRPLPHIVVVTAEPTPSRISSIALGTGEIDCVYHFALYELEQILQS
LNYEDALDLFYIMVNGIRLKDIDLPLDLAF

SEQ ID 197

ATGACCACCGAAGTCAACAGCGGACAAGTGCGCGGCCCGGTGCAACTGGCGTTTGCCCAATCCATCGATCCGATTGTGCGCCCGG
AAGTTTCCATCACACGCATGGCGGTAACCAATGAAAAAGACTTGGAAAAAGAACGCACCATGGGGCGCAATACATCGTCCCTTA
CGTGGTCTACCGCGTCATGGCTTTATCTCCGCCAACCTTGCCGCCAAACCGGTTTTTCAGACGACGACTTAGCCAAACTCTGG
CAAGCCCTGACGTTGATGTTTGAACACGACCGCTACCGCCCGGTGGAGAAATGGCGGCACGCAAACTGGTTGTTTCAAACACG
ACAGCGCACTTGGCAGCCAGCCTGCACATAAACTGTTTACGCCGTGAAAGTCGAACGCGTAACGCGCAATCAGGTACGCCCCG
AAGCGGTTTTGGCGATTACAAATCAGCGTGGTTTACAGCGGGCTAAATGGCGTGAGTGTGAAGAGTATTTG

SEQ ID 198

MTTEVNSGQVRGPFVQLAFAQSIDPIVPPVVSITRMAVTNEKDLEKERTMGRKYIVPYVYRVHGFISANLAARTGFSDDDLAKLW
QALTLMEFHDRSAARGEMAARKLVVFKHDSALGSQPAHLKLFDAVKVERVNGESGTPASGFGDYKISVVSGLNGVSVEEYL

SEQ ID 199

ATGAATGCTGTCCAAGTTTAAACTTTCAACAAAACCTCCGTCCTGACTGTGCGGATAACAAAGCGAGTTGTGGTTTTTGGCAA
ACGATGTTTTCGAGATTTTAGGCTACACCAACCCCTCGCCGAACGGTTGACCTGCCTGCAAAAGCAGGGCGCTAACAAAACGGTA
CACCCCACCACAGCGGCGAACAGGAGATGACCTATATTAACGAGCCGAATCTCTACCGCTTGATTATCAAAATCCCGCAAGCCT
GCCGAGAAAGCGTTTGAAGAATGGGTAATGGAACCGTCTGCCCGCCATCCGCAAAACAGGCGGCTGCCAAGTCGGACCAAAAA
CCACCGCCGACGACCGTACCGGATTGCGCCAAGCTGTTGCCGCGCTTGTCCGACGCAAAAGGTATAGACTACTCTCCCGCTACAG
TATGATACACCAACGCTTCAACGTCGAATCCATCGAAGACCTCCCTGCCGGAAGCTGCCGAAGCGCTCGCCTACGTCCACGCA
TTGACACTGCACAGGGCTTGACAGGCGAAGTGTGGACGCAACGCCCAAGCCGAGCCGAACTGCCCATCGACGGCAACTCTT
TAGCCGACATTGCCGCTATGGTTTATTACGGCACATGGATGATTGAATCGGGCAAAAGACATCTCCGCGCGCTGAAGCAGCTCGG
CTGACAGCAGCGGTTACGATGTGGACGGTTTGGCAGCAAAACCGTCCAATCTGAAAAGATCCGCGCGCGCCCTCGAAGTGTG
CGGGATATGCGGACAAAGACGCTCCGACCGCATAGCCGATGTCTTGAAGGCATTTACGGCAAGGCTACGGTAAGG

SEQ ID 200

MNAVQVLNFQNSVVRTVADNKGELWFLANDVCEILGYTNPRRTVDLHCKSRGVTKRYTPITTSGEQEMTYINEPNLYRLIIKSRKP
AAEAFBEWVMTVLPAIRKTGGCQVGPKTADDRTGLRQAVAAALVGRKIDYSSAYSMIHQRFNVESIEDLPAGKLPEAVAYVHA
LTLHFTGLTGEVLDAPPKAEPLPIDGNLADIAAMVYYGTWMIESGKDISAPLKQLGCRQAVTMTWTVWHETRPILKRSAAALEVL
RGYADKDASDRIAACLEGIYKATVR

SEQ ID 201

ATGGCAGAAAAGACGAATACGGCCTACGGCGACCCGAGGCGATGATGAAGCAGGCGGCGGGGCTGTTTGCATGTCATATGCAGC
GCAACAGTACGCTGAACCGTTTGGCGGGCAAGATGCCTGCCGGTACCGCGGCTGCGGAGGCGACTTTGCGCAAAACAGACGACCCA
GCATATGCCGGTCTGCGCTGTGAGGATTGACGCGCGGCGATGGGTGACGAAATCCGTTTCAATTTGGTCAACCCGTGTTTCCGCC
CTGCCGATTATGGCGGACAAACACGGCGGAAGGCAAGGCGCTGGGGATGAGCCTGTCCGAGCGCGGTTTGGCTGTGAATCAGGCGC
GTTTCCCCGTTGACGGCGGCGGACGATGACGAATCAGCGCAGCCCTGCCGATTATCGCGCGCTGATTGCTCGGCGCGCGCAAG
CCTGATGGACCGTTATGCCGACAGACGCTGTTGGTGCATATGGCGGGCGCGCGGTTTTCATGACAAATATCGAATGGGGCGTG
CCTTTGGCGGGCGACCCGAAATTCATGATTATGCCGTCAATCCGGTCAAAGCCCCGTCCAAAACCCGCCATTTTACGGCTTCGG
GCGATGCCGTACCGGGCGTTGGGGACACGGCGCGCGAGTTGAAGATTGCCCTTACCGATTGTTTACGATGGATACGGTGGACAG
TATCGTACCGTGCTCGACAGATTCCGCTGCCCGCGCGGATTGTGAAGTTGAGGGCGACAAGGCGCGGGGTGATTGCGCTTTG
CGCGTGTGGCTGCTTTCCCGCGCGCAGTACAACCGTTTGGCGCGGATCCGAAATTCGCGCAGCTTCAGGCTTCGGCAATCGCGC
GCGCTCCAGGCAAAATCAAATCCGCTGTTTGGGCGATGCGGGTTGTGGAACGGCTTTATCTGTTGAAAATGCCGCGCCC
CATCCGTTTCTATGCCGGCGATGAGATGAAGTATTGCCCGGATAAGTTTACGCGAGGCGGAATCGGGCTTGAAAATCCCGGCTTCG
TTTGGCGACAAGTTTGGCGTGCAGCGTTTCGGTTATTTGGGCGGCGAGGCGGTGTTGGAGCGTTTGGCAATACCGGCAAAACAG
GCGGTATGCTTTCTTTTGGTCTGAGAAGGAGCTTGACCACGGCAACCGTGTGGAACCGTCTCGGTACGATACCGGCTGTGGC
GAAAACGCGCTTTCGCGTGGATGTCGGCGGGGTGCGAAGGAAATTACCGACTACGGCGTAACGGTTGTGGATACGGTGTCTCT
TTGCACGGCGGTATCCGC

SEQ ID 202

MAQKTNNTAYGDPQAMMKQAAGLFAMHMQRNSTLNRLAGKMPAGTAGAEATLRKQTTQHMPVVRCDLTRGMGDEIRFNLVNPVSA
LPIMGDNTEAGRGVMSLSEAGLRVNQARFPVDGGGTMTNQRSPADYRALIRPAAQSLMDRYADQTLVHVMAGARGPHDNIEWGV
PLAGDPKFNDYAVNPFVKAPSKNRHFTASGDAVTGVGDNNGELKIASTDLFTMDTVDMSMTVLDQIPLPPPVIKFEKGKAAGDSPL
RVWLLSPAQYNRFADPKFRQLQASALARASQANQNPFLGDAGLWNGFPILVKMPRPIRFYAGDEMKEYCADKXSEAESGLKIPAS
FADKFAVDRSVILGGQAVLEAFANTKGHGMPPFFWSEKELDHGNNRVETLVGTIRGVAKTRFAVDVGGGAKEITDYGVTVVDTVVP
LHGGIR

SEQ ID 203

ATGACAGTCCGAAACACGCAAAACCGAAACCGTCCGGACGGAAGCCGCGCCGCAACAAGGCGGCAATACCAACCCGGGCTATTACA
AAAACCGCGCTTCGAGTGCCTCGGTTTGGCGCAATACCTCAACTTCAACCTCGGCAACGCTTCAAAATACATCTGGCGGCACAA
GGAAAAGGCGGCGCAAGACTTGGAAAAGCCCTCGGCTACTTGAACGCGCAACGCGCGCGCGCGCGCAAGTTCAAGAAACTC
AAACACCGCGCTATGAAAAATGTACGCCGCTGTAAGATTGCGGGTTGACGCGGCGACGAGGCGCGCTGCTTGGCGTCA
TCTCCGCGCTTATTACATCCGCGACGCGCAAGACAATTTGCGTGGCGCGCGCTGTGTGCAAGATTGTTGGAATAAATGCG
GCCTGAAGCGGGCGGGCCCCCACCCTGAAAGCCCGATGCCCGCTGAAACGGCGGGCGGAGGCATT

SEQ ID 204

MTVRNTQTETVRTEAAPQGGNTNPGYKYNRAFECEVGAQYLFNLFNLFNAFKYIWRHKEKGGREDLEKALRYLERQAGAPKFKKL
KHRRYEKMYAGLKDCCGFDGGTEALLAVISAAYYIRDGEDNFAWAAACVEDLLEKMPPEAGRAPHPEPMPPETAGGGI

SEQ ID 205

ATGAACCGAATCGAGGAAACGGAAGCCGTCCAATCCTGCGCCAGCGTAGGGGCGGAACAGAACATTTTGGCGCGCATCTTGATTG
AACCGACGGCGATTGCGCGGTGCGCAATCTGACCCCTGAAAAGTTTACCAGGCGCAACACAGGATTATTTCCGCGCTCTGCT
GGATATGGCGCGGCAACAGAGCTATCGACATCATCAGCTGAACGACAAGCTGGAAGCGCGCGGCGAGGCGGAAACGCGGGT
GGCCTGGCTTACTGTAGACTGAACCAAAACACCCGAGCGCGAAGATATCAGCCGTTACGTTGGGATTGTGAACGACAGGT
TTGTGCGAGCTTGTGCTGAAGGCTTCGCGCGCGATTGAAAAAATCCGCGTTTCCAAAGACGCGGGACGCTCGCAGAAAAGCT
GTCTAAGGCGGCGGATGAATTGGCGGCGAGTCCGCAAGACGCGGTAAAGCGTGAACCAAGACATTGCGCCAGACCGTTGAGGAT
TTGATTGGCGGTTTGGACAAAAGGCTTGACGGCGTGCCTTTCGATTGCTTACCGCTTGATGAAGCTTGACGGGATGACCGGCG
GTTTGGCGGATGGAACCTGATTGTGATTGCGCGCGCTCCGTCTATGGGTAAACCGTTTGGCGGAAACATTGCGCGATTTCGC
GCTGAAGCAGGGCAAGGCAGTTTCAATTTCCAAAGCTACGAAATGAGCGCGGTAGAGCTGGCAAGGCGCGGATGGCGGCTGAGTGC
AATATCCCCATGCAAGCTGAAAACCGGCAATCTGACGCAAGACGATTACGCCAATATGCCGATTACGTGACGCAAGCGAAG
AGTGGAAAGTTTGACGTGAACCTGCGACCTGCTCAACGTTGACGAGCTTTGCTTTTGGCTAAGGAGAAAAAACTCACTACCGCTT
GGATTGTTGTTGTTGTCGATCACCTTCAATCATGCCAAGGGCAGGGAGGGACGAGTGGCGGAGTTGGGGAATATATCGCGCGCT
TTGAAAACCTTGGCGGCGAGGCTGAATACCCCGTCTGCTTGGTTGCCAGTTGAACAGGGGAAACACAAAGCAGGCAGACAAAC
GCCCGAATATGGCAGACATTGCGGCGAGCGCGCGGATTGAGCAAGACGCAACATCATCATGCGCGACCGCGAAGCTACTA
CGACGGAAACGAGAATCCGAGCATGCCGAGCTGATTATCGCAAGAACCGGGACGGCGAAATGGGAACGGTGGTTTGGCGCTG
AAAGGCAATTTATGAAGTTGAGGAAGAGCTGATTGGCATGGCAAGCCCCCAACATGATGAATATGACCCTTACAGTGTCT

SEQ ID 206

MNRIETEAVQSLASVGAEQNILGGILIEPTAIARCAITPEKFYQAOHRIIFRALLDMAAANEPIIDIITLNDKLEARGEAEANAG
GLAYLIDLNQNTPSAKNISRYVGVINDRFVERGLLKASAAIEKIAVSKDGGTVAEKLKAADELAAGVGDVAVKRETKTFGQTVED
LIGGLDKRLDGVRFGLPTGLMKLDGMTGGLPDGNLIVIAARPSMGKTVLAENIARFALKQKGKAVHFQSYEMSAVELARRGMAAEC
NIPMQNLKLTGNLTQSDYANMPIYVSQAKWKFDVNCDDLNVDELCLFLAKEKLLTTGLDLLVVDHLHIMPRAGRDEVAELGNISRR
LKNLAAELNTPVVLVAQLNRGNTKQADKRPNMADIRGSGAIEQDANIIIMPHRESYDGNENPSIAELIIAKNRDGMGTVVCGW
KGQFMKFEEDPLAWQAPKHDEYDPYSV

SEQ ID 207

ATGACCGCCCTCACACTCTACCGGTGCGCGGCAGACGTACAGCGCGGGCTGGATTACTACTTTGACAGCGAAACCGAGCGCGAAG
ACACGCTGGAAGCGCTTATCGGGCAGTTCGAGGTCAAAGCGCAATCCGTTATCGCTTATATTAACCAAGAAATCACGGAATA
AATGCTTGAAGGGCACATCAGGCAGATGACCGGGAAGCTCAAGCGCGCAAAAGCGCGGAATCAAAGCCTGAAAGACTACTTGGCG
CGCAATATGCAGCGCGCGGCATTACCGAATCAAAGCGGATGACGGCATTTTAAAGCCTCGTTCGCGCAATCCGAAGCCGTCG
TGATCTTAGACGAAGCACAAATCCCCCGCAATTTATCGGTGAGGCGGTCAAACCGAACCAGCAAAACCGCCATCAGAAAAGC
GATTGAAAGCGGTGCGCAAGTAGCAGGCGCAAGATTGAAGGGCGGAAGATTTCAGATTAGA

SEQ ID 208

MTALTLYRCAADVQAGLDYFFDSETEREDTLEAVIGQFEVKAQSVIAYIKNOBITEKMLEGHIRQMTGKLKAAKARNQSLKDYLA
RNMQAAGITEIKADDGTFKASFRKSEAVVILDEAQIPAEFMREAVKTEPDKTAIRKAIESGRQVAGAKIEGRKNLQIR

SEQ ID 209

ATGTTGTCTGGCGCAAAGGTATCGGAAGACGAAGCCCTGACGTGCGGCATCATGATGCGGCTGTCCCTGCAGGATATGCGCTATG
CCTGCAATCAGGAATTAATCAACTTCGCCGAACATATCGTCAAACAGGTGCAACGCTTGGGCTGTACTGCAACACTGACGACCC
CGCAACGGGGAAAGCGTACTGTTTGCCTGCCGGAAGCATCGCAGGCGCTCGCTCAATGGACTAAAGATTTTGACAATTTAAGC
CCGAATCAGCGCCAACCTGCTGCTGCTCCGCTGTCAAATCTCTTCGCGCGGTACGAAGAATTTCTGAAAGACGCGCCCTGCACGGC
TGATAGCCGAAGTATCGGCATACTCATTTGGCCGTGCGGGTTCGCAAGAAAGCCATGGCGTTTTTAGAGCTTGACGGCGGTTTGAT
TTCCGGCGTTGGCAAAGTCGTCAACGGCGCGGATTTCGCGCGCGGAAGCCCGCGCTTAAATGCCGTACGCGGAATTTACAGGC
CGGATCCTACACGCGCGCAACCTGCTTTACGATGTGGGCATTTCAGGCGGACAAGGAGCTTTTCGCGCATGTACGCGCAAGCCGCTGA
ATCCCGTGGCGCCCCGACGGATAAGCGACGTGCGCGCGCGCATGATGAAATGCTTGTTCGCGACAAAGCGCGCGCTTGGTCCG
GGCCGTAAAAGACTCGGAAGACGTCAATCCGGCATTTCGACAAACGGCGCGCGCTTACGTGCTTCAACTGGACCGAACAATTTCAA
CGGACGGCAAACCTGATCAGCCTCATGCACAGGAAGCGCGCGCA

SEQ ID 210

MLSGAKVSEDEALTCGIMMRLSLQDMRYACNQELINFAEHIVKQVQRLGLYCNTPDPANGESVLFACREASQAVAQWTKDFDNL
PNQRQLVLRPLSNLFAAYEEFLKDAAPARLIAEVSAYSLAVRVARKAMAFLELDGLISAVGVVNGADSRARRLKMPYAEFTG
RILHAANLLYDVGIQADKELSAMYGKPLNFPVRPRRISDVRRPMMKMLVADKGGALVRAVKDSESVIRHCDNGAGFSCFNWTEHFK
RTANLISLMHREAAA

SEQ ID 211

ATGAACAAAGAAGACAGTTCACTGTCATCTTACTTGGCTTCGCGCGCGCTTCTATGCACGCGCAAGGGCGCGCGCTGCAACA
CGCGAAGCATAGAGAGACAGACAAATACACCTCGTCTCGCAAAACAAGGGCAAGAGAACAACTATACCTTAAATGGCGGAAC
CGAAGTCAAACCTTAAATTCCTTCATCATTTGCCGCCAAGCGCGGTACGAACAACATTACGATAAAAGGCAATTTGGCAGACGGT
CCTGCCGATGCCCCCGCGACGATTGACAATAACTCGATTGAAAGAAATAAATAAAAACGGTTACACGTACGCATGGCAGAATTT
GGAGCGCGCGGTGATGTTGGTGGATCAAAGCTATGAGGGAGAAATAAGGTTACTTTTGAAGAACGTAACCATAGCCGCCATAA
CGCGCTTCCCGGCAATTTGTCTGATGATAGGCATAAATCCAGTAGCTTGGCGCGCGCGATGCTTGCCTTTAAAGGGCGCAATACC
ATCAATATGGACGCGGACTCAAATGCCAATCTAGTAACGAAGGTATCCTATTGCTTAATAATGGTGAAATAATGGGAGAATATC
GTCTTGTTCGGAAGAAGGCTCGACGCTGAATATCAACATCAAATCAGGAAAGATAAAGGACAGGGCATTACCGCCAACCACTA
TGGTAACCTCAGACATCAACTTCAACAGGCTTCTCCAAACATCACCACAATGGAGTTCAAGGGCGATGTAAACATTAATTAAGT
AGGAACGGACAGGAAGAGCGGAAAGCAACGGTTTGGCTTCTATTCAAGCCGCAATTAGGCAATAAGAACGAGATTCCGGAAG
GTTCTAAGATGGAAGCGATTTCCTGCGGAACGTGATATCTGTTGCAACCGCGGTTATGACGAGCAAGGCAGGCCAAAAGCAT
AGGCAGCGCTTTCGATGACGGGAATAACAGCAAGTCAGGTTGTTCGCGGGGAAGGCAAGGTTGTCAAATCAAAGCGCAT
ATTTTCGCTTACAACGGCGCGCGAGCGTGAGCGTGAACCTTGCCAAACAAGACTCTTATTTGAAGGGGAAGCCCATATCGGAAAA
GGAGCTTTGCCAAAGGGAAGATATGTTTGCCTTAACCGTGGATGCGGACGGATATGAATTAACCCCGGATACAAAGTCGATTGA
AAAGAAAAGAAAGAGCTGAATGTTAGGGGCTGTACTAGATTATCCCTAAATTCACACCGATCCCGCAGGATTTT

SEQ ID 212

MRQKKTVCILLGFAAASMHQAQGAANAASGTIEKTDKYTLVLAKQOENNYTLNGGTEVKPLNSLIIAANGGTWNITIKGLADG
PADAPPTIDNNSIERNINKGYTYAWQNWGSVAVMLVDQSYEGENKVTFFENVIAAHNAPAGILSDDRHKSSSLAPAMLAFFGRNT
INMDADSNANSNNGILLNNGEKMGEYRLVSEEGSTLNINIKSGKDRGQGITANHYGNSDINFNKASPNITTEFKGVDVNIKID
RNGQEEAESNGFGFYSSRKLGNKKQIPEGSKMEAIFRGNVDIVATPVYDEQGRPKSIGSAFIDGKYSKVEVVGGBGVVKIGKD
IFAYNGGSVSVNLANKDSYFEGEAHIGKRSFAKGKDMFALTVDADGYELTPDTKSIEKKKKELNVRGCTRLSLNSTPIPDQF

SEQ ID 213

ATGAAGCGCGGCACAAAAGAACTGATTGGCCTGCTGCACGCGCGCGACGAGTTTCAGATGGCGGATTTGTACACCATTACGCTTT
CGGGCGCGCGGTGCTGCGGCATACCGGCGCGGATATGCCCGTCTGTTGGGACGGTCAGGCCTACGGGGCGCACGAGCTGGTTAT
CAAGCGCGCGCGGACACCGGTACCGCGTGGATTGGAAGTGGATTCCAACACCTGCAGATTTCAGCCGCGCCGATTACAGGCTT
GAGGGCTGCAATGGGCGGAGCGCGCTTGGCGCGGTATGGACGCGCGCGGGTCAAATAGACCGTGTGTTTTTGTATGCCG
GACTGCGCCCCGTGGTGGTGAATATTTTTCAGGCGCGGTGTCGACGATACGGGCGCGAGGTGTCATGAGGACGCTCTATGACGCGC
GAAATCCGACATCGAGCTTTTGAACGTTTTCAGCCCGCGCAACATTTATCAGGCGGGCTGATGAGGACGCTCTATGACGCGC
TGCAAGGTCAACCGTGAGAAATTCAGGTAACCGGCGGTAACCGGAAACAGCGGACGCGGAACCGTGTGAAGCACAACTGTA
CGCAGCTGACGGCTGGTTTTTCGAGGGCGTGATTAAGTTTTCGCGCGGGCGCAACCGGGTTTGTAGCAGGACGCTCAAGGCACA
CGCGCGCAACACGTTGCAACTTGCCTTCCGCTGCCCTACCCGCGCGAGCGGGCGATGCGTTCAAGGTTTATCCGGCTGCGAC
AAGCGCGCGATACCTGCAAGGATAAGTTTGACAATATCGTGCATTTTCGCGGCTTCCCGTTCATCCCTTCCGCGATACGGTGG

TG

SEQ ID 214

MKAATKELIGLLHGGDEFQMDLYTITLSSGRVLRHTGADMPVVDGQAYGAHELVIKRGATRTAVGLEVDSENTLQISAAPDYRL
EGLQWABAALGGVLDGARVKIDRVFFDAGLRPVGAVNIFSGRVSDVSGGRSSVKVDVKSDELLNVSSPRNIYQAGCMRTLYDDG
CKVNREKFTVNGRVNTENSRTGTVLKHNLTQPDGWFSGQVIKFAGGRNAGLSRTVKAHGGNTFELALRLPYPPQAGDAFKVYPGCD
KRRDTCCKDFDNIVHFRGFFIPFIPADTVV

SEQ ID 215

ATGTCGGTTCAACCAAGCGTTTCGGAACAACTGAAAGACAATGCAAATGTTGATGCGAAAGATGAAAAAGTTATTGAATATCTGA
AGAAATCATCATTAAGAGATGTACCAAAAGAATTGCAAGCCAAAGTATTAAAGGTTAAAGGTGATGAATATACAGGAGTGCGAAA
ACAATATGCAGGTAGCTCGGTAGGGTGAATCTGTCAAGGCAATGCTATTTCCTAGACGGCGAAGAGCCGTTTAGTAAGGAACAA
CTTCAGAAAGATGGATGTATATGTTAATGGTAAAAAATACGAAGGTAGTAAGGGGGGGAACCTAGATGTTCTCCCAAAGGTTTGA
GTGAGCAAAAGATTGAGTTTACGGTGGGATAAAGAACAGAATTATGCGCTATTAAAAACTTGGGTTTATGAGCAACCGTATTC
TGTGGTTAGAGGCTATTTCGGCTACAGTCGAAAAGACGGTAATCCTATAGAAGGGGATGGACAAAATCCTGAAGAGATTCTTTT
GACTTGTATCTGGGCGACATTAGAGGCGTGGCAACAGATGAAGACAAATTACCCAAGGCTGGGAGCTTTCAATATGAAGGTGCGG
CATTTCGGCGTAATGGGTTTATCCAAAGAATCGTTAGATAAACCATAATGGCGTATTAGATACACAATTGATTTTGATCGTAG
AAAAGGCTCTGGCTCAATTGAAGGAATGGAACAATATGCAAGATCAAATTAGAAGAAGCTGCTATTGAGAGAATCCCTTATCGA
GAGTCCGCTCAGCTTGGGGTTGAAAGACCGGGTTCTTATTTCGGCGTGAACGAAGGGGTGCTATTGAGAGAAGGATTAATG
AGATTAAGAGTATCATTTGGGTATTTTCGGCGAAGCGGCTAATGAAGTAGCAGGTGCTGTAAGCCAAGAGCATAAACATCAAGC
TGTTATCGGTTTCGGCGCGGAGAAGAA

SEQ ID 216

MSVQPSVSEQLKDNANVDAKDEKVIKSLKSDVPKELQAKVLKVKGDEYTGVRKQYAGKLGKGSVKAMFLDGEPPFSKEQ
LQKMDVYVNGKKYEGSKGGLDVLPKGLSEQKIEFYGADKEQNYALLKTVWVEQPYSVVRGYPGYSRKDNPIEGDQNPBEIPF
DLYLGDIRGVATDEKLPKAGSFQYEGRAFGNGVLKESLDNHNGVFRYTTIDFDRRKSGSIEGMBQYGIKLEBAIERIPYR
ESGSSLLGLKDRVSYPGVNEGVMLEKDNEIKKYHLGIFGEAANEVAGAVSQEHKHQAVIGFGEKK

SEQ ID 217

ATGGCCGGCTGCCTGACCGACTTGAAAACTGTCTGAAAAATACCTCGAACAGTTCGGGCCGGTATCGGAAAGTATCGAAGCCT
GTACCGCCAACTGCAGGAGCAACCGTCGTTCTTCAACAGGCTGATGAAGCCAACGACAAGCTCAACAGGCAGATTGACGTGTT
GCAGAACAGTCCGCGAGCCATCCACAACGAAGCCTATATCGAAATGAACACGCTGCTTTACCGCCATCGCGAAGTAGTTTCCATC
CACAACCCGCAAGAGCAGATTATGCGGAAAAGGCAAGAGCGGATTGCGCTGTTCCCGCGCGGTTTGAACGGCATCACCAAGCTGC
CTGCCCGCTCTGTTGCCCGAGCGTCCCTACCATTGATATGAAGGAGGTTCTGTATATATTTCCCGAATACCGAGA

SEQ ID 218

MAGCLTDLENCKEYLEQFGPVSEIEACTAKLQEQSPFNRLMKANDKLNRIQIDVLQKQSAIHNEAYIEMNTLLYRHRREVSI
HNRKADYAEKGERIALFPRGLNGITKLPAVLLPERPHYFDMKEVLYIFSRIPR

SEQ ID 219

ATGGGAATACACATATTTGAAATAACAGAAAAAGCGGGGGCAAAACCCGCCGCTGCATCTGTGCGTGTACATCCCTGCTGTCGGA
CTTACCGCTTCAACTTCGCAACGCATCCGCCATCGCCGAATTGGTTGGGACACGCTCGTTGCGTGTGTTTTCGGCCGGCTGT
CCGTTTCGGGCTGCGGTTTTCAGCTCGGACAGAATGTCAGAAATGGTCGGCAGTCCGAAGTGTTCGTGCGGTGAAGTCGGACCC
TTTGATTTGCTTCACGCGCTCGCGGTTAACTGCCTAAATATGAAATTCCTGGTCTTCTTG

SEQ ID 220

MGIIHIFEITEKAGAKPAAASVAVHPCRTYRFNFANASIAELVGRSLRCLRPVRSRLRFFQLGQNVQNGRQSEVFGVEVGR
FDLLHALAVNCLNMKFLVFL

SEQ ID 221

ATGGGATTATAGAACCGTTTTTATCAAGCTATACACCTTTATCACGAGATTATGTACAAGCTCGTACTAACCGAAAAACGACAAA
CCCTACTTTCCAAAATCGTATATACGCACTCTGGCTTTTACGCGTTTCACTAAGTAACTGAAACTCTAATATTCGACAAATAAATTTCTT
GATTAAGCGCTGGTCGAGCATCCACAAGGCAAGCTAAATAAAAAAGAAATTTGCCGCCATGATGTTAGTAGACTTAAACAACTTT
CAACAAAGATTATCTAACCGAAACAGAATTGAATGATTATTTTCAACAGGGAATAGAATCAGGATTATTGAACGAAAAATACAATC
AAATAAGTTATTTATGGAACCTATTAGACAAATTAGACGACTTAAACGAGTAGGTGATGACTTATATTTTGTGAGGATGCCCA
ACGTATTTTGGTAAATTGGATGAAATTACTGTAAGGAAACGCGACCCCTTATTTACATCGCCTATACAAAAACCACTTCAAGAA
GAAAGTGAAGAACATTACGGTAATGTGAAATGTATGCTGGAAAACTTGCTATCTGTATTGATTGCCAGTCATATTAAGCCTT
TCATCTGTGCGGATGATACCGAAGCATACGACCCAAATAACGGCTTGCTATTAAGTCGTACCTTGGATAGCCTATTGATTTGAA
ATATATTTGCTTTGATGATGAAGGAAATATGTTGAAATATACGCGTTATCGGCGTATTGGCGACGTTGGTGTGATGATGTAAG
CTAGATAACAATCTGCTCAACGACAAACGTAATCTTACTTGGCATATCATCGAGAACTTATGCTACAAGAAGACCAAGAATTTT
ATATT

SEQ ID 222

MGFIEPFLSSYTPLSRDYVQARTNRKQTLISKIVYTHSGFQORSVTENSNIQINFLIKTLVEHPQGLNKKEIAAMMLVDLKTFF
QQDYLTETELNDYFQQGIESGFIERKYNQISYLNWLLDKLDDLKRVGDDLYFAEDAQRIFGNLDEITVRKRDPLYLHRLYKNQLQE
ESEEHYGNVCKMLEKLAYPVLIAHLKPFILSDDTEAYDPNGLLLSRLTSLDFDLKYISFDDEGNMVKSKRLSDDVWRRWCDDVK
LDNNLLNDKRSYLAHRELMQEDQEFHI

SEQ ID 223

ATGACGCTGAAGAACAACAAGCCAAAGAAGCATTGGACGGCATTATCAAAAAATCCCGTGTCCACCTTTATAAACCCATTCAAA
TTGCAGAAATTTTATATCATGACCGTTGTATAAAACAGTTGGATTTTTTAAATTTAGATACTTACCGCAACCAATCTAAACGCTG
GAGGGATGAAATCTGCCGTCGGTTTTTAGGGCGGATTCTACTTTCATCTGCAAAATCCCAAGATAATCTGTTTGAAAAAATGCA
ATACCGCTTGAAAACTAGCGGTATTGGGAACATTAAACAGACAGCTCGGACGGCGGGGTAGAATCGTACATTTATAACAGTTT
TCAATCGTTTTTCCAAATGAGCGAAGCATTGGCTTATGTGCGCAATACAGACAGATACTCCTTCCAACTGTCTGAATTTCTAAA
TTTATTTTGGCTCGAGCCGGGATTGAAAAGAAGTATAGACAAGATATATGAAATCGTTGTTTATGCGTTGTTTGTATGCATTGGTT
TCAGAAATTAGGCATAACGTTTCAATTGATTTTCTAAGGAAAACCTGTTTTATGGGAGGAATATCAAGATTTTGCCGAAAAAA
TCATCACTATGCCGAAAAATGAGCATTAAAACCTTCTGCAAAAAATCCATCGTGTAGGCGTAACCAATGCTGCCGATAGAGGGTT
GGATATGTGGTCTAATTCGGATTGGCCATACAGGTCAAACATCTCTTTAGACGAAGAGTTGGCAGAAGATATTGTATCTCTCC
ATTAGCGCAGATAGAATTGTCATTGTCTGCAAAAAGGCAGAACAAATCGGTGATTGTTTCACTTACTGACGCAATAGGCTGGAAAA

GCCGAATTCAAACATCGTAACTGAGGATGATTGATAAGTTGGTACGAAAAAGCATTGAGAGGCCAATATCCGATTGCAGAAGC
GTTGTTGGAAAATATTAACCTGAAATTATGCGTGAATTTCTGCCGTAAATGAAGCCAATGAATTTTATAGATTTCCGCCAAAAT
CGCGGATATGACATTACTGTTACTCATTTT

SEQ ID 224

MTLEEQAKEALDGIKKSRVHLYKPIQIABILYHDCIRQLDFLNLDTYRNQSKRWRDEICRRFLGRISTSSAKFQDNLFEKNA
IPPEKLAVLGLTLNRQSDGGVESYIYKQFFNRESQMSSEALAYVGNTRYDFQLSEFLNLFWLEPGLKRSIDKIYEIVVYALFDALV
SELGITVSIDFPKENLFLWEEYQDFABKIIITMPKNEHLKLPKIHVRVGTNAADRGLDMWSNPLAIQVKHLSLDEELAEDIVSS
ISADRIIVVCKKAEQSVIVSLLTQIGWKSRIQNIIVTEDDLISWYEKALRGQYPIAEALLENIKTEIMREFPAVNEANEFLDFAQN
RGYDITVTHF

SEQ ID 225

ATGAACTGGCCTTATTTAATCGATGCCGTACCCAAATTCGCCGATGCCGCAAAGCTGACGCTGGAATTGTCCGTTTACGGCGTTG
TTTTGTCGTTGCTGTTCCGCCCTGCCCGTCCCGTGGTAACGGCATAACCGCATCCGCCCTTCTACGCATTGGCGCGCGCTATAT
CGAGCTGTCGCGCAATACGCCCTGCTGATCCAATTGTTTTCCTATATTACGCTCTGCCGAAATGGGCATCAAATGGGACGGT
TTCACCTGCCGCGTAATCGCGCTGGTTTTCTTGGGCGCAAGCTATATGGCGGAAGCTGTCCGCCCGGCATCCTCGCGCTCCCA
AAGGGCAGGTCGGAGCGGGCAAGCAATCGGTTTGAGCCGCTTCAAGTGTTCCGCTATGTGAATTGCCGAGGTTTGGGCGGT
CGCCGTTCCCGCCATCGCGCAAATATATTGTTTTTAATGAAAGAAACATCCGCTCGTCAGCACGGTCGGCATTCGGGAATTGTTA
TTTGTTACAAAGACGTCATCGGTATGGACTACAAACCAATGAAGCCTTGTTCTGCTGTTTGGCGCTTATTTGATTATCCTGC
TGCCTGTTTCTTGTGTTGGCGCGCGGATTGAAAACCGGTACGGAGTCCGAAATATGGCGTT

SEQ ID 226

MNWPYLIDAVPKFADAAKLTLLELSVYGVVLSLLFGLPVAVVTAYRIRPFYALARAYIELSRNTPLLIQLFFLYYGLPKMGIKWDG
FTCGVIALVFLGASYMAEAVRAGILAVPKQVQVAGKAIGLSRFQVFRYVLEPQVWAVVPAIGANILFLMKETSVVSTVGIAELL
FVTKDVIQMDYKTNELFLLFAAYLIILLFVSLARRIENRVSARKYGV

SEQ ID 227

TTGGGCGAAGGCTGCTCTTAACGGCACAATTTCTTTAATCTCTGTTGCGGCTTCTTGCGTATTGGGCACGCTGTTCCGCTTGG
TTTTGCGTTCCGCGCAACCGGCTTGTCCGCTTTGTCCGACGGTTTATCTCGAAACCATCCGAATCGTCCCGATTTTGGTGTGGCT
GTTCCGGCTGTATTTCCGCTATCCGTCTGGACAGGCATCCACATCGCGCGATTTTGGGTCTGCGTCTGGGTATTTCCCTGTGG
GGCGTTGCCGAAATGGGCGACTTGGTGCGCGCGCGCACTGGAATCGATTGAAAAACACAGGTCGAATCGGGTCTTGGCGCCGGCT
TGAGCCGGGGCGAGGTATTCGCTGTCATCGAGCTGCCGCAAGCATCCGCCGCGTATTGCCCGCGCGGTCAACCTGTTACGCG
CATGATCAAAACAGCTCGCTCGCTGGCTTATCGCGCTGATCGAAGTCGTCAAAGTCGGGCAGCAAATTATTGAAAACTCGTTG
CTGACGCAGCCCAATGCTTCATTTTGGGTTTACGGCTGATTTTTATGCTGATTTCTCTGTTGCTGGCGCTATCTCTACTGG
CGGCAAACTTGAACAAAATGGGAACAC

SEQ ID 228

LGEGLLLTAQISLISVAASCVLGTLFGLVLRNRNLVRVFRFYLETIRIVPILVWLFGLYFGLSVWTGIHIGGFVWVWVSLW
GVAEMGDLVRGALESIEKHQVESGLAPGLSRGQVFRCIELPQSIRRVLPGAVNLFTRMIKTSSLANLIGVIEVVVKVQQIISNL
LTQPNASFVWYGLIFMLYFFCCWPLSLLAAKLEBQKWEH

SEQ ID 229

ATGAAATTGAACGCCAACTCAAAGCCCTTTTGCGCTTCCGCCGCCATCGCCGTCGGTCTGACCGCTTCCGGGGCGGCTCCGGCG
ATGCCCAATCTTCAAAAGCAGCGGTGCGGCAACCGCTTGCCGCCATCAAAGAAAAGCGTTATCCGCATCGCGCTATTCCGCGA
CAAACCCCGTTCCGCTATGTTGACGCAACCGGCAAAACCGGCTTTGACGTTGAAATCGCAAGACCTGGCCGCAAGACCTG
TCGGCAGCCCGCAGCAAAAGTCGAATTCGTCTGACCGAGGCGCGCAACCGCGCTCGAATACGTCCGTTCCGGCAAAGTCGACCTCA
TCCTCGCCAACTTTACCCAAACCCCGAACCGCGCGAAGCGCTCGATTTCGCCGATCCTTACATGAAAGTGGCGTTGGCGGTGGT
TTCCCCCAAAACAAACCGATTACCGACATGGCGCAATTGAAAGACCAACCTGCTGGTCAACAAAGGCACACCCCGGACGCT
TTCTTACCAAAAGCCATCCCGAAGTCAAGCTGTTGAAATTCGACCAAAACACTGAAACCTTCGACGCGCTGAAAGACGGTCCGG
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TCCTGCCGAATTTATCGCCCCCGCGTTCAAAAGGCAACCGGCACTCTGAACTGGGTCAACGGCGGAATCGCCGCCATGAAA
AAGACGGCGCTCGAAGCGCCTATGAAAAACCTCTTGCCCGTGTATGGCGAGAAAGTCAAACCGGAAGCATTTGTTGGCCG
AA

SEQ ID 230

MKLNALKALLASAAIAVGLTACGGGSGDAQSSQSSGAATVAAIKEKGVIRIGVFGDKPPFGYVDANGKNQGFVLEIAKDLAKDL
LGSPDKVEFVLTEANRVEYVRSGKVDLILANFTQPERAEAVDFADPYMKVALGVVSPKNKPIIDMAQLKDQTLVLNKGTTADA
FFTKSHPEVKLLKFDQNTETFDALKDGRGVALAHDNALLWAKENPNFEVAIGNLGPREFIAPAVQKGNADLLNWNNGEIAAMK
KDGRLLKAAAYEKTLLPVYGEKVKPEALLAE

SEQ ID 231

ATGAGATTAAACGAAATATCCTTATAACTCCATAAGAGAGTTAGAAGACTATTTAATAACACCTATCAAAAATATATTATTCTAC
AAGAGGGAGGAAAAGAGATTTATCGATGTTTTATTCTTTCTTTTATAAAGAATTCAATATAGGTATTGGATTAGCTGTTTCTTG
CATAAGTATTTCCCAAAAGTATTATGCTTGATGATAAAATATTTTATCGGATTTGATTCAGTCGTTTTTGTATTTCCTATA
CAAAATTCAAAAGTTAACATACTAATAGATGGAATAGTTTTTATGATATTATTATTGGATAATCAAAAAATTTGTATTATTC
ATGAGTTGGGTGCAATTATTACAGATAAAATTTAATAAGAGAGAATTCAGTATCTACCGATATAATATCAGACTGGGAAATAGA
TAAAGTTAATAAGTTAATCATATTAAAGAGTTAGACTCTGAAAAATAATTTCTCTAAATTATGAT

SEQ ID 232

MRLTKYPYNSIRELEDYLINTYQKYIILQEGGKEYRCFILSFYKEFNIGIGLAVSCISIPPKVLMDDKNIFIGFDSVVFCSIS
QNSKVNILNIDGIVFDIYLLDNQKICIIHELGAIIIDKNLIRENSVSTDIISDWEIDKVNKLIILKELDSEKIIISLNYD

SEQ ID 233

ATGGTTGCGCTATGCTTTCTTATTTTGTGTTGTAACGCGCGCGGTGCTGCTGATTGTCAGGTCGCACTACCGCTGGACGTATTTTT
TCGCGTCGGCGCTGTTTGTCTTTTGGCGGGCGGTATGCTGATGTTGACGGCGCAGTGGCAGCGCGCTTGAATTTCCGTTCCGT
CTGGTTTGTGGTGTGATACTGTTCCACAGGCTGAAAATCCATTATACAAACAGCCGCTGTTGATTTCGCACTTTTTGCTGATT
GCCGACTGGCGGAATTGGGAAACGCTGTTTCATTATAAGGAAGCGGTTATCGGTATGGCGGGGCTGCTGGCTTTGGCGGGGATG
CGGTTTTCGGCTGGAGCGGTGCGGATTTTGGGTATGCCGTGGCGTTGGGCGGGCGCGGTTCTGTTTGGCGGGCGGTTCCGTGTC

GGTGCGGCATTTTTCACGACCCCGCGCGGTAAAGACGTGGCTGGATTTCGCTGCCGGACGACGGGCGCGACGTGTTTTTGAAC
CTGCCGATGTCCTGTGCGGCGGTGTTTTTCCAAGTACCCGTGTTTCGAGGGCGACGGGGAAGCGTTTGCAGGCAGATGCCGTCTG
AAACCCGCGCGTACGGCATGTCGGATGAAAAGCCGATATTGTCTGTTACCTGATGGAATCGACGCTCGATCCGCACTGTTTCGA
TTTTTGCCGCCGCCAAAATTCGGATTGAAAATGTTTCGACGGCAGGAAGATACTGTATTTTCTCACCTTTTGGCGGTGCATACT
TTCGGCGCGCAACGTGGAAGTCCGAATTTGCGTTTTTGGCGGGTGTTCGCTCCACAGATTTCGGCGCGTTGGCAAGCGCGGTGT
TTTATTGCGTCTGATCCGCAATTTGACAGCCGGTTTTGTCCGCAACCTGCGCGAACACGGTTATTTTTCGCTGGCGCTCTCGCGGT
TACCAAGGGCACTACAATGCCAAGGCAGCATATGACCATTTTCGGCTTTAATCTGATGTTCCAGCCGCAAGATTGGGCTATCCC
GCGCGCATGGGCAAAACCTGTGGCAGATTTCCAGTGAGGAAATGATGCAGTATGCGCGGATGATTCTCGAAAACGCCATCCCG
ATTTGGAAAACGTGCGGCGCCGATGTTTCGTATATGTCTGACCATGAAGGAGCACGGGCCGTATCGGACGGATACCGACAATGT
GTTTGATTTGGATGCGCCCGATTGAAATGCGAAAACCGTATCCGCGCTTAACGACTACATCGGGCGCATTGCCGATTGGACAAA
GCGGTGGAAGTTTCGACCGTTATCTGCACGAACGCGCAAAACCTTTGTTTTCGGTTATTTTCGGCGATCATCAGGTACCGTTTG
AGGGCGTGTCCGTCAGGAAGAAATGGGATTACGCTCAGCCGGATTATGTAACGCAGTTTGCCTGTCAGGAGCAATATTGCCGGCGG
ATTCGTACAGCGCGAGGATTTCCTCGACCTTGCCTTTGCAGGCGCGGTACTGATGGAGCGCGTGGTTTGAAGCCAAAGACGGC
TTCATGCGTGCAGAAATATGGCGATGCGCGGTTTGTGCGCGGAGGGTTGAAGACTGCCCGAACCGGGAGTTGGTCGGAAATTACC
GCAACTATCTGTACGACGTTTTGAAAATTGCCCGT

SEQ ID 234

MVAYFLFLFVTAAVLLIVRSHRWTFYFASALFVFLAGGMLMLTAQWQALNFASVWFVVLILFHLRLKIHYKQPLLI.SDFLLI
ADWRNWETLPHYKEAVIGMAGLLALAGYAVFGWSGADSLGMPWRWAGAVLFAAAFVSVRHF.SKHPGA VKTWLDSL.PDDGRDVF LN
LPMSCRAVFFQVVFEGDGEAFARQMPSETRPYGMSDEKPDIVVTLMBSTLDPHCDFDFAAAKIPDLKMFGRQEDTVFSSPLRVHT
FGGATWKSEFAFLAGVPSTDFGALASGVFYSVVPHLQTGFVRNLREHGYFCVALSPFTKGNYNAAAYDHF.GFNLMFQPD LGYP
APMGKNLWHISSEMMQYARMILEKRHPDLENVRQPMFVYVLT.MKEHGPYRTD.DNVFDL.DAPDLNARTVSALNDYIGRIADLDK
AVESFDRLYHERGKPFVFGYFGDHQVFPFEGVSVRKWDYAQPDYVTFQFAVRSNIAGGFVQRQDFLDLAFAGGVLM.EAAGLEAKDG
FMRANMAMRGLCGGLEDPCNRELVGNYRNYLYDVLKIAR

SEQ ID 235

ATGAAGCACGCTCCGATTATCCTCCTGCTTACCGCTTCGTCCGCGCCCTACTTTCGGCGGGCTGCACCGCCCTTCCCTCTGACC
GGCGCGCGCTTCGCACCCCTGCCGAAAAGCGCGCCCATCAACCCGCCAACCCATACAGCCGCGCCCTTCAGGCACGCGGACGG
CGCATTCAGCACCCGCGCCTCAAACGGCGCGCTCTTGAAAAGCATCGTCAAAAACGGCGGTTCGACCGCTTTGTTCGATTTTAC
CATCCAAACGGCAACTGCATTTCGCACACGCGCGTTGAAAACGGCGTGGCGCAAGGCTATACCGAACAGGGCATATTGCGGACGG
GCATCCTGTACCGGACGGGCATATCGTCCGAGCGCAAACTTTGGATGCGTCCGGCAAGGTGGAACGGCAATGGCAGCGG

SEQ ID 236

MKHAPI.I.L.L.LTASSAALLSAGCTALPSDRPPLRTL.PKSAPIQ.PANFYSRPPSGT.PDGA.FSTRASNGRVLKSIVKNGV.FDR.FVDIY
HPNGKLHSHT.PVENGA.QGYTE.QGILRTRILYRDGHIVRAQTL.DASGKVEREWQP

SEQ ID 237

GTGTCCATCCCCACCGCCACGCCGTGCCCCGCGCGGAGGTAACGTTATCAAGCGATAACGGCAATATCGAAAACATCAACACCG
CCGGCGCGGAAGCGCATCCGACGCGCGGAGCCGACGAGCGCTCGTTCGATGCGCGCCCGCAAAACACATCCGGCATTTCCAT
TCGGCAGCGGGAAGTAGAAAAAGACTATTTCGGCTATAAATCAAAAGAAACATCATTCATCTTCAAAACACCCGGCGCGCGCAA
TACGCCCTTTTCATCCTACGCCGACCCCATAAACGTCAGCTACTCTCCCCCGATTTCAAAATTTCCGACCGCCACGCGAGGCGAG
GGCTCGCCGACGGCAGCCGCATCTTTATCTGCTGCAGCGACTCCGGGGCTACTTCGTATGCGGAAATTACCAAAACAAGATTATAT
GAAATTTCGGGCGGTGATAGGTCTTAACGGCGAAATCGACCTCTTCGCGCGCGGCTTCCCGTCCGCAAAACGCGCCTCTGCG
TTCTCCTACGGCAGCAGCAGCCCGAAACCGCATTTGTCAAAGGTAATAATCACTTATCAGGTTTGGGGCATCCGCGTCAGAAACG
GGCAATTTGTTACTTCTCTTATACGCCCGCGAAAAGCGGTTCTTATTATGGGACACTTGCCAAATACCCCGCTCTCTTCTTTAT
CACCGCCAATTTCAACAGCAACACACTGGCAGGCAAAATCCTCGGCAACAGCGATTACGGGCGGGATGTGGATATTCAAACGCA
ACGATTACCGGTCCGACCTTTTCCGGCGATGCCACGTCGCGCGGGAAGCGGCAAAATGGAAGGCAAGTTTTTGGCAAGTTTCG
CCAGCACCCGACGAGCGAAGTCAGCATAGGCGCGCAAAATCACTTTTGAAGCGGACCGCTCCCTCGATACCGTATTTCGGCGGTG
GAGTTATGAAAAAAACTTGATGACACCAGTCAAGATACCAACCACCTTACTAAACAA

SEQ ID 238

VSIPTATPLPAGEVTLSSDNGNIENINTAGAGSASDAPSRSRSLDAPQNTSGISIRQREVEKDYFYKSKETSFIKFTPGGAQ
YALSSYADPITVSYSSPDFKIPDRHAGQRLADGSRIFCCSDSGATSYAETKQDYMKFGAWIGPNGEIDL.FAGGF.PVGKTPPPA
FSYGSSTPETALSKGKITVQVWGI.RVRNGQFVTSSTYPKSGSYGTLANTFVLSF.I.TANFN.SNTLAGKILGNSDYGP.DVDI.QNA
TITGPTFSGDATSGGKSGKLEBKFFGKFASTRSEVSIGGKI.TFDGDRSLD.VFVGVS.YEKKLDDT.SQDINH.LTKQ

SEQ ID 239

TTGCCGCAATTTGCGGGGGGGGGGGGGTAATATCCGCTTTATAGACGTAAACCCGAAGATTTCGCGCGCTTCCCTTAAACA
TCAGGCACATTTCCATTACGACTTATGCCCAGCTGAAATTTGGCGGAATACATTGCCGATGCGACAAAGTCCGTATCTGGATAC
GGACGATTTGGTCAGGACCGGCTGAAGCCCTTATGGGATACCGATTGGGCGGTAAGTGGGTCGCGCGGTGCATCGATTGTTT
GTCGAAAGGCAGGAAGGATACAAACAAAAAATCGGTATGGCGGACGGAGAATATTATTTCAATGCGCGGTATGCTGATCAACC
TGAAAAGTGGCGGCGCACGATATTTCAAAATGTCCTGCAATGGGTGGAACAATACAAAGGACGTGATGCAATATCAGGATCA
GGACATTTTGAACCGGCTGTTTAAAGCGGGGTGTGTTATGCGAACAGCCGTTTCAACTTTATGCCGACCAATTATGCCTTTATG
GCGAACGGGTTTTCGCTCCCGCCATACCGACCCGCTTTACCTCGACCGTACCAATACGGCGATGCCCGTCGCGGTACGCCATTAT
GCGGCTCGGCAAGCCGTGGCACAGGACTGCACCGTTTGGGGTCCGGAACGTTTACAGAGTTGGCGCGGACGCTGACGACCGT
TCCCGAAGAAATGGCGCGGCAAACTTGCCTCCCGCGGACAAAGCGTATGCTTCAAAGATGGCGCAAAAGCTGTCTGCCAGATT
TTACGCAAGATTAT

SEQ ID 240

LPPICGGGGNI.RFIDVNPEDFAGFPLNIRHISITTYARLKLGEYIADCDKVLVLDTDVLVRDGLKPLWDTDLGGN.WVGACIDLF
VERQEGYKQKIGMADGEYFNAGVLLINLKKWRRHIDFKMSCEWVEQYKQVMDQDQDILNGLFKGGVCYANSRNFNFMPTNYAFM
ANGFASRHDTPLYLDRTNTAMPVAVSHYCGSAKPWHRDCTVWGAERFTELAGSLTTVPEWRGKLAVPPTKRMLQRWRKLSARF
LRKIY

SEQ ID 241

ATGATTTTTCGCAGACCCGCTTACTTTCTTTCCAATGACGGTTTCAGTTGTCAAAACGGGCAAATGGTTTCCGTCAATAAGGGCA
ACTGGGATAAATCCAAAGGAATGGCGGCAGATTGGAATTTTACGAAGAATGGCTCCGACTGTGTACGCCCTATTAAAAACCAA
CGGCACAATTTGGGTTTGCAGCAGATTTTATAATATCTATTTAATCGGCTACCTGATGCAACCGCTCGGCTACCATATTTTGAAC
AATATTACTTGGGAAAAACCAATCCTCCCCCTAATTTGTCTCGCGTTCTTTTACCCATTCGACAGAAACAATCTTATGGGCAA
AGAAAAATAAAAAAGCCAAACATACGTTTCATTATGAAATGATGAAAGCACAAAATAATGGCAAACAGATGAAATGTGTTGGAC
ATTTCGACCTCCAAATAAAACCGAAAAACATTTCGGCAACATCCGACACAAAAACACTCCCTTACTTGAACGCTGCATACTA
TCGGCTTCAAATATCGGAGATTAAATTTTGACCTTTTATGGGAGCGGCACAACAGGCGTTGCCGCTTAAACATGGTCGGA
GATTTTGGCGTTGCGAACTGGAAGAAGATTTTGAAT

SEQ ID 242

MIFADPPYFLSNDGFSQNGQMVSVNKGWDRSKGMAADLEFYEEWLRLCYALLKPNGTIWVCGTFHNTYLYGYLMQTVGYHILN
NITWEKPNPPNLSRFFTHSTETILWAKKNKAKHTFHYEMMKQNNGRQMKCVWTFAPPNKTEKTFGKHPTQKPLPFLERICIL
SASNIGDLIFDPMGSGTTGVAALKHGRRCGCELEEDFLN

SEQ ID 243

ATGAAATACACAGCCGCACTCTGACTTTTCTTTTAACTGCCTGCATGAACCCGAACGATGCGTTTTCACAAAACCGGCGTTATC
AAATGCCGAGGCGCAATTGAACGGTTCAAACGCCGTTTTCATTACGGTTATTCACAAAATCCCGATCATGATTTATTTGGTCGA
CCAAGTCCGCGTCCCGGACCGGTACAGGGCTTCATTTCGCGGGGATGGATAGCGAAGGAGCAAGGTTACCGCAAAAACGACTGC
GTACTGGAAAAAGCGGAAAGCGGGGTGTGACGTACTACACCTCGCATGCGGAAAAAGGATTCAACGGCACAGTTTCGTCTATCT
ATGTCGTGAATATGAAAAACGACAAAGGCTACGTCAAAGTTTACCGGGCATGAATAAGCCGAATCAGGAAGAGTTAACCAAATT
GTTGCCGATTTGAATAAGTTTACCCT

SEQ ID 244

MKYTAALLTFLLTACMNPNDAFFQNRRYQMPAQNGSNVAFHYGYSONPDHDLVDQVRVPDAYRASFARDWIAKEQGYRKNDK
VLEKAESEGGVITYTCDAEKGFNGTRFVIYVNMKNKDGIVKVRGMNKPNEELTKLVADLNKFPY

SEQ ID 245

ATGGAAAGCAACCTGCAGAAAAACCGAGCGTTTGATCCGCGAAATCAACCGCTGCACGCACAATATTTCGAGGATTATTTTGAAA
CCGGCAAGGTGCGGAAAAATCAATTGTAGCCACAGCTCAAAAACGTTCCGACCGAACATATTTGTCTTATCGCCTTAATTTGCA
CGAAGCAGTTAACGATTATTTAGCCTTTGCCGATACGCGCGCATAGACTTTTCTACCGCGTGAAAACCGCAGAAAGCATACAT
GATAAAATCAACCGCTATCTGGCAGCGCGCACCAATATCCGACCAACAACATCTGAACGATATTTTCGGCGCGCGGCTGATTT
GGCGCTCTGAAACAGTCCGCGGATTTTAGAAAACTTGACGGCTGAAAAACAGAAATACGGCTTGAAAAACGGTATTTGCGCGA
TGCCGCGCGCTATATCGGCATACACATTTATTTCAAAAACAGCAGCAATTTCTACTATCCGTGGGAATTCAGGTTTGGGATGAA
AAAGATGCCAAAGCCAATATTGAAAACCATATGGCGTACAAACGGAATTTCTGTGCGT

SEQ ID 246

MESNLQKTERLIREINRLHAQYSQDYFETGKVRKINLSHTLKNVPTZHLISYRLNLHEAVNDYLAFAADTRGIDFFYRVKTAESIH
DKINRYLARGTQYPTNNILNDIFGARLIWSETVAGILEKLDGWKTEYGLKNWYLRDAGGYIGIHIFKNSSNFYYPWELQVWDE
KDAKANLENHMYKRNFR

SEQ ID 247

ATGCGTAACACCGTAGGATTGGACATATCCAAGCTGACATTTGACGCAACGGCCATGGTCCGCAAAACGGAGCATTTCGGCAAAGT
TTGACAAACGATTCAAAGGTTTAGATCAGTTTTCGGACCGGTTGAAAAGCTTGGGATATCAGAACTGTCATATCTGCATGGAGGC
AACCGGCAGTTATTTATGAAGAAGTTGCCGACTACTTCGCGCAGTATTACAGCGTTTACGTAGTGAACCCGCTGAAAAATAAGCAAG
TATGCAGAAAGCAGGTTCAAGCGAACCAAAACAGACAAACAGGATGCAAAACTGATAGCGCAGTATTGCCGCGTCCGCGCAGGAAA
CGGAGCTTGTAAGAGGCAGAAAGCTACGGACGAGCAATACAGGCTTTACGGATGACCGCAGCATACCGCGCAATCAAAGCGA
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GAACAGCTTGAAGTTTAAAGGAGAAGATAAAAGAGCAGACGGAGAACCTTAACGCAAGGAAGCGGTGAAGCGCTCTTGAAACCA
TACCGGCAATAGGCAGAAATGACCGCAGCGTATTGTTTCATCATCTAACATCTTCGAAATTTGAAACATCAAACAAATTTGCAGC
ATTTCGAGGCTTAAGCCCGCAACAAAAGAATCCGGGACAAGCGTAAGGGGAAAAGGCAAACTGACCAAGTTTGGCAACAGGAAA
TTACGCGCCGCTCTGTTTATGCGCGCCATGGTCGCATACCGGATAAGGGCATTTCGCCGACTTCATCAAAGGCTGGAAGAAAAGA
AGAAGCCTAAAAAGTCATCATCGCAGCATTTGATGCGTAAACTCGCGCTATTGCGTATCACGTACATAAGAAAGGCGGAGATTA
CGATCCATCGCGTTACAAATCGGCG

SEQ ID 248

MRNTVGLDLSKLTFDATAMVGKTEHSAKFNDNSKGLDQFSDRLKSLGYQLNHICMEATGSYEEVADYFAQYYSVYVNNPLKISK
YAESRFKRTKTDKQDAKLIQYCRSAQESLVKQKPTDEQYRLSRMTAAYAQIKSECAAMKNRHHAAKDEEAAKAYAEI IKAMN
EQLEVLKEKIKEQTEKPNCKEGVKRLETIPAI GRMTAAVLPHHLTSSKFETSNKFAAFAGLSPQOKESGTSVRGKGLTKFGNKR
LRAVLFMPAMVAYRIRAFPDFIKRLEKKKPKKVI IALMRKLAVIAYHVHKKGGDYDPSRYKSA

SEQ ID 249

ATGTTGCGAACCTACTTGAACCAATTGACCCCTCCCGAATTAGCTGATTCTGTAAAAATACCGTTGATGGTTTATGAAAAAAT
TGTCACAAACCGAGCCGAAAAATCGCCCAAAATGTTTTATTGCTGGGCAATGTTCAAAGTGGCAAAACGGCACAGGTTTGGGTGT
ATTAAGTGGCTGGCTGATGATGGCGACCACAAAGTTTTTTTGTATCTTACTACTGACAGCGTAGATTACAGGATCAAACAGTC
AAACGAGCCAAAGCCAATCTGAAAACTTTATCGTATTGTCGAAAGCTGACGACCGAAGTTTATGGAAGTAATGAAGGCAGAGA
ACCCCATCTTGGTCGTGATTAAAAAGAATGCCCGTGTATTGAAACGTTGGCGTAATTTGTTTGCCAGTCAAAGTAGCCTGAAAGG
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ATCAATAAATGCTAAACGACATCAAAAATCTCTGTGTCAAAGCCTGTTTATCCAGTTGATGACCGCCTCAATCGCTTTTAT
TACAACATGAAGAATCTGATTGGCAACCTGAATTTATCCACTTCTTTGAAGCAGGCGAAAAATACATCGGCGGCAACTTTGTCTT
TTCTGATCCACCAAGCTATATAGTTTCGTTTTATTGATAGCGAATTGGATGATATGAAAGACGAGAGTGGTGAATTTGCCGAAGGA
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GAAAAATTGACAGCACTTTTAGAGAATAAAACAAATCTCTACTCTTGTGCTTAACTCGCAGACAGAAACAGATTTTGACTTAGAAA
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TGCCAAAAAACCGAATGCAGATACTTTCTGGCAACATTCGCGTATTTTGGATATGACCGCGATAAATCATTATTACGGCTTTAT
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ATATTCAGGTTATTTATCCGAAAAATATCAATCAACTCGAAAAATGTATTGAAATTCGATATCAATCAAATTTGGGTGG
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CAATCTGATTATATCAATAGATATAGAAGATTTATCTTGGTCTAGATAAATGGGTGCTTATGTTCCAGATGACTGGAATA
AGGAAAAATTTATGCTGGTGTAGAAGCATTAAAGCACAACGTCGAAGTTTAAACCTATGTTTGGATCAAAACCGGACGTA
ACTTCTCGAGCAACCGGCACAATGCTTTGGAAGACGACCGTAAATAGGAGAAAAATATCCCAATGATTTATCTTACGCTT
TATCAAGTAGTAGGAAATAAGACAAAGTTGGCAGGGAAGATTTTGGTTACCCAATATCAAGCTACCACACAATGGCTTGG
TGTACCAAAGTGCAAAA

SEQ ID 250

MLRTVLNQLTPPELADSVKNTVDGFMEKLSQTEPKIAQNVLLGNVQSGKTAQVLGVLSALADDGDHVKVFLYLTTSVDLQDQTV
KRKANLNKFNIVLSEADDRSFMEVMKAENPILVVIKNARVLKRWNLASFQSSLLKGYPLVIVDDEADAASLNTNSDKPAKDA
INKLLNDIKNSCCQSLFIQLTATPQSLLLQHEESDWQPEFIHFPEAGEKYIGGNFVFSDFPSYIVRFIDSELDMDKDESGEIAEG
AKQALLSFLITCAEFALCDKANCNFALHPYKIQDHQAFSKKIQAFLNDLVQAVMNGEDLAGSFKESYLDLQKTKPDIIHFDEY
EKLTALENKQISTLVNSQTETDFDLERGFNIIGGNVIGRGLTIPKLOTVYYSRTAKKPNADTFWQHSRIFGYDRDKSLRLY
IPFDVYVFFVQLNQANNLIIGQAKNSGGNIQVIYPKNINPTRKNVLFKFSINQIVGGVNYFPLHPNEDNLSEINKILPSILKDEI
QSDLYQIDIEDLFLVLDKLGRYVPDDWNKEKFIAGVEALKAQRPSPKTYVLIKTGRKLSRATGTMLESDDRKLGKEYPNDLFLTL
YQVVGNKDKGWQKDFWLPNIKLPNGLVYQSAK

SEQ ID 251

ATGAATACAGTTTTTTTCCAATATCGCCAATGCCAAATCACTGAAAAATCTCTTAATGCGGTTTGGATGGATTATTTAAATCAG
CGGATGAAGTGTGTATGGCGACAGGTTATGTATCTAATGACGAGTGGTTGAGTTACATAAAATTTGGAGCTAAACGATCATAT
TCAAAAAATAGATTTATGGTCGGAATGCATTATTTGGAGAGTTTATAGCCATTATACAATATGACAGCTTATGTAACATAAATGAT
TTTTTGGCGACATGAGAAAAGAGGAGCGCTATGTTTCCCTTTTGTGAAATTTACGCGCAAAATGTATCTCTTAAATATATC
AAAAATCAATGGATTAAATGGTCTGCTAACTTAACGTGTTTTTGGGATAGCACGGAACGTACTTATGAACTATGTTGCATTT
GAACGGTAAGCCTGCACAGATTTTGCAGGCAGATATTCAAGTACTATTCATAAGCTAGGCAAAATATCCAAGAAGTTGAAAGA
CCAAGTAAATTTATTGAACATAATAGCCATTTAGAAAATTTGTTTGGGTGTTTCAAGAAATGACACGAGAACAGATTCCGCAATAT
TGGCCCAACGTCAGAAATATCATTTCTCAATTCAGCTAAACCGAAGAAAAAGTAATTTGAATGATTTTTTGGAGAAGGTCG
ACGAGATAAACGAGGGTTTGTCAAACACGACCTTGGTATGAAGTAGAGTTGATTGTATCCAAAGACATCACTTCCAGAAGGG
TATCCGGTTCTGAAGTCTTTTACAGTTATTACCGATGATGGTTGGCAATTTCAATGCAAGACATCGGGGATTACTCCAAAAC
TCCGCTCAGAAAATGATTTAAAGACACTTGGTAAATGGATTAAAGGTCGTTTGGAAAGTCATGGCTGCCTGCAAAATAACGAGAA
GATTACGATGAAACCCACGCGAATACGGTAACGATCATTTTGAGTTACGTTCAACCGATAATCCTGATGTTTGGCTGCTCTCA
TTTAAGGGGAAAAAC

SEQ ID 252

MNTVFSNIANAKITERSLNAVWMDLFSKSADEVLMATGYVSNDAVVELHKILELNDHIQKIDLLVGMHYLEGFSLQYDSLCKLND
FLRHEKRGAVYVSPFVKFHGKMSYFNKYQKINGLIGSANLTCFWDSTERTYETMLHLNGKPAQILQADIQSTIHLKGNIEVER
PSKFIENSHLENCLGVQKIAPEQIRQLFAQTSEYHFSIPAKTEESNLNVFFEGERRDKRGFVKPRPWYEVLELIVSKDITSQEG
YFVLKSFTVITDDGWQFQCKTSGDYSKNFRSENDLKLTKWKIKGRLESHGLQNNKITHETLREYGNDFELRSTNDPVDVWLLS
FKGN

SEQ ID 253

ATGACAACAGAAAAATAACGCTTTTGAACACGCCAAACACATCGACGAAACAGGCAATGAATATTGGTCGGCGCGCACCTTGCAGC
AAATCTTGAATATTTCCGAATGGCGCAATTTCAAACGGGCCATTGATAAGCCATAACCGCTTGCAGAACATCAGGAAATGACAA
AAATCATCATTTTGTGTAACCAACAAATGATAGCCCTTGGGAAAGGCGGCGAGCGCGAAGTGGCGGATTACCGCTTTCCCGC
TATGCCTGCTACCTGATTGTGCAAAACGCGCATCCGTCCAAAGCGTCAATTGCGCGAGGGCAACCTACTTTGCCGTGCAAGCCC
GCCGCAAGAGCTGCAAGACGAGGCGAGCATTAGGAGTTTGGGCGAAGACAAACACGCTGCTGCTTGCAGGCAGCTGCGCGA
ACACAATACCGACCTTGGCGCGCGAGCAGGATCGAGGCTAGAGAAACCCGTTGAGTAGCGCTTCCAAAACACGCGTAT
CGGGGCTATACGAGGACTGGACAAGCAGGGCATACACAGCCGCAAGGCTTGAAGAAAAGCCAGAGAATCTAGACCACATGA
ACGCCAGCGAACCGGCTGCCAATCTGTTTCCGCCACGCAAAACGAAAGAACTACGCCGCAAAACATCCAAGCAAAACACA
GGCAAACCGGCTGCATTTCGAAGTCGGACAAAAGTGCGCCAAACCATTTGAAGAACTGGCGGCATCATGCCTGAAAACAGCCC
GTACCCGAGAAAAGCATCAACAGCTTGAGAACGAAGAACAGAAAAGGCTTGGCGCAACCGAACAGCATCAAAACGGCAAAAAA

SEQ ID 254

MTTENNAFENAKHIDETGNEYWSARTLQOILEYSEWRNFQRAIDKAITACETSGNDKNHVFETNMIALGKGGQREVADYRLSR
YACYLIVQNGDPSKSVIAAGQTYFAVQARRQELQDEAAFRSLGEDKQRLLLRRQLREHNTDLAAAKDAGVEKPFVEYAVFQNHGY
RGLYGGLDKQGIHSRKLKKSQRILDHMNASEPAANLFRATQTEELRRKNIQKQTQANRVHFEVQKVRQTIEELGGIMPENQF
VPEKSIKQLENEEQKRLAATEQHONGKK

SEQ ID 255

ATGAAAGATTTATGTGCTCGTCCCCATCATTCCTGCTGTTTTCTGTATGCTTGGCGTTACCTGCCCTACCGGTTAATCGGCTTTT
TCGCACTGCGTAACCGAACCTTAAGCCGCGCGCCAAACCGTTATGGAAGCCGCGCGCGGCTGCGTCTCATTTCCGTCAATTCG
CCCCATTTTTGTATCCGACAAGCCGACGAACCTATTGCCATCGCGTTAACCGCTTGGCGGCTGCGGTTTTCTATGTTGTTT
ACCGTATTGATAGGGGTCGGCTCGTCAGGCATCTCGGATGTTGATGGCA

SEQ ID 256

MKDLLSSPSFLLFSCMLAVTCPTRLIGFFALRNRTLSRRAQTVMEAAPGCVLISVIAPYFVSDKPHELIALTAFACRFSMLP
TVLIGVSSGISGWLMA

SEQ ID 257

ATGGATAAAGAGAAAGTCTTAGACAAAAATCAAGAAATGTTTGGCTTTGGGTGCGTTCGTAATGAACATGAAGCCGCACAGGCGT
TAAGGACGAGCGCAGGCTTTAATGGAAGTACAAAGTAAATGCCGAGGATATCGCCTTATCAAAAGTCTCCGAACAGAAAGCCGA
TCGGAATATGGCTTTTAAATGGCAGGCTGCAATGGGCGTTGCAATATGATTGCCGATATATTCGGGTGCAATCTTACCAA
CGCGGAAACAAATGATGTTTTACGGCATTTGGAATCGAGCGGAACCTCAGCCTATGCCTTTGATGTAGTCTATCGTCAGATTT
CCGCCGACCGCGCAATTTTTGAAACCTGCCGGCGGGAAGCCCTCGCACAGAACTATCTTGGCGACCGATTTTGGCGCGG

TTGGATTGCGAGCGCTTGGGAAACAGTCAAAAAATTTGAGATGTCAGATGAAGAAAAAGCCATTATGGACGGATACAAAAAGAAA
GAATATCCGGATATGGCCGAAGCAAGGACAAGAGATGCGAAATCGTCAATCCTACAAGGGTCAAAAAATGGAATATGAGGCATTAA
CCCGAGGAATGGAATCGGGTAAGCAAGTGAAGTTACACTATGCCGTGAACGGTACGGGCTTCGTAAAACAAATCGGAGGGCAAAC
A

SEQ ID 258

MDREKVLDRKIKCLALGRSVNEHEAAQALRQAQALMEKYKVNAEDIALSKVSEQKADRKMAFKLAGWQGVANMIADIFGCKSYQ
RGKTMMFYGIGNRAET SAYAFDVVYRQISADRRKFLKTCRAGKPSHRTYLADRFCGGWIASAWETVKKFEMSDEEKAIMDGYKKK
EYPDMAEARTDRDAKSSILQSGKMEYEALTRGMESGKQVKLHYAVNGTGFVKQIGGQT

SEQ ID 259

ATGGAAGCAAAATAAATTTGAAGTGAAAAGTTTGTGACACCTTATAAAAAGTCTTTGCAGGCATTGCTGCCGATTTCGAAGCGGCAA
TGGGTGTAAAACCGCGCCGACATTTCACCGAATTTGACGAACCGCAACATGAGCCGCAACCGCCGGTAACAGTTGCCGAGCAAAA
AGGTATCAACGACTTTGCCATCGGCAAGGAAGTCATCATCCGCACTTATTCGGCAGGCGTTTGGTTTGGTGTGTTGAAACAAAA
GCAGGCAATGAAGTGATTCTGACAAAAGCGCGCCGAATGTACAGCTGGTGGGCAAAGGAATCAATCAGCCTGTGAGGTGTCGCAC
GACACGGCATCAGGCAAGACGGCAGCCAAATTTGCGCGGAGCTTGATTCCGTATGGCTCGAGGCGATTGAGATTATCCAGTAAC
AGGCGGCGCGGCTGAATCAATCCGCACCGCGCTGGAGGTGCGCCAGTCA

SEQ ID 260

MEANKFEVKSLSDLIKVFAGIAADF EAAMGVKRAISTEFDEPQHEPQPPVTVAEQKGINDFAIKKEVIIRTYSAGVWFVGLKQK
AGNEVILTKARMYSWWAKESISLSGVARHGIRQDGSQICGELDSVWLEAIEIIPVTGGAABSIRTALEVAQS

SEQ ID 261

ATGATTCACTTAAATGTCCACTATTGCGATGAAATTATCCGCCATGCGGAAAATGACAAATACAGCCTGATAGGTATATTCCCCG
ATATATGCCATATTCGACACCGCAGGCCATTCTAGGCCGCTGTGCCTGTCTGTTTCATTTCCGCCGAAGGCATGGATATACA
GACTATGAAAACCGGTCAAATTTTCTGGAAATCGTCCGCAACGATGATGTAATCTCTGCACCTTGAGATTCCATCATATGACGGC
AGTGATACAGAAGAAAACGTGTCTATTCATGTACACCAAACAATCAGCGGACTACCCGTTTCAGACAACGACCGCATTTATGTAA
GAATGACAACACACAACCATATCTCTCCGAGAGCGCTCTTTGTCTTTTCTTTGGCTTCCTTACCCTCA

SEQ ID 262

MIHLNVHYCDEIIRHAENDKYSLIGIFPDICHIPTPQAILGRLCLSVSFSAEGMIDIQTMKTGQIFLEIVRNDVISALEIPSYDG
SDTEENVSFMLHQITISGLPVSDNDRIYVRMTTHNHILSESRPLSFSWLPYHS

SEQ ID 263

ATGGAGCTGACCGTCCACTTTAACGCCGAGCAGGATTTAGACCGCCTCTTTGAAAAAGACGAAGAAGCGGTTCGTTATCTCGAGA
ATGTCATTGCGATGATTACAGCGGACTCTGCTATTTTGTAGCGCTTATACAAAACAGATACCTCAGGGAATATGGCGAACCCTAT
AGGCCCGATTGACTTGGAAGTGAAACCCATATTTGTCTATTATGGGGAAGACATCAAAGTTTACCGCTCCGATTGACAGCGAA
GAAGCCGCCGATACAGAATAATTTACGCACCATGCCATGAAAACAGCCAAACGGCAGTATATCCGCCCATAGATATATTTGG
CTGTTGTAAACAAGAAGACAGACGAATTTGACTATCAGGCAGAACACCAATCACAAAACGGATTATCAAAGACTATGAAGAAT
GTACTCCAAC

SEQ ID 264

MELTVHFNAEQDLRLFEKDEEAVGYLENVIAMIQADSAIFDGLYKNRYFREYGEPIGPIDLEVKPILSLWGKDIKVLVRVDFSE
EAAGYRIIYAPCHEKQPNGTYIRRIDILAVVNKRTDEFDQAEHPITKRIKDYEELYSN

SEQ ID 265

ATGAATCAACAAGAATTTGAATTTATGAACGACTTGGCGCGTGCTTTTGAGCGTCGTTACCGTGATACGCGCAGCCTAAATAGAT
GTTTCAGTATCGAAGGCCGTTATATGGGGGAGGAAGCTTGCCCGCATAAGCCTGAAATCGGCTTGAGATACGGCGAAGATGCCAT
GTTTCTTACTTTACAGGCATGGCGGAAGGTGGATGCGCCGCAACAAGAGCCGTCCTGTTTTCGTTCCGCATCGGTGCGAAGTCG
CAGGCAGCTACGAGGAACGTTTGCAGGCTGAAATCAGGCGCGCGCGGAGGGGCCCCGTCATTTCGACAGCGGATTGCGGCTTGG
CCGCGTGGTATAGGGCGATACGGCAGGCGGCGAGGAATGATTTTGATTGCTGTTTGAGAAGGTT

SEQ ID 266

MNQEFEFMNDLARAFFERRYDRTRSLNRCFSIEGRYMGEACPHKPEIGLRYGEDAMFLTQAWAKVDAPOQEA VRISFGIGAKS
QAAYEERLQAEIRRRGEGPLHLQTDLGLAAWYRAIROAGNDFDLLEK

SEQ ID 267

ATGAGTAAAGCTATTAAACAAGTTAAATGAAAAGGAAAAGGAAAAAATACGCCTGCTTTTCGCACAAAGAGAAAAATTTATCGTA
TCTTGAAAAATCCGGAACAGGGATTACTCTCTCTACCGCTCTTTTAAAAAGTGCGGAACTTGTTTTCGATTGATTATGTTAA
TATGGGCGAGGTGGTTACTGAGAGGTCAGAACCTATACAGGACACGTTTAAAACTTGGCTCCACACCGGTTTATTTAGGGGGC
GGGAAATCCGTAGCAAATGAAAAACAGAAGAATGTTGCGTACGGAGAGTTGGTATTGACGAATTTAGGTTGATTGTTGTTAGGGA
ATATGAGAAGTATAGATTGCGCGTGGATAAAATAAACAGCGTGGAATGTTTCAAAGCAGCATCCGAATCAGCCAAAGCGGCAA
AAACAAACCGATTTCCTTTAATACCGTTTTTAAATCCGCAGTTATGGAAGAGGCTATATTGGTACTTTCCGATAAGAAG

SEQ ID 268

MSKAINKLEKEKEKIRLLFAQREKFYRILENPEQFTPPPTALLKSGETCFLLIDYVNMGEVVTERVRYTGTRLKLGSTPVYLGG
GKSVANEKQKNVAYGELVLTNFRLLIFVGNMRSIDLPLDKINSVECFQSSIRISQSGKNKPIFFNTVFNPQLWKEAILVLSDKK

SEQ ID 269

ATGAGCGGCACGAAACGCAAATTAGGCCGTCCGACAGATTACACGAAAGACATGGCCGATAAGATATGCGAAAAATCGCAAATG
GCAGAAGCCTACGTTCAATATGCGCCGAAGATGGTGTGCGCCCAATGAAACTATTTACCGTTGGTTGGAAGCTAATGAAGAATT
TCGCCACCAATACGCGCGCGGAGAGAAAAGCAGGCGGACTATTTGCTGAGAAATCATCCGAGATTGCGGATAGTGCACAAGCA
GAGAGCGCGCGGTTTCAAAGGCGAAATGACAGATAGATGCGCGAAAGTGGGCGGCTTCCAAGATTGCGCCGAAGAAATACGGCG
ACAAATCGGAGCTTGACGTTAAATCGGGCGATGGGAGCATGAGGGCGGCTGTACGGCTTGATGCTGAGGAATATCGCAAGATAGC
GGAAGATGTGTTGCGTAGGTT

SEQ ID 270

MSGTKRKLGRPTDYTKDMADKICEKIANGRSLRSICAEDGVPPMKTITRWLEANEFEFRHQYARAREKQADYFAEEIIBIADSAQA
ESAAVSKALQIDARKWAASKIAPKKYGDKSEL DVKSGDGSMAAVRLDAEEYRKIAEDVLRV

SEQ ID 271

ATGGGCAATGCGGTTTTCCTCCGAGTTCCCGGCTTGAAGTGGGGGCGGAAGAAACGCGCGGTATGGAGTACGGGGACGCAGAAAT
CGGCAAGCGCGCGTGTAGTTCCGAACCGCTACTACACCTACCGCAATGGCGGTTTTCGCTGTCTGAGGTATTCGGGACAAA
AGCGTCCGTAAACGAGTTGGAAAACTGGCGGGATTCTTCAACGCCCGCAAGGCGAGCTTTGAAAGTTTCCCTTACGAAGACCCG
GCCGACAAACCGTAAACCGACAGCCTGTGCGAAACCGGTGACGGGCGTTGCGCGTTATCAGCTTGTCCGTTTCGATGGGCGGAT
TTATCAGACCTGTGTGCGGCGTCAAGGAACGGCCCGCGTCAAGGTGCGGCGCACGGCGTTGGCGTACGGGCGCGATTACACCGT
TACCGACAAGGGCGTTTGGTTTCAACACGCCGCAACCGCGGGCCGCGCGATTACATGGACGGGCGGCTTTTATTTCCGCGTG
AGGTTTACGTCTGACACGGTGGATTTTGAAACGTTTGGGCGAGCTTGTGGGCGGCCAAAAGATTGAGTTTACGAGTGTGAAAC
TA

SEQ ID 272

MGNAVFPPEFPGLKWGRKKTAVWSTGTQKSASGREFRATAYTYPQWRPFLSFEVLRITKASVNELEKLAGFFNARKGSPFESFLYEDP
ADNAVTDQFVGNVTQGVARYQLVRSMMGGFIEPVSAVKERPAAVKVGGTALAYGRDYTVTDKGVLFVNTPPPPGRPIWTGGFYFRV
RFTSDTVDFENVLGLSLWAAKIEFTSVKL

SEQ ID 273

ATGCCGTCCGAAACGATTGAGGGCGCGGATCGTCGAAGAGGCGCGGTCTGGCTTGGCACGCCGTACCATCATCATGCAATGG
TCAAGGGCGCGGTTGATTGCGCGATGCTCTGGTCCGCTCTACGGGGCGGTGCGACTGCTTCCCGAAGGGTTCGACCCGCG
CCCTTACCCTCAAGATTGGCATCTGCACCGCGATTGCGAGCGTTATTTGGGGTTCGTCACGCAATTTGCGCGTGAACCGGAATCG
CCGACGGCGGGCGACATTGCAGTATGGCGTTTTCGGGCGGTGCTTTTCGCACGGCGGCATATTGGCGGGCGGGCGCAAGGTTATTC
ACAGCTACATCGGGCGCGGCGTGGTGTGCGACGACATCGGCCAAGCCGAACCTATCGGGCGCGGGTTCGGTTTTCATATTTTC
ATTT

SEQ ID 274

MPSETDLRARIVEEARSWLGTPTYHHAMVKGAGVDCAMLLVAVYGAUGLLPEGFDPFPYQDWHLHRDCERYLGFVTQFCRETES
PQAGDLIAVWRFRSFSHGGILAGGKVIHSYIGRGVSDDIGQAEIIGRGVRFPTFSF

SEQ ID 275

ATGCCTCGTTTCCCCCGCACTTTACCCCGCTGACCGCTGTCTGCTGTTGGCTGTACCGCTTCTCCGCCGCCGCACACGGCA
ATCACACCCATTGGGGCTATACCGGACACGACTCTCCCGAAAGCTGGGGCAATCTGTGAGAGAATTCGGTTTGTGCTCCACCGG
CAAAAACCAATCTCCGGTAAACATTACCGAAACCGTTTCCGGCAAACTGCCGCCCATCAAAGTCAATTACAAACCGAGTATGGTT
GACGTGGAAACAAACGGCCACACCATTCAGGTCAATTATCCCGAAGCGCGCAATACCTGACCGTGAACGGCCGCACCTATACCC
TGAAACAGTTCCACTTCCACGTGCGGAGCGAAAACCAATCAAAGCGCCGCACTTCCCGATGGAAGCTCACTTCGTCCACTTAGA
CGAAACAAACAGCCTTTAGTATTAGCCGTGCTGTATGAAGCCGGCAAAACCAACGGCCCGCTGTCTTCCATCTGGAACGTCATG
CCGATGACCGCAGGAAAAGTGAACTCAACCAACCGTTGACGCGATCCACCTACTGCCGAAACGGTTGAAATACTACCGCTTTG
CCGGTTCGTGACCACGCCCGCGTGCACAGAGGGCGTATCATGGTTGGTGTGAAAACCTATGACCACATCGACCAAGCGCAAGC
GGAAAAATTCACCCGCGCGCTCGGTTTCGGAACCAACCGCCCCGTACAGCCTCTGAATGCACGTGTAGTTATTGAA

SEQ ID 276

MPRFPRTLRLTAVLLLLACTAFSAAAHGNHHTHWGYTGHDSFESWGNLSEEFRLCSTGKNQSPVNITETVSGKLPAIKVNYKPSMV
DVENNGHTIQVNYPEGNTLTVNGRTYTLKQPHFHPVSENIQKRTFPMBAHFVHLDENKQPLVLAVLYEAGKTNGRLSSIWNVM
PMTAGKVKLNQPFDASTLLPKRLKYRFAGSLTTPPCTEGVSWLVLRKYDHDIDQAQAEKFTRAVGSENNRPVQPLNARVVIE

SEQ ID 277

TTGAAGACTGATACTGCCAGAATGAACAATCTGATTCCCGAACATTAGCCGCTATGCACATAGTGATAACCTGCAAATTGAAG
GCGGGCATCGTTGCTTTTCATTATCCTGCCAAGGTAGAGATACTTCCACATCCGTTACTATGGAGAGCCTTTTGATGGATTGAT
TACCGATACTGATAAGGCGCGGTAAAAATGTGGCGGTAGAAGCTGTAAGCGCGGATGAAATCGTATTGTTTGATGGGGCGGAA
CATGGCTATAACGCTATGTTCTGCGACAAATATAGCCAAATCAAAGCAAAACAGAACGTTAACTGATTGGATGAATATACCT
ACCGAGTTCGATTCACTTTATTAACAATATAGACTACGAAGATGAATATGAAGATTTTCGTCAATTCTGAAGGACAAGTCCCTT
AATTGATGGCGCATCATTAGTTTGACTCATTAACGAAATGGCTTTGATGCAATCAGCATTGATCTAATTGATGAAAAACAC
TCTGTTCTGTAATTATTGAATGAAGAATTAAGC

SEQ ID 278

LKTDARTMNNLIPEHLAAYAHSDNLQIEGHRCSLSQGRDFTFHIRYYPEPFDGLITDTRKAPVKIVAVEAVSGDEIVLFDGAE
HGYNAMFCDKYSQNKQNRLLTDLDEYTYRVPIHLNYNIDYEDEYDFVNSEGVPLIDGRIISFDSLKRNGFDAISIDLIDEKH
SVRELLNEELS

SEQ ID 279

ATGCTCGAGAATCTGCCCTATTTCCAGCGACATCTGCCCTGAAGACCTTGCCAAAGTCAATGAAGTCATCAACCGTGCCTGCAAT
CCGATGTGCGACTGATTTTCGCAATCGGTACATATATCATCAGCGCGGGCGGCAACGCCTGCGTCCGATTATGACGATTTTGGC
GGGTAAGGCGGTGCGTTATGATGACGAGAACTGTATTGCTGGCAGCGATGGTTCGAGTTTATCCACACTTCCACACTCTGCAC
GACGATGTCGTGATGAAAGCGATTTCGCGCGTGGGCGGGCAACGGCAAAACATCTGTTCCGGCAATGCGCGCGGAGTGTGGTTG
CGCACTTTTATATACCCGTGCATTCAACTGATGGTTGCCCTGGGCGAGTATGCGCGTTTGGGAAGTGAATGGCGGATGCGACCA
CATCATTTGCCGAGGAGAGGTATGCAGCTGATGAACATCGGCAATACGGACATTACCGAAGAACATATATCCGAGTCATCCAA
TATAAAACCGCAAAATTTGTTGAAGCTGCCGCTCAAGTCGCGCAATTTTGGGCAAGCTTCCCGGGCACGAACAGGCGCTTGA
AAGACTACGGTATGTACGTGCGGTACGGCATTCAGATTATTGACGATGTGCTGGATTATTCCGGGGAAACCGAAGAAACAGGTAA
AAACGTGCGCGACGATTTGGCGGAAGGAAACCGACCTGCTTTGATTTATCTGATGCGTCAGGGTCCGAACAGGTTGCGAAC
GATGTGCGTACTGCTTTGGAAAATGCAGATCGCGGCTATTTGAAAAAATCCCGGATATGTGCTCCGTTCCGATGCTTTGGCAT
ATTTCGATAGGCGAGGCGCGCAAGCAGTCGATTGTGCCGTTGCCGCGTTGGATGCCCTGTCCGACAGCAAGTGAAGGATGCTAT
GATTACAGTGGCGAAGGAATCTTTGGTCAGGGTGTGCG

SEQ ID 280

LMQVRVLSVNDKAFVTADLDYELPQAYYVDDPKAPPVEISAPVEAVPAAASDTASDGAEDASAENGVSQNLWKQIWKAKQGQIV
VVGIALTILLVLFQDWIVRYEKWYDRFRFAFLTFTLFYIGWYAQAQLSVVNTLTLSAILTEPHWFFLMDPIVFIWLWFTAA
TMLLWNRGTFPGWLPFGSLQELTNRIAKKLGVKQITVPHMLHTRLNVIKYLILFGLAISLYDLGTAEKFAEVEPFRKTAIILKF
MCDWFWFAFAVALLIAGLFIERFFCRYLCPLGAGIALPGRFRVFDWLRRYKMGCPQICTHECPVQALAEPEGDIHPNECIQCLH
CQVMYHHDTRCPQVVAENKKKQKQAAAKSGELENVSKQPQEQVVRVFKPETAQSEK

SEQ ID 281

ATGAAAAAATTGAAAAATATTTCCGTTGTTGCTGTGTGTGCCGTTTTCGTTGCTGCGCTTCTGAAAAATCTGTAGCCAACT
ATGCTATCGGCGACGATTCCGCCGTAATCAAGGCTGGTCGTAACCGTGCCGAAGCGGAATTAGCCGTGCGGAACCTGGCGCAACA
CCGCCGTCAACGTAAAAATGTTTCTGAGGAGTTGGCTTTGGAACGTGAAAAACGTGCCAATAAGCATGACGCAATCCGTCAAGGT
ATGGGTACGGCTGCCGGTGGTCTGATGCTGCTGAACGGTGTGGTTGGTACCCTGGGTGTAATGAAAAACGTGTTT

SEQ ID 282

MKNLKNISVVAVCAVLLAACASENSVANYAIGDDSAVIKAGRNRAEARI.SRAELAQHRRQRKNVSEELALEREKRANKHDAIRQG
MGTAAGGLMLLNGVVGTVGVMSVF

SEQ ID 283

ATGAAAAAAGCACTGCTTGCACTGACTATTGCCGCCATCTCCGGTACTGCTATGGCCAGTTGCCCGACTTTCGGGTAAAGGCG
AATATACCGTCCGTACAGACATCTCCAACAAACGCTGAAAAATGCCGATTGAAAGAAAAACACAAAGTACAAAAAACATCGG
TTTCCGTGCCGATATGCCGTTTGACGATATTACCACGGCATGCGTTTCGAAGTATCACACAGCCGAGACAAAAAGACATGTAC
GTTGTGACCGAAAGTACTACTAAACCATTCCGCAAGACGTTGAAGAAAAACGACCGACGTGTATGCCGGTTACACCTACACTC
AACCGATCAGTGAAGCCACCAACTGCGTGCCGGTTTAGGTTTGGGCTATGAAAAATACAAAGATGCCGTAAGTAAAGGAAAG
AACAGTCAGCACCGAGCGCGAAGCCTTCTATACCAAGCGCACGCCGACTGACTTCCGATTGGGCGCGCGCTGGTATCTGAAT
CCTTGGGCGAGAGTTAAGGTTGACCTGGACGCCAAATTGAAACACAAACGCAACTGTAGCCGGTGTCTCAGCCGACATTAACGCAA
AAACACGCGGATGGGCGTGGGCGTAGGTGCGAATATCGGCAACAAATTACCGATACCGTCGGCATCGAAGCCGCGCCGTTCTA
CAAACACCGTCACTTCAAAGCATCCGGCAGCTTCGTTTGTAGACGCGGGAACATCCGAGTCGATCCTACCAAAATCAACGAATAC
GGTGTTCGTGTCCGCGTGAAATTC

SEQ ID 284

MKKALLALTIAAISGTAMAQLPDFLGKGEYTVRTDISKQTLKNADLKEKHVKQKNIGFRADMPFDDIHGMRFEVSHSRDKKDMY
VVTSTTKPFKGVDEKRTDVYAGYTYTQPISEATKLRLAGLGLYEKYKDAVANEKGTVSTEREAFYTKAHADLTSDLGGGWYLN
PWAENVKVDLDAKLKHNATVAGVSADINAKTRGWGVGVANIGKQITDTVGIEAGFPYKHRHFKASGSFVLDGGNIRVDPTKINEY
GVRVGVKF

SEQ ID 285

ATGTTCAAACGACCTGAAGAAATCATCGTCTGATACTTGCCGCTCTCTGGATTGCCGGTACGTATTTCTCGCCGCCCTGTTTG
GAGCGGATGCTTATACCGTGTAAAAATCACTGCCCTTACCCTGCTTTGGTCTGCCGCATCATTCCTCCTTTGGCAAAAAAAC
TCAGCCGGCATATCTGCCCGCTGCTGCTCGGCTGCCGTGACCACCTGTTGGTGGCGGTATCTGAATCAATCGGTGCGACCCGGTTC
TTTACCTTGGCATGCATCATGACGTTCAAACCATCTTAGCCCTGATTCCCGCAACCGCAGGTTATCTGTT

SEQ ID 286

MFKRPEEIIVLILAVLWLAGTYFLAALFGADAYTVLKITALTLLWSAASFLLWQKPPAYLAAAARLPDHLVAVSESIGRTRF
FTLACIMDVQNLSPDSRNRLSV

SEQ ID 287

GTGATGATTTTGTCTGGACACGAATGTGATTTCGAACCTTTGCCGCCACAACCCAATGAACGTGTGGTGGCATGGTTGGATAGTT
TGATATTGGAAGATGTGTATTGTCTGCCATTACTGTGCGAATTCGCTTTGGGTGTGGCGTTGTTGCTCAATGGCAAGAAAA
GAATGTGCTGCACGAACGTTTGAACAATCCATTTTGCCCTTATTGTGCGGGCGGATTCTGCCTTTTGATGAACCGGTTGCCGCA
ATCTATGCGCAAAATCGTTCTTATGCCAAAACACATGGCAAAGAGATTGCTGCCGAGACGGCTATATTGCCGCCACTGCAAAAAC
AGCACAGTTTGACAGTTGCTACCGGTGATACCGGCTCATTTTTTTCGGCCGATGTCGCGGTGTTCAATCCGTGGCAGCAT

SEQ ID 288

VMILLDTNVISEPLRPQPNERNVVAWLDSLILEDVYLSAITVAELRLGVALLNGKKKNVHERLEQSIPLPFAGRILPFDEPVAA
IYAQIRSYAKTHGKEIAAADGYIAATAKQHS�TVATRDTSFFAADVAVFNPWHD

SEQ ID 289

TTGAAAAAGCCGTGGTGCCAAGGGGGCAGGGGATTCAATTATGAGGTGCTTTATGTTTTCGACTGTGATTACTGCTGCTGTTTAT
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TATCGGACAATATTTAGGTTCTGTAATTTTAATATTAGTTAGTTTATTTCTAGCTTTTGTGTTTGAATTATGTTCCGGAATAATGG
GTGTTGGGTTTATTAGGTTTAAATACCGATTACTTAGGTATTAAAGTTGCTATTACGACGATTGTGAGGGCGAAAAAGAGCTA
AAAAAGAATTGGATGAAAAAGGTTGTCAAATATTAGTCGGTATTGTTGCTTTGGTTACAGTTGCTAGTTGTTGGTGCAGATAATAT
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TTAGTATATACGACCAAAAGATTGGCTAATATTTCAGTTGTTGGTGAAATTGTAGAGAAGTTTACTGTTGGTGAATAATGGCTGTTA
TTTATATTGGTTTAGGTTATTATTATTATTGAAAAATAATACAATTGCAACAATAATATCAATAATA

SEQ ID 290

LKKPWCQGGRGFIMRCFMFSTVITAALVLIATAVDLLVILLIFFARANTRKEYRDIYIGQYLGSVILILVSLFLAFVLNVPEKW
VLGLLGLIPIYLGKIVAIYDDCEGEKRAKELDEKGLSKLVGIVALVTVASCGADNIGLFVPYFVTLDLVLLVTLVFLILIFV
LVYTAQRLANISGVGEIVEKFSRWIMAVIYIGLGLFIIENNTIRTIISII

SEQ ID 291

ATGACCGCACTTTTAAACCGAAACCCAAAGGGAATCAGGATACGCGCTGATTCCCTTTCCGCCCTGCAACACTACGCTTCT
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GGTGGATTCCGACGAGCCGGAACGTCGAAGGCGTGCGCTTTGAGTGGACAGTGCATGTTTGGCGGATAAGCTGGGCATCAGC
GGCATATTGGATTGTTGGTGAAGTGGATACAAAAACAGGCCGTCTGAAACCTGTGGAATACAAACGAGGCAAGCCAAACCTGACC
CGGGGGATGAAATCCAGCTTTGCGCCCAAGGCTTGTGCTTGAAGAAATGACGGGGCAACCGTCTCTGAGGGCGCGCTGTGGTA
TATGCAAAACCCGCCACCGTGTCCCGTCTGTTTTCAGACGGCCTGAGACCTTTGCAA

SEQ ID 292

MTALLTETQRENQDTRLIPLSALQHYAFCPRQCALIHNEQAWAENYLAQGKALHERVDSDEPETCKGVRFEWTVHVLADKLGIS
GILDLEVDTKTGRKLPVEYKRGKPKPDGDEIQLCAQGLCLEEMTGQTVSEGA LWYMQTRHRVPVVFSDGLRPLQ

SEQ ID 293

ATGAGTGATATTGATGATTTCAAAGCTATTTAGAAAGCCACCAAGCGGCATTTTCCGCTTGGGGTAGATTGTGGCTGAAGAAA
TTCAAAATCAATTATCCAATGTCATTTCTCTGTTCCGGTTGCCAATTTCTAAAAATGAAGCAAAGCCTGGAGTCAAAGAGAT
TTCTTCAGCTCTAGCCAAGATTGGCCGAAAAAATTACACTTCACCTCAAACCTCAAATGACTGACTTGGTGGCGGTACGTTTGTG

GCATTGCTTGCAGAACATATTCAAATAGTTTGTGAAATCATTTGAATCCTCATCTCAGTGGAATGCTAAAGTTTCGAAAGATTTTG
CAGATGAAATTCAGCAAAATCCCAAAGCAAT

SEQ ID 294

MSDIDDFKSYLESHQAAFSAWGRFVAEBIQNQLSNVISPVFVANFLKIEAKPGVKEISSALAKIGRKNYTSPTQMTDLVGVRFV
ALLAEHIQIVCEIIESSSQWNAKVSDFADEIQONPKAI

SEQ ID 295

ATGAAACTGTTTCCAACCATCTGACCGGCATCTTTTGGCAACCGCCCTTCCCGCATCCGCACACGGTATGCATAAGAGCAAAC
CCCTGGCTATGGACGAGCTGCCGCCGATTGTGCAACAATATTTCAAACGCGCCGAAACCTGTTACAACAAAGCCGGAACAAAGC
AGATTTTCGCACGCAACAACACCAAAATTCCTATTCCAAGCCCTACCTGCCGCCGATTGGGACAGCGTAAGCAAATGTGCCAAATC
GCTATGGATTCTGTTGCAGAAAAAACCCGCAATCTGAATTGCGAATAAAGCCGCATCAGCAA

SEQ ID 296

MRTVPTILTGILLATALPASAHGMHRSKPLANDELPPICQYFKRAETCYNKAGNKADFARNNTKFLFOALPAADLGQRKQMCQI
AMDSFAEKNPQSELRIKPHQ

SEQ ID 297

TTGCTCAACCCCTCTTCTCACCTTCTCATTTCTATAAATGATTTTACCGCCGGCCGTTTCTGACCGTTCCGGCTTAAAGCCCAAC
GCCGCTACAACGCTTCTCGCGCTCTCCGCAAACTCCACATCCAAAGGCTTGCCCGTCCGCAATCGACAATCCCTCGCGCTTCG
CCGTCAAGCCCGTATCCGGGTCGGCAACCTCATACTGACAGTCTTGAACACATTCCGGGTCAAAGCCCTTCTCCCTTGCCTC
AAACTTCCCGTTAAGCGCATCAATCTGCGCGCAATCTCCCGCGCTGCCCGTCCGACTTCGCAAAACCATAAGCCCGCGTCAA
TCGGCGATGCGCTTCTATCTCAAGCTCCAGCGCATCCGCCTCAGCTTCATCTCAAACCCCTGCCGCTTCATCCCCAGCTCGG
CCTGCTGCACATCAAACGCCCTGTCCGCATTCTCTGCGCATCTCCGGGTTCAACGCACCCCTCGTTCCGCTTAAACGCCGCATC
AAACCGCCCTTCTGCAACACACCGCTCAGGTTGCGCGCATCTCCGCGCAGCCGCCGCCAGCCCTTCCCTGCCCAATTCCCTG
ACCGCCGCTATTTTATTATGTTCCGCCACAATCCCGCGCGCGCATTAAGCTGTGCGCGCGTCAACTGACCGTTCAAGGCCCGG
CATAAGGCGTAGTCGCCCTCTTATAAGCTCCCGCTCCTCAGGCGACAGCGCATCCGGCCCGGCGAGACCAAAGGACGCTGCCG
GTCAAATCAGCGACCGGCTTGCCTGCCCGGATACATCTCCCGTCAAATCCCAAAGGCGCGCGCGCTCCGTCGCCCGCATCCGTC
GGGCGCGTATCGCGCCGCGGAAATCCGCCCGCGCGCATCCGGGGAAAGCGCTTATCGCCGCCCGGAAACCCCAACCGG
CATCCGACCCCGTTGAAAGCACCCCGCCCGCGCAACCGCGCGCCCCATCTCAATATGTTACGGCTCAAATCCATCACATT
CCGATAACGCGCCCGCCCGGCTCATAATTGCGCAACGCTACGCCCGCACCGCATCGGCACGCTGCGCTGTGCGCGCCCGCTCC
CGCTCTCCGCCCGCTTCCGGGCTTCTCTTTTCTCTCTTTCTCTCATCTCCCAAAATCCCGCGAGCGGCTCAAACAAAC
CCATCGCAAACCTCCGAACAAATAAGTCCAAATAAGCAAAACCAAGCCCAATCAAACGCTTAAAGTTAAGAACAACAAACAA
AATCGCAACCCCGGACCAATTACAAACAACAAGTTACAAAAAAACACACCGACGGGCCATTTCCGGGGGCAATAAAAGC
CGCCTTGTGCAAGGCGGTTGCATTTAGAACAGTCTCGGCTGTTTACGGTCCGGTCTT

SEQ ID 298

LLNPLILLLILINDFTAGRFLTIVRLKAQRITLLALSRKLIHQRLARPQIDNPLALRRQARIRVGNLITDSLEHIRVKALLPLPL
KL PVKRLNLPRLPALPVRLRKTISPROIGDALPILKQIRLTLHLKPLPLHPQLGLLHIKRPVRIPLRHLAVQRTLVRLNRRI
KPPLLQHRLTVRRILRRSRQPPPAQFPDRRIFFIMFRNPARRIKLCRRQLTVQGPRIIRSRPLIKLPLLRQRIRPGRHQRTLR
VKITHRLAAPIHIIPVKSQRRRPSARIRRRARIAPREIRPGPRIGGKRLIAARKPQTGIRTPEFSTRPAQPPRPILNIVTAQIHII
PITRRPGLIIRNGTPHRI GTVRLCRRPLPLRLPLGLLFFLLFLHLPLKIPGRRLKQTHRPSEQIKSKISKNPSP IKRLKLRTNK
NRNPGPIKQQTQKHTDGPFPGANKRPFLCKAVAFQNSLGLRSL

SEQ ID 299

TTGGGCATCTATGGAGCATGGTGTTTTATGGGATTAACACAAGAGGTTTAAAGAATTATTAAGATATGATGACAATACGGGAA
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GGTTTTCTTATACAAAGGCAGGTTGGGGTATTTGAAGTTAAAAATATTAAAGAAACATATAATGCACATAGATTAATTTGGCTT
TTTGTATTATGGGAAACAGCTTCTTCAATAGGCCATATCAATAGGATAAGACAGATAATAGAATATCTAATTTGAGAGATGTTA
CACATGCTGAAAAATATGAAAAATAGAGGGAGTTTAAAAATAATACCTAGCGGGCATACTGGGGTTTATTTCCATAAGCCGCTTAA
GAAATGGCAAGCTAGGATTATGGTTAATAGAAAAATAAATAATTAGGTTTATTTGAACATATTGAAGATGCAGCGAAAGCGAGA
GAGGCAGCATCTAAAGATTTTGGCTTTGTAGTG

SEQ ID 300

LGIYGAWCFMGLTQEVLEKLLRYDDNTGKLYWAERPRKYFNSGLHYKSWNTGFSGKEVFLYKGRGLGYLKLKIFKKQYNAHRLIWL
FVYGKHASSIGHINRDKTDNRISNLRDVTHAENMKNRGFKNNNTSGHTGVYFHKPSKKWQARIMVNRKNKILGLFEHIEDAAR
EAASKDFGFV

SEQ ID 301

ATGAACGGGGCGGAATTTACACTGACGCCCCAAACAAAAGCAGGTTATGCGGTCGATTGGGACAGCCCGGACGGGTGGTTTG
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TGAAATTCAGAAAAAGTTTTATCGATGGGAGAAGGTTAGTCAAGATGTATGGCATGAATTTTAAAAAGAAAATTTATTTGGA
TGTATTGAAATGCCTAACGGGCAATTAATGGGTATATCAACGACAAAAATTATCAGTTCGGGAAATGTCTGAATATCAAGAAAAGA
TTATATCTTGGGCATCTATGGAGCATGGTGTPTTATGGGAT

SEQ ID 302

MNGAEFTLTPOKQVMRSIWDSPDGWFENGLEITIRPKSKRSVEQNRLWFLYREISEKVFIDGRRFSQDVWHEFLKRKF IG
CIEMPNGQLMGISTTKLSVREMSEYQEKIISWASMEHGLVWD

SEQ ID 303

ATGCCGTCGCCGCAAGGAAGGGGGTCTATTATTACAAATCGTGCAAAACCTGCCGCAACAGGCAGTCCGGCAAAAGCGCGCG
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GCCTGTGGACGCAACCGCGAGGGGAATGCGCGTGACGCGCTTATCTGCCTTACCCCGTATCGGCAAAACCGATATTGGCGGATT
TGGCGCAACAGGGCGGTCAGGAGCGCGGAGGCGCGGCTATAAGGAAACCGTCCGCGTATCGCGCAAGGGCGGGCGCGATGC
CGTCCGAAGGCGCGGTTGCCGTATATGTGCGGCTGATACCCAAAGCGAACAAGACGCGCGGCGCAACAAGACCGTGATCGATTT
GGACAACGCCCTGAAGGTTACTCTGGACGCGCTTCAAGGCGTTGCCTATCACAACGACAGGCAGGTGCGGCGCATTTGCCGCCGAA
TATGGCGGCGAACCAGGTAACGGCGCGCGGTTTGGCGGTGGAGGTGGGGGAATTGGAGATGGAACAGACGGATGCGGCAGACGAGG
GTTGGGATTTTATCGGACAGGAGGTTGGGATGTC

SEQ ID 304

MPSRARKGGLLLQIVQNLPPQGGSPAKARGGSSRRDDGGKAAIRIHPRRARRLPDIGRRPVDATGRGMVRTRLILPYFVSANRYWRI
WRNRRAVRSAAEAAAYKETVRRRIAQAGAMPSEGAVALVYVRLIPKANKDGGANKTVIDLNLKVLTLDALQGVAYHNDQRVRRIAAE
YGGEPVTGGGLAVEVGELEMEQTDAADEGWDFIQGEGWDV

SEQ ID 305

ATGCTGAACGCGTACGACGTGGCAGATTTCTTCCTTTCCCTTTTGAAGAAGAGGACGGGGAGCAAATCTCCAATCTCAAACCTTC
AAAACTCCTGTATTACGCACAAGGCTACGCCCTTGCCATACTTAACCGCCCCCTGTTGCGGAAAATATCGAACACTGGCAGCA
CGGTCCGGTAGTCCCCTGCATTTACCGCACCTACAAAAAATACGGCGGCAGCCCATTCCTGCGGCCCATATCGAACCGGACAAA
TATCGGACGAGAAGATTGGTTGTCTCAACCGTGTCCGTAAAGAGCAGGGCTGCTACACCGCTTGGCGATTAGCAATAAAACCC
ATCAGGAAGCGCCGTGGATACAGACCCGGCAGGGCGAAGTCATAGGGATTGCGCTGATGGGGGAATATTTCCGCCATGCGCTGCC
GCAGACGGATTACAATTTCAATCTTGAAAAACTCAAAACAGCCGTTGAAGACAGCTTTGTACGCTCCCGCATTTCAACGGCGCC
GACGACTTGAAAAATGGTTGGAGCAG

SEQ ID 306

MLNAYDVADFFLSPFEEEDGEQISNLKLOKLLYYAQGYALAILNRPLFAENIEHWQHGPVVPPIYRTYKKGSSPLPAAHIEPDK
YADEELVVLNRVRKEQGCGYTAWALRNKTHQEPWIQTRQGEVIGIALMGEYFRHALPQTDYNNLEKLTAVEDSFVSVPHFNGA
DDLEKWLEQ

SEQ ID 307

TTGTCCGATGAAGGCAGGCATAAACCTACTTCCGCCCAAACCGCGTTTATGATGAAAGGTATGGATAAATTGAGATACCAAC
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TTTAACCGACTCCGTGCGTAATATTGAAGAAATCGGTATCGATTTGTGTACAGTCTGCCAAATGGAAGGAAACACTTATAAT
CAATACGATACCGCAGGATTGCTTAAACTCGGGCAAAACCGAGCGGAAGTTATATTCCGATGCGCTTAATGTTAATCAACCTGA
GGGAAAGTTTCCGCCACTGCTGTCCGGTTTGGACAGCCCAAGCCGTTTGACTGGTTGGATTTCTTAAAAACCAACCCACAGCCT
GATTTCCGAAAACCTTACTGAAAAAGGCTCCGGCGCGTAGTCCGCCGCGACAGCGTTACTATAAGCGGGACAGACTACACCCCT
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GGCGATTACGGTTTATTCAAGAAATATTTATTTCCGCATACGAAAATACCGTAATAAGTACGGTCCCAGCCTGATGTGGATA
TTTTCCGAAATTTCTCCATT

SEQ ID 308

LSDEGRHKPTAPNRVFMKGMKDLRYQRDFLNIRPIFTAGEQEYLTELSRPLSVLTDSVRNIEBIGIDFVYSPAKLEGNTYN
QYDTQALLKLGQTAGGKLYSDAVMLINLRESYRHLISGLDSPKPFDWLDFLKTTHSLISENLEKSGGVVRRDSVTISGTDYTP
LSNPQSLDTLKLWLLQEPKIEPNFDRAVYLHNNLAYLRYFKDCNKRTARNCMTSLMLRSGFFPCVFPSPDSYPAYAEAVVAYET
GDYGLFKKYPISAYENTVNKYGPQPDVDFRNFISI

SEQ ID 309

TTGAACAAAAATGGGAACACTGACATGGCTTTACTGAGCATCCGCAAGCTGCACAAACAATACGGCAGCGTAACCGCCATCCAAT
CCTTAGACTTGGACTTGGAAAAAGGCGAAGTCATCGTACTGCTGGGCCCCGTCGGCTGCGGCAAAATCCACCTCTGCGCTGCGT
CAACGGTTTGGAGCCGCACCAAGGCGGCAGCATCGTATGGACGGTGTCCGCGAATTCGGCAAGACGTTTCTGGCAAAACCGCC
CGGCAAAAGTCCGTATGGTCTTTCAAAGCTACGAACTGTTTGGCCCATGACCGTCATCGAAAACATCCTCTTAGGCCCGGTAA
AGGTACAAAACCGCGACCGTCCCGAAGCAGAGGCGCAAGCCGGCAAACTGTTGGAACGCGTCCGACTGCTAGACCGCAAAACGC
CTATCCGCGCAACTTTCCGGCGGTGAGAAACAGCGCATCGCCATTGTCCGCGCCCTGTGCTGAATCCGGAAGTCATCTGCTG
GACGAAATCACCGCCGCACTTGACCCGAAATGGTCCGCGAAGTCTTGGAAGTGGTTTGGAACTCGCCCGCAAGGGATGAGTA
TGCTCATCGTAACCCACGAAATGGGGTTCGCACGCAAGTTGCCGACCGCATCGTCTTTATGGACAAAGGCGGCATCGTCAATC
GTCCGACCCGCAAACTTTTTCGCCACCAAAAAGCGAAGCGCCCGCAATTTCTGGCAGGTATGGACTAC

SEQ ID 310

MALLSIRKLHKQYGSVTAIQSLDLLEKGEVIVLLGPSGCGKSTILLRCVNGLEPHQGGSIIVMDGVGEFGKDVSWQTARQKVMVF
QSYELFAHMTVIENILLGPVKVQNRDRAEAEQAQGLLERVGLLDKRNAYPRELSGGQKQRIIVRALCLNPEVILLDEITAALD
PEMREVLEVLELAREGMSMLIVTHEMGFARKVADRIVFMDKGGIVESSDPETFFSAPKSERARQFLAGMDY

SEQ ID 311

ATGACGAAGTTATACGCGCAAATCGCCAAGACGAGGCGCAGGACGACGGCACGGTCAAAGTTTGGGGCTATGCTCGAGCGAAG
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AATGCACGGCTCAAACGCGCGCGGAACGCGGATTGAATCAACGTGGAAGACGACGGCGCACATTTTCCGGGCGCATATCGTT
GACCTGTGCGGTGACGAAAGTCAAGACAGGCGTTTACAAAGGCTTTTCCATCGGCGCGCAGGTTACCGCCCGCAATGATTGA
ACAAGTCGCAATACGCGGCTTGAAGCTGACGGAATCAGCCTTGTGACCGCCCTGCCAATCCGACGCGGTGTTTACCTGCTT
TAAGGCGGACAAACCGAAAGATGAGGCAGGGCGCGGATAAAGACGGCAAGCCGTCTGACAAACCAACCGAAGGAAGATGAA
AATCTAAAGACGGCGATAAAGGGCTTAAACCGCAAGATAAAGGCGATAAGGACGCGCGCAAAAGGACGCGGAAATATCGG
CAAGCGTGAATTTGTCCGAATCTGAAATCGCCGCTTTGAAAGCGGTATTGGCTAAAGCCGACAAAGCGGAAAGCGGGCGCGCGC
CAATCAATGTACCAAGTCAATCACCGGCTGATGTATTGATGTGCTGAAATGGCTGGTTGAGGACGCATCTACGACAACATC
GATGAAGCGGTTACCGCGCAAATCAAAGATCGGCGCGCGCTTCCGAATCGCTGAAAGCGTTGGCGGCAAGCGAAGCCGATA
AGCCGCGCGACGTTTGGCGGCAAAAGCGCGCAATCAGGCGATCTTGCCAAAGCGGAATCGGCTGACGAATGGCAAAGGCACA
AGACGCGCTGAAAAAATCGAATGACGCCCTTGCCAAAGCACAGGCGGAAATCGAAAGCCTGAAGAAACAGGCAGTACCGCGGAA
GGCAGTACGAAAGCTATCAGTAAGGCAGAAGATAACGGCGAAGACCGTTTAAAGGTTTTACCGCGATTGTAAAGAATGACGGCA
CGCTGGATGACGTGGCGACACTCATTAAAGCAAAACAACAGGCCGCTG

SEQ ID 312

MTKLYAQIAKTEAQDDGTIVKVGYSASSEAVSDSEGVAAEAMKAAIPDYMKGAVREMHGSNAAGTAIEINVEDDGRTEFFGAHIV
DPVAVTKVKTGVYKGSIGGSVTARNDLNKSQITGLKLTETISLVDRPANPDVFTCFKADKPKDEAGAADKDGKPSDKPTEEBDE
NPKDGDGKPKTEDEKDKDAGKDEAGKSASVNLSESEIAALKAVLAKADKPKGGPAKSMYQVKSADVLMSLKLWLVEDASYDNI
DEAVTAQIKESAAGLAESLKALAASEADKPADGLAAGKSGDLAKAESADELAKAQDALKKSNDALAKAQABESLKKQAVFPK
GSTKAISKAEDNGEDPLKGFQPIVKNDGTLDDVATLIKAKQTGR

SEQ ID 313

TTGACAATCAAAATCGGGGGGATAGCTGATGGCTATCAATGCCGCTCGAAAAATGTGGTTTGGGAAGACGTTGGGGGAGGTTGCCG
AATATTCAAAAAACCGTATTTGTTCCGATAAACTGAACGAACATAATTACGTTGGCGTGGATAATCTCTTACAAAAATAGAGAAGG
TAAAAAGTTATCCGGTTATGTTCCAAGCGAAGGAAAAATGACAGAATATATTGTCAATGACATTTTGATTGGAAATATTCTGTCGG
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ATCCAAAATATCTGTATCAGGTATTGGCCGATGATAAATTTTTGCTTTTAATATGAAGCACGCCAAAGGTGCAAAAATGCCGCG
TGGCAGCAAAGCAGCGATTATGCAATATAAAATCCCCATCCCCCGCTCCCCGAACAGGAAAAAATCGTCGCCATCCTTAGGCAAA
TTCGATACCTGACCCACTCCGTCAGCGAAGGCTTCCGCCACGAAATCGCCCTGCCCGCAAACAATACGAATATTACCGCGAAC
AGCTGCTTGCCTTCCCCAAGGCTGCC

SEQ ID 314

LTIKSGGIADGYQCRLKNVWVKTLGEVAEYSKNRICSDKLNENHYVVDNLLQNRGKFLSGYVPSEBKMTEYIVNDILIGNIRP
YLKKIWQADCTGGTNGDVLVIRVTDKVNPKYLYQVLADDKFFAFNMKHAKGAKMPRGSKAAIMQYKIPIPPLPEQEKIVAILGK
FDLTHSVSEGLPHEIALRRKQYFYREQLLAFPKAA

SEQ ID 315

ATGCTGCCGCCCAACTGCGGAACGGCAACCCCTTATATATTGCGTAACGCCGTAGGATTGGACATATCCAAGTTGACTTTTGAAG
CAACGGCCATTGTCGGCAATGCCGAATATTGCGCAAGTTTGAACAACGATTCAAAAGTTTAGATCAGTTTTCGGACCGGTTGAA
AAGCTTGGGATGTCAGAATCTGCATATCTGCATGGAGGCAACCGGCAATTATATGAAGAAGTTGCCGACTACTTCGCGCAGTAT
TACAGCGTTTACGTAGTGAATCCGCTGAAAAATAAGCAAGTATGCAAGAACGAGGTTCAAGCGAACCAAAACAGACAAACAGGATG
CAAACTGATAGCGCAGTATTGCCGGTTCGGCGCAGGAAAGCGAGCTTGTAAAGAGGCAAGCCTACGGACGAGCAATACAGGCT
TTCACGGATGACCGCAGCATACGGCGCAATCAAAAGCGAATGCGCGGCAATGAAAAACCGTCATCACCGCGCAAAAGATGAAGAA
CGCGCCAAAGCATATGCGGAAATCATCAAGCCATGAATGAACAGCTTGAAGTTTAAAGGAGAAGATAAAGAGCAGACGGAGA
AGCCTAACTGCAAGGAAGGCGTGAAGCGTCTTGAACCATACCGGCAATAGGCAGAATGACCGCAGCGGATTGTTTTCATCATCT
AACATCTTCGAAATTTGAAACATCAACAAATTTGCAGCATTCGCGAGGCTTAAGCCCGCAACAAAAAGAAATCCGGGACAAGCGTA
AGGGGAAAAGGCAAACTGACCAAGTTTGGCAACAGGAATACGCGCGCTTGTGTTATGCCGGCCATGGTCGCATACCGGATAA
GGGCATTTCCCGACTTCATCAAAAGGCTGGAAGAAAAGAAGCCTAAAAAGTCATCATCGCAGCATTTGATGCGTAAACTCGC
CGTTATTGCGTATCAGTACATAAGAAAGCGGAGATTACGATCCATCGCGTTACAAATCGGCG

SEQ ID 316

MLPFCGTATPYILRNAVGLDISKLTDFDATAIVGNAEYSAKFDNDSKGLDQFSDRLKSLGCONLHICMEATGNYYEEVADYFAQY
YSVYVNPPLKISKYAESRFKRTKTDKQDAKLIQAQYCSAQBSSELVKRQKPTDEQYRLSRMTAAYAQIKSECAAMKNRHHAAKDEE
AAKAYABI IKAMNEQLEVLKEKIKEBQTEKPNCKEKGVRLETI PAIGRMTAAVLFHHLTSSKFETSNKFAAFAGLSPOQKESGTSV
RGKGLTKFGNKRKLRAVLFPMPAMVAYRIRAFPDFIKRLBEKKPKKVI IAAALMRKLAVIAYHVHKKGGDYDPSRYKSA

SEQ ID 317

TTGGAGAAGCGTAGCGAAGACATCCCGTTTATATGATTATCAGGGCAAGAAAGACCGATTGGAAGAAGTCATCGGCTTTCCGAAGACCCGAGCTTTGGAACGACCCGAAACGTCGCC
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AGGTTTTCGCCCGCTGAAGGAAGACGTCGCGGGCTGGAAGAAACAGATGCGCGATTGGAAGTTCAACCGGATGTTCAACCGAGCCCGCGACCCGAAACCTGCTTATCGACATCACCGC
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GCATCAACCGCGCCACCATCCGAGTGAAGCGGAATACGCTTATGGTTTGCCTGCTACGAAACCGCGCTTACCGCTCGGTGCGCTACTCGCGCTTGGATTGGAACAAACGCGCATAC
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GCTACAGGCTACGAAGTCGCGAACACCAAGCCGATTGAGCGGCGATTGAGCGGCTTTATCGAAGCCAGCTTGAACAGGGTGCT

SEQ ID 318

LEKRSERIVMDYQKKDRLEEVIGLSEDPFLWNPKAQIEIKESKILEGIVLTLDNIASSIEDNRMLIEMAVEENDEEGFAAVKEDVAGLEKQADLEFKRMFPNPADPNCIFIDITA
GAGGTAEEDWAGMLFRMYSRYAERKGFKTEILEEDGELAGINRATIRVEGEYAYGLLRTEGTGVRHLVRYSPFDSNNKRHTSFASVFPVIDDSIEIEINPADLRIDTYRASGAGQHIN
KTDSAVRITHEPTGIVVQCNDRSQHANKAAAMEMLKSKLYLEMRKRNEEKQALEBEGSDVWGWSQIRSYVLDSSRIKDLRTGYEVGNKAVLDGLDGFIEASLKQGV

SEQ ID 319

GTCTCGGATGCACACCGGACAGGCGGTAAAGCGGGTCTGCTCGGACAGTCAATTCCTCTAGGCATACCGTTGCCGTATGCTCAAGCAACCTACCCGAACGCTCGGCGGGCAGCGTCATT
GCGTTCGTTTGGTCTGCTCGGAATGGGGTTTGGCTGCCGATATTGTTACCAATGCGCGGTGCGCCCTTACCGCACTTTTACCCCTGCTGCTGCTGCAAGAGCCATCGCGG
TTTTGCTTTCGTTCCATTTCCGTCGCTTACCGCGCCCGCGCT

SEQ ID 320

VSDAHTGKGPGSVSDSHSRHTVA GMLKQPTRTLGGQRHCVLFLGAPNGVWPAAYCYQMRGAPLPHLFTLACAATAIGGFAPCSTFRFRVTARGR

SEQ ID 321

GTGTTTTATATTCCGTTGATGCAGCCCTGATGAGTCGGACAAAATGCCCTTTTACTCAATAGGACCGGTTTCCGCCCAAGCGGAATAAAGCGCTATTTCCTTCGAAACAGACGGAATCA
GGCGGTATTTAA

SEQ ID 322

VFLYSVDAALMSRTKCLLLNRTGFRPSGNKRLFLQTDGIRRVFK

SEQ ID 323

ATGCGCGGATACCGTCTGAACCTTTCAGACGGCATTTTCCGCATAATGAACCAAAACCGTTTCCACCGCAGGACAGGCTTTCCCCCCCCAACCGGAAGGCGAGCTGCTGATTGTCAAT
TAAATACCGCGCTGATTCCGCTGTTTTCGCAAGGAAATAGCGTTTATTTCCGCTTGGCGGGAACCGGCTCTATTGAGTAAAGGCAATTTGTCGACTCATCAGGCTGCATCAACGGA
ATATAAAACACAGCC

SEQ ID 324

MRRYRLNPSDGIIFHNETHKPPFDRTPPTTGRQPADCHLWTRLIPSVCKGNSRLFPLGRKPVLLSKRHFVRLIRAASFEYKNTA

SEQ ID 325

ATGTCCCGCATCCCGCCCGCAGCGGAGAAAAACATTTTTCGGCCACCCCTTCCAGCTTTCCACCTCTTCCATATCGAATTGTGGGAACGTTTTCATTTTACGGAATGCAGGGCATCC
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GGGACGTAAAAACCTGCCCAACCCCAACCGTCCCCATCCGCTTTCAAAGGACAGGGCAAAACTGCGGCCGCCGTGCGCATCACCCTCATCGCCGCACTTGCACACGCCCATCAAAACCGGG
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GCGGTATTTGTTACCGCGCGCTCGTTTTCGGGATTCTGTTCCCTTAATTTCTCTCCGAACCGCATGCCCTATTTCCGGTTTTCGCATGATCGTCTTCGCCATCAGATAGGCGCAACTGATGA
TTTCCCGGATTGGCGCTGTCCATCTCCACCAAAATCGCACCGCCTTTATTTCAAACCCAAATGTGCGCCCTTAATTTCTTCCTCGCTTTTCACTTTAGGCTCTCACTTTGGCGCGCGTATTTGTTGA
AAAGGCATATCAGCGGGCGAGAAATCGGCTTCTACCGCGCTGCTTCTACATCGGGCAGCCACAGGCTTCTCTGCTGCTCGTCCCAAAATTTGAACAAATGCTCGAAGGCACA
GAC

SEQ ID 326

MSRHPARTGEKTPFGHPQLSTLPHIELWERPSFYGMQGILLILTYLYTTADKGGGLGIDKTLFAGGIVGAYSGSVILSTILGANFADRVWGAEKTLFLPSGIWVMLGHIVLAAAPGLYGLLIGLI
PIALGSGGVKSTASSMVGALYEQDEMRPLRDAGFSIPIYIAINIGGFLGPLTLGLQENIGFHYGGAAGVMAPLWRYSLGRKNLPHPTVPHPLSKGQCKTAAAVGITLIALAATAIKTG
LVNLDNFSGILLSTVLLAVIAYFARLLTNPRVSSDNKRHIIAYIPLFLITCMFAWVWQIITYTVTYFDETIVNRITIGSPVFPVANKDSMQSLWVILFSGLMAAMWTKMGRQPKTPLKFAH
AVFVTGASFLGFVFPISSGTPMPIAVPALIVLAIITIGELMISPIALSISTKIAPPLFTQMVNLNPLAFSLGFLTGGVLFERKQYQAGEIGFTRLLFYIAGATGFLLLLLVPKINKMLEGT
D

SEQ ID 327

GTGCGGGCGGGATGCCGGGACATAAAGGTTCTCTCTCAATACCGTCTGAAACGGATGCGGACGGCGGCGGTGTTTTTGTATGAAATATCGGTTTTTAACCGATATT
TTCATCTTTGTGCAACGACGGCTGCGCGTTTTTCGCGGGCGGATGTTTTATATTGTTTCAATTCAATGGATTGTATTTTAGAGGACGTGTTCGATACGGCGCGGGTAAATCCCTTTTC
TGTCATGGCTTATCCGATAGGGCGGPTTTTACT

SEQ ID 328

VRAGCRDIKVLKDFLSIPSETDADGGGVFCMKLSVFNRYFHSLSNDALPFFAGGCFYICFNSMDCILEDVFRYGAGKSFSVNGLSDRAWFT

SEQ ID 329

TTGATGTGCGAGAGAAATATGATGAATCCCAAAATCGTGTTTTTCGACATATGACGATACGCTGTACC CGAAATATACCGGATACCTTCGCCGCTCTCCGTGAAACCGCGGTGGCGGCTTTGC
TGGCGCAAAAGGCTATCGACGGGTTGTGCACCGGCGGGCTCTTTGGCGACGATTCCCGCAAAAGGTCAGGACCATGTGCGGGAACCGGGTATGAGTATCGCGTGTGATCGATAAACCGGACGAT
TGCCGCTGTGTCACGGTAAATCTGTGCGGAAGTACCGATGGATACCGGTTTGATGTGCGAGGGTTTGTGCGCATTTGGATGGTCTGGGCATGGAATTATGCTTATGTCGCCGACAGAGGATC
GCCGTGTCCGCGCTGTGCGAATCGGTGTGCCGCGCCTTGCACGATATCGCCAGCGATTTTTTTTGGCGATAAGGATTATTTTTTCAAGCAAAACCGGTATCAGATGCTGGTGTTTTGC CGGAAG
AAAACGAATGCCCTTTTGTGCGGATATGTGTGAACCGGGAAGCTTTGAAAACCGTGCCTGGCACGAGGAACCGCTCGATCTGCTGCTCGCGGAATGTGAAAACAGACGGCATCAGAA
CGTGCTGTGAAGCATTTGGTTTGGAAATGGCAGACGTCGTGGCGGACGGTTTGAAACGATGTGCGGAATGCTGTGTAAGTCCGGTTTCGCCGTGGCAATGGGTATCGGGGGAACAGCA
CGCAAGAAGAACCGCGGAAATATGTTTGGCCCGCGTGTGATGAAGACGCGTGTGTAGGGGCTTGC AAGATTTCGGGTGTGATT

SEQ ID 330

LSARENMMNPKIVFFDIDDTLYRKYTDTLRPSVKTAAALRGKGILTALATGRSLATIPKVRDMMATGMDAVVYTNQGFALLHGKTVREVPMDTGLMGRVCAHLDGLGMDYAFVGGEGI
AVSALSECVCRALQHTASDFADKYFSSKPVYQMLVFAEENEMPLMSIDIVERGLKTVRWHEEAVDLLPAGMSKTDGIRSVVEALGLEMDVMAFGDGLNDVEMLSVVGFGVAMNGEQA
AKEAAKYVCPGVDEGVLRLGLDGLVI

SEQ ID 331

ATGTCCGACAACAGCAGACGCGGATTTCTGGGGCGCGGGTTTGACGGTGAAAAGAAATGTGCCCGCCGCAATGAAGTTTCTCGGATAACCGCCCATAGGATTTTGTGTTGTGGTGTGGGTGTG
GAGAAGGAATGGTTTGTGTTGTTAAAGTTTAACTTTGTGGACCTGATGTTTCCAAACGACATGGAGGCGCTGAAAGCACTAGCTTCAACGAAGTTAAAGT

SEQ ID 332

MSDKQTRFRGGGFDGEKECAAGNEVSAITRHRI FVCGWGVGEGMVCC LRFNFVGPDVSKRHWRPSESTSFNEVKS

SEQ ID 333

ATGACCGGATACCCACCGGACAGATACCGATTCGACCGGAAAAAGGGCACGGCGCAAAATGCGCGTCTGAACACCGCGCCCGCCCGCGCGGCAAAAAAAGCGCGCCGCTGCTGAAGCTGTGCGCGG
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AAACCTTCAAAGGACACATGCTCGACCGGTTTCGACGGCGGACACATGCTCGATAGAAAACCGAGGGGGCAGACGTTAAATACACCGGCTTTCGCGTTCGCGGTGGAAACCTGCTCCGAATGATGCG
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CTGGACATCCGTTCCCGCGCATTCGACCTTCGCGCATCGATCGCAATTTTCGGGACGGCATATCAACGGCTGTGACCTTTCGCGGTGAATCGGAAAGGAAATTTACCGGCAAAA
TGCGTTTTCGCGCGTAGCTGTCAACGGCGTCCGATTCGCGGACGAGCGGACATGTTTACAGATCCCGCGACCTTTCGCGCGCGCGCGTGTGATTTCGGTTTCGGGGCGGACATCTGCTCAAA
AACAGACGGCGGCTTCGGCAAAAAAGGCGACCGGCTTAACTCAATATACCGCACCCGATTATCCCGTTTCGGTTTCGACTCGCGGGGCTTTAAATGTACGCGGACACCTTTCCGGC
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CAAGCGCCCGATTCGCGCGCGATATCAAAGGCGCGCGCTTTCCCTGTGCGGGCGGCGCGGCTTGTGATACCGCGGCTGACGCTGGAAGGTACGGCGCGCAGCACCGCATCCGCAT
ACACCGCGCCATGACGCTGGACGGCAACCGTCAAACTCGAATTTGGACCTTCAGGCGGCATCAACAGGGAATTAACCGATGGAAGGAGGACGATTCGACCTCTCGCATCTCGGCGGCA
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CGGGCACACGCGCGCGGCTACCTCAATATCAGCGCGCAAGCGGCGGATGCGGTATTCGCGCGGCGGCGAGGCTTTGGGTTTGAACGCAATTTCCCTGAAAAACGCGCTTCAAACAGACCG
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CGCAACTTCTCATCGGTCGAGCAAAACCGTCAAAGGCAGCTGAAATGCCGCGGTAACCTTCGCGGCGAGCATCGCGACCGCGCACTTGGGCGGCGATATCAACGGCGACAAGCTCTATTACC
GCAACCAAAACCAAGGCATCATCTTGGACAACGGCTCGCTCGGTTTCGCAATTTGACAGGCAGGAAATGGTAAATCGACAGCTGAAATTCGCGCACGAAGGGACGGCGGAACCTCTCGGCAC
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CCGCAAAAAGGCATATCCGTTACCGGTATGATTAATACTGATCAGGGCGTGTTCGGTTTCGCAAAAATCTCGATGCGGCTCGGCGAGTGTGCTGATTTGGGGCAAGTCAAGAAAG
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AACCTGAACATCCGCGCGCGAAGCCGCGCCTTCCGCCGTCGGTGGCGGCTGGAAAAATTGGGCAGCCTCAACAGCCCCGCCATTACGCTGACGGCAACGAACCGATGAGTGAAAAAGACA
 AGCTCTCTCGGCTCATCTCTCAACCGTGCCGCGCAGCGGACAGCGCGGACAATGCGCCGCTGTGCGCAGCGCAGCGCGCTGCTTGCCGGGGCAAACTCAACGACCCGATCGGGCTGGTGG
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 GGCATCTCCAGCGCGGAACAGTCGCTCAAACTGATTATTCGCGGTGACCCGCGACATCAGCGCGCTTGGCCGATTTAGCCGAGCGCTGCTGACCGCGGCGGACGATACACCATACGTTTCG
 AACCGCTCTCTCGGTTGCGGACAAAAAGACTCCGACGAAACCGCAAGGGAAA

SEQ ID 334

ENDTDTTDPDPTENGTRKMPSEHRPAPPAKKRRPLKLKLSAALLSVLILAVCLGWIAGTEAGLRFGLYQIPSWFGVNISSONLKGTLTLDGFDGDNWSIETEGADLKISRFRFAMKPSLMLR
 RSLHITDISAGDIAIVTKPTPKPEKRRPQGLPDSIDLPAAYVLDYRFPETGKISMGKTDRQTVYLERLNAATYRDRKGRRLDLKAADTPWSSSSGSAVGLKKPAPALDTAITYTKGFGEGFTI
 RSTARLSGSLKDVRAELITDGGNTRLSGKSVIHFPAESLDKTLBEVLVKGFININPFAVPSPSLPAGLNFDTAIPSPFSDGIALEGSLLDEWTKAGFADRNGIPVRQVLGGFVIRQDGTVHI
 GNTSAAALLRGGRIRLSKGIKDTEKDIIDLNTIGINSVGAEDVLQTAFGKRLDGSIGIGTTASPKISQLGTGTARTDGSALASDPANEQRKLVDTVNI SAGEGSLTAQGYLELFDKRLIKL
 LDRISRAFDPSPRIDQTPAGNINGSIHLAGELAKEKTFKGMRLFPPTFGNVIAGSADVIYESRHLPPRAAVDLRLGRNIVKTGGFGPKKGDKRLMLNITAPDLSRFGFLGAGSLNVGRHLSG
 LDGGRITAFDVLDSGTARNHLKGAADIRSLDPTFKGSPSPRMRADIKGGRLSLSCGAAVVDTAGLTLBGTGAQHRIRTHAAMTLDGKPKKLDLDSAGGINRELTRWKGSGIILDIGGA
 FNLKLNRMTELEAGAEHVAASAANWQAMGSSNLQHFWSDRKTGISAKGGARGHLIEAHNFFKPPFEHNLVLNGDDVAYGHNARGYLNISROSGDVAIPGGQALGLNAFLSKTRFQNR
 IGIILDGGARFGRINADLGIGNAPFGGNWAMPFGGRITASLPDLGALKPFLPAAQNTITGSLMASAQIGGRVGPSPVNAAYNGSSNYGKINGNTIVQGSRSYDTAPLGGRLNLVADABAR
 RNFLPVGQTVKGSILMAVTLGGSTADPHLGGSSINGDKLYRNRQTQGIILDNGLSLRSHIAGRQWVIDSLKFRHEGTAELSGTVSMNSVPDVIDKAVLQYRILSRPNRRLTVSGNTRLYS
 POKGTSVTGMKTDQGLFGSGKSSMPTGDDVVVLSEVKKKEAASLFPVNMNLTLGLDNDIGRFSQYADVLTYGGLKLTAGGVNVRGVTGVGLKGRYKRAYQDLDITKGTYSFVGPLNDP
 MLNTRAERRLSPVGAQGLGLSLNSPRTITANEPMSGEKDKLSMLLINRAGSGSSGSDNALSAAGAGLACQINDRIGLVDLGLFTSKRSRNAQTEGLNPABQVILTVGKQLTGKLYIGTGY
 GTSSABQSVKLYRLTRAIQAVARIGSRSSGGELTYTTRFDRLPGSDKKDSAGNGKKG

SEQ ID 335

GTGTGGCGGATTTCGATTCTAACACTGTTTCGGACGGGGCGGGACGCTTCAGACGGCATACCCCGCCGGTATTTCGGAGGTTCGGGCCCGCCGAAATGTATCTGCTTGTTPTAAGGCATT
TTCATTCTCAATCCGCATATGGAAAAACAGGCTGCCGTTTCGGAAATGATGTTCGAAAAATAGGCAGGAT

SEQ ID 336

VWRISILTLFGRGGTLOAYRRRYFGGCGPPEMYLLVLRHFVSNPHMENLRFGTIVSKNRQD

SEQ ID 337

GTGTAGTAATCGAAATCCGCCACACCGATGCACGACACCCGTACCATGATGATCAAACCGACCGCCCTGCTCTGCGCGCTTATTTTCTTTCCGACGACATACGGCCCTGCGCGGAC
TTTCCGAAACAAAGCGCGGGTTTCGCAATTGTTCAAAGCAAAAGCCCCGACACCGGAATCAGTCAAATTAACACCCAAATTCGCCGTCCGCATCGACACGACGAGCAGTGAATCAAAGA
TATGGTCGAAGAACACCTCGCCGCTCATCAGCAGCAGCAGGAAGAGGTTTGGTAATGAAGAACAGACGCGGATTCCTTGCCGAAGAAGCACCGGACAACGTTAAACAAATGCTCCGACGAA
GGCTATTTACGACGAAGGTTCAGCTTCACGGAATAAGACGGAGCTTACAGCGTGCAATCACACCGGGCCCGCGCACAAATCGCCACGCTCGCGCGTCCGCACTCTCGCGGACATCTT
CAGACGCGAACCTTCGCGGAATATCAGCAACACCGCTCGGAATACTTGACAGCAGCGGTAGGCAGCGGATTTCGATCAGGACAGTTGGGAAAAACAGCAAACTTCGCTCTCGCGCGGTAAC
CGCGAAAGGCTATCCCGCTTCGCAAGCTCGGCAACACCCGGCGCGCTCAACCCCGATACCGCCACCGCGGATTTGAACCTGCTGCTGGACAGCGGGCGGCCCAATTCGCTCTCGCGGACATTT
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AGCCACGCGCGCAATCTTCGGGCAACTATCGACGAAGTCAAGTCTTCTCAACCGCTTCGACACCCAAACCTCGAAGAAACGCGCTTCTCCGCGGCATCTGGTATGTGCGGACCGCG
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TTACGCGCCGAAACAAAAATCTGGGACGTTCTATCATACGCGGACAAGCGGGTTACACCGTTGACGCGCAATGCGGATGTCCTTCCGCGGGCTGATGTTCCGCGGCGCGCGCTT
CGGTGCGCGGTTACGAACTTGACAGATCGGGCTTCCCGGTTCCGACCGATCGGCTGACCCGAAACCGCCCTCTTGGTGCGGCACTTGAATTAACCAATCGGCTTTACGCGCACCGCTGTC
CGGCGCGGATTTCCAGATATGGGCAATGCGCGCGGCTTCTCAACGCTTATGAGCTGACCAACCGGTTTCGGGATCGGCGTGCCTGGTTACGCGCGCTCGCGCGCTTTCTCTCGACATC
GCTCACGACGACGCAAAAAAAATTCGCTGGCAGATCAGCTTGGGAACCGGTTTC

SEQ ID 338

VLEBSKATPMHNDTRTHMTKPTALLPALFFPHAYAPAADLSENKAAGFALPKSKSPDTESVKLKPKPPVRIDTQDSEIKDMVEEHLPLITQQQEEVLDKBQTFGLAEBAPDNVKMTLASK
 GYFSSKVSLETKDGATTVHITPGPRTKIANVGVAILGDILSDGNLAETRYNALENWQQPVGSDFDQDSWENSKTSVLGAVPTRKGYPLARKLGNTRAAVNPDATADILNVVDSGRRPTAFEDF
 EITGTRQRPQETVSGLARFPQGPYDILLDLDFQALQNGHYSGASVQADFDRLQGDVRPVKVSVTEVVRKHKLETGIRILDSEYGLGGKIAIDYDNLFNKGYIGSVVMDVKRYETTLAAGI
 SQPRNYRGNWYTSNVSYNRSTQNLKRAFSGGIWYVRDRAGIDARLGAELFAGRKRIPGSDVDLGNSHATMLTASWKRQLNINWHPENGHYLDKGLTITGLTFISLTALIRKTSARAGYF
 FYPENKLGTFYIIRGQAGYTVARDNADVPGLMFRSGGASSVRGYELDSIGLAGPNGSVLPERALLVGSLEYQLPFTTTLGSAFVHDMGDAAANFKRMKLKHSGLGVRWPSPLAPPSFDI
 AYGHSDKKIRWHIFATGTFP

SEQ ID 339

SEQ ID 339
TTGGCGCGAATGATAAAACAAAGCCTGTCCCTGCATAGGGCAAATCAACGCACCTCAAAACACAGCTTGAAAAATAAAAAACACAGAGAATGAGTTTTCCTTTTAAATACAACATTTTT

SEQ ID 340

LRMIKOSLSLHRANORTSKHSLKNKKTQMSFLLKYNIF

SEQ ID 341

ATGGCGGTTCGGCAAACTCTTATTTCATGCGATCGGCGCGTGCAGCCTGGTTCAGGCAGATTGCGCGCGGTTTGGCGTTGGGCATCGTAATCGGTTCGGTTTCACCGCAACTGGGCTTGGCGG
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GATTATCTGCTCTTACCTCATCGGCACGTTTTCGCGCAGCCGTCAGCCCGGTCATCGCCGGTATGTTTTCGCGAGCGACATATGTTTGGCGGGCGCGGGCGATGTGTCCGCGCGCGCGCCT
TCCGGCATTTGGAAGTGTGAAATCGCTGCTGATGAACCTGGTCGCGCAACCCGATTAAACGCGATTGCCAATGCCAACTATATCTGGCATTTTGGCTTGGGCTTTGGTTTGGGCGCGCGT
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CACAAATCGCGAGACGGGTTTCGGCGCGCTGGCGGGTTATCGGAAGCTGCTTCCGGTGCTGTTGGGCTGTATGGCGTTTATCGCGCTGGCGGTCAATCCCGCATCGTGTGGTGGAAAAATC
CGCGCAACCCCTTATCCGCTGGTGTTCACCTGCCGTCGCGAAGCGGCGGTGATGCTTCTTTACCGTCTCTTCGCGCGCAATATCCCGCTGAATATGGCTTTGGCGAAAAAGCTGGGGC
TGCACGAAGACACTTATTTCGATTTCATCCCGTTGGGGCGGCTGACCTCAATATGGCGCGCGCGCGCATGATACCGTTTGGCTATGGCGGCGCGCGCACACCCAAGGCATACAGGTGTA
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AGAGAAACCGTCGGGAA

SEQ ID 342

MAFGKSLPFAIGRVSLVRQIAGLALGIVIGSVSPQLGLAAGLFGSLFVGALKAVAPVLVILVAATIAQHQKGNKAHRIPIIVLVIGITPFSAALTAVIAGNVFPTHIVILAGAGDVSAAPP
SCIVEVLKSLMLNIVAMPINAIANANYIGILAWALVGLAALRNHGSDVTRQVVADLAEAVSTVVKMIIIRFAPIGIGFGLVSSSTIAETGPGALAGYAKLLAVILGCMHPIALAVNPAIVWVKI
RNNPIYPLVPTCLRESGVYAFPTSSAANIPVNMAKAKKLGHEDTYSISIPLGATVNMGGCAITITVLMAAAHTQGIQVDFATALLLSLVATVSACGASGVAGGSLILLIPLACSLFGISN
DYAMQVVAVGFIIGVIODSAETLWSSSTVLPATAADLGRQRNRAE

SEQ ID 343

ATGCCGCTCTGAAGCCCGTTTGGCGTTGACAGGCATATTTTACAATTTTATGGCATATGGCGGAAACAATACCGGCTGCTTGAATATGTTTCAACACACAGGGCGATACATAAAGCGT
CGCCCTATGAAGGAGATGATGATGT

SEQ ID 344

MPSEARLAFRRHIFTILWAYGNNVPGCLEYVSTHRAIKASPYEGDDV

SEQ ID 345

ATGAAGGAGATGATGATGTTTAAACGCACTGTGATTGCAATGGCTTGTATTTTCCCTTTTCAGCTGTGGGGCGGCGGTGGCGGATCGCCCGATGTCAGTCCGCGGACACGCGTCAA
AACCGCGCCGCCCCGTTGTGCTGAAAATGCCGGGAAGGGGTCTGCCGAAAGAAAAGATGAGGAGCCAGCGGGCGGTGCGCCGCAAGCCGATACGACGACGCAACCGCGGAGA
AGGCAGCCCAAGATATGCGCGGAGTTTCGGCAGAAAATACAGGCAATGGCGGTGCGGCAACACCGGACACCCCAAAATGAAAGACCGGGGGCGCAAAATGATATGCGCGCAAAATGCGCGC
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AGCGCGATGATTGTCATATGGGTACGCAAAATTCAGGCGCCATCGATGGAACGGCTTTAAGGGGACTTGGACGGAATGGCGCGGGGATGTTTCCGGAAGGTTTACGCGCCGG
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SEQ ID 346

MXEMMFKRSVIMACIFPLSACGGGGGSPDVKSADTPSKPAAPVVAENAGBVLPEKKDEBAAGGAPQADTQDATAGESSQDMAAVSAENTGNGGAATTDNPKNEAGAQNDHPQNA
ESANQTGNNQAGSSDSAPASNFPANGSDPGRNVNNSVVIDGPSQNTLTHCKGDSWGNMLLDEAPSKSEFKLSDEKIKRYKDEQRNFVGLVADRVRKDGNTKYLIFYYDPR
PTRSARRSLPAEILPIPNQADTLIVDGEAVSLTGHSGNIFAPBGNRYLYTGAELPGGSYALRVQGEPAKGEMLVGTAVYNGEVLHFMENGRFPYSGGRFAAKVDFGSKSVGLID
SGDDLHMGTKPKFAAIDGNGFKGTWTENGSDVSRFYGPAGEEVAGKYSYRPTDAERGGFVAGKDRD

SEQ ID 347

TTGATAAATCCTTATAAATTTCCCGCAAAATTGACCGCGAACACGAAAGCGGATAATCCGCCATCTTCAAAACCCCTTCAGACGGCAATTTGACGCAATGCCGTC

SEQ ID 348

LINPYKFPKIDREHEKADNPPIFKHPSDGICSNV

SEQ ID 349

TTGATGTTGATGCCCGCGAAGCGCAGGTATTCAATTACGGCGGACGACGCGTTCAATCATCAAAACAGCCCGCAAAAGGCGGATCCCAAAATCCGGCACTGAAATGCGCGCGTA
TCGCGCGCATTCGCGAGCTGCCGGGAAACCGTCGCGAGCAGCGGAATGTCGGGTATTTCGCGCCGCTTTTTCGGGCTGT

SEQ ID 350

LMLMPFEAQVFTAGRRVQLIKQAPKEGIPKSGTEIARIGIIPQAGETVGSRRNVGYFRPFSGC

SEQ ID 351

TTGCACCGCCCGGATTTCGGAAGGCGATGCCCTTCCCAACACCGGCGGAAACCTCGCGCCCGAAGAGCGGGTTCAAGGCATTATCTCCCTGCTGCTGCCGTTGGAACCGCGGAGTG
TTGAACACACGCGTTAAAAAACAGGCGCTC

SEQ ID 352

LHRPDSERRCLSPNRPEPCRPERRSRHYLPAAGWNRRESVETPLKQAV

SEQ ID 353

GTGCAACGGGGTGCCTTATGTGCCGAAAGGTTTGGCGCAACGATATGCCGCTGAAAGCGGGTGCCTTCAGACGGCAATTGTGATGTTTGGGGCGGGGTCCGGTTCAATCCGCAATCAG
TTGATAAACCCGTTGTCTTTCAATTTTCTTTTCAGAAAAATCTGGCGCATACGACGAGGGCGGAGGATGATGACAAACAGCCCTGCCATAGTCAGTGTGATTTTGAAGAACAATTCCG
CTTCGAGAAAAGAAAAACCAAGTTGCACAATCAGCAGCAGCACCAGCGCGCAACAGTCCGAGACAGGCATAAACCGCGAGCTTAAACACGGTCCCGCTCAAAA

SEQ ID 354

VQRGAPVYPKGFAATVCLKRVSDGIVMFGARVRFKSASVDKPVVHFHFKILAAAYQGGEDDKQCHSQCDFEEQPGFEKRRPKLHNOQHPAGKQSETGINAEKHPAPK

SEQ ID 355

GTGCTGCTGCTGATGTCGAACCTTGGTTTCTTTCTTCTCAGAACCGAATGTTTCTTCAAAATCACACTGACTATGGCAGGGCTGTTTGTCTATCTCTCGCCCGCTGCTGGTATGCGGCC
AGTATTTTCTGAAAAGAAAATGAAAGACAACGGGTTTATCAAC

SEQ ID 356

VLLLVQLWFSFLEAELEFKITLTMAGLFVILAAALLVCGQYFSEKMKDNGFIN

SEQ ID 357

ATGAAGAATACAAAGTCGTCAATTTATCAGGAAAGCTGTTGTCCAGCCTGTTTTCGGCGGGCAAAAGTCAACCCGCTCAATTTACAGCGGTTCTTCAACAAACAAACCCCGAAGGCT
GGCGGGTCTGATGATGGAAGAAATTTGCCCGTATGCTGCTGTTTTCACAAACGCGAAGCCTACGCTGCTCAATTTGGAGCGGACCGGTGT

SEQ ID 358

MKEYKVWIYQBSLSSLPFGAAKVNPNVNSAFLNKQTPGMRVVMKEKDLRMLLFFKREAYVVLERDRV

SEQ ID 359

TTGTTTGTGAGGAACGCGCTGAAATGACGGGGTGACCTTTGCCCGCGGCAAAACAGGCTGGACAACAGGCTTCTGATAAATGACGACTTTGTATTTCTTTCATCGTATTTCTTTT
CGGTGAAACCCCGCCTTTGGGGCGGTAGGATCAGACTTTATTTGGGAGGAAACCCCTTCCAAATCAGGACGATACATAGGCGGTGCTTTATGTATCGCTCTGTGTGT

SEQ ID 360

LFVEERABIDGVDLCRAERQAGQAFLINDDFVFFHRLSFSVETPPFGAVGSDFIWEGTPSKSGRYIGRCFMYRPVC

SEQ ID 361

ATCGCGCAAAATTTATGCTTATGCCCCAATGCGGCAATACCGAGCCTTCGCCAGCGAGAGCAAAACCGCTTTGCGAATAAATACCCAGTTTGGCGCGGGTGTGCGGTGATGTCGAGGTTG
CGCATCGTGAGCTGTCCGATGCGGTGAGCGGTGTGAACGCGCAGCTTCGACTTTTTCATACTCAGGCGTTCGGGTGTTAGTTCAGGTGCGGATCGGTTGTCAGAAATCGAGTAGT
CGTTGCCCGCGCGAGTTTCGAGGGAATTCGCGCGTAACGGCTTTGGCGACCCAGCGCTTGGCGGGTTTCGCGCAACATCAAGCTTTGGCTGTGCAACAGCGCGCTTGGTAGAGCAAAAG
TCCGAGGCGCAGGCGGTTGATGCGGTATTTGTCGATGCTGTCTGTTGTGATGCGGTAACCAAGCGTTTCGAGCGATGCGGAACAAATCCATGCCCGGGCTTCGTAGATGCCGCGC
GATTTGGCTTCGATGATGCGGTTTTCGATTGTCGCTCATACCCAAAGCGTGGCGCGCGCGGATGCGGTTGGCTTCGAGGAAGAGTTCGACGGGTGCGGCTATTTCTTTCGCGTTCAATG
CAACCGGCACGCTTCTTCAAGCGCAGCTGACTTCTTCGGGTTCAATTTTCGAGGTTTTCGTCGAGAGGCAACGCCATGATGGCTTAACGATTTTGTATGCCGAGTTCAAAAATTC
CAAGTCTTTGGCTTTCGGGTGCGCGGAGCATATGGAATCGGTGAGTAGGCTTTTTCACCGACATTTTGTAGTTGAAGCGGTTCGCAATCAGAAATTCGCTCATTTTCGTGACGCGCG
CCGAGTTCGTGATAAATTCGTGTCGAGCCAGGCTTTGTAGATTTTCAGCGCGGATTTGGTGAGCAAGCGGTAGCGGTAGAAACGCTCGATGTCGTTGCTTTGTAGGTGCTGCCGTCGC
CCAGATATTACATCGCTTCTTTCATGCGGAAACGAGCATGTCGCGGTACGCGCGCGCCAGAGCGGTGTTGAAATAGCGGATGCCCGCGGTGGAACGTCGGAACGCGCGCGCA
TTGGATGCGCGGATGCTTCTGTGTGCCAGTTGTGCGCGGAGTCGATCAGCGCGGCTTTTCCGACCGTATTCATTTCTTTTGGGAATGGCGTTGTAATCGCTTTCGTGCGGCTGTG

CCAAAGGTTGGCAGTGTAGGCATAAGGCAGCGCCCTTTGAGTTTCATCCACAACAGCGCGCAGAGGTATCAAGACCGCCGGAAGGCGATGCCGACTTTCTGAACGACGGGAGGTTT
G

SEQ ID 362

MRRNLLLTALRLQYRAFAQREBTALRINTQFAGVGDVEVAHRELSDAVERCERRTFDFHTQAFGLVQVGRFVQNRVVAAPQFEGNFAGNGPGDPALGGFAHQGLAVEPALVEQT
SEAQAVDAVLFDGVFVVDAGNQAFVGDVEQCHARGFVDAARPGFDDAVFDLVAHTQAVAAADAVGPEEFBDGVGVFFAVQCNRHAFPAHADFPGFNFVDFVPBGNADGLNDFDARVQRF
QVFGFVRAEHIGIGGVGFNRHFVVEAVGNQKFAHFVTAAEFVDKLLVEPGFVDFQRGIGEQAVAVETLDVVAVFGAAVAPDHIIVFPHGGNEHGAGHGAQRGRVETGDAAGGNVERAA
LDGGDAFVQCQLCAANDQAGVFRVPHCFPGNGVIVFVGLAKVGSVGLRQRAFEFHPQQRGRGIRKTAGEGDADFLTDGEVL

SEQ ID 363

ATGAACCAAAACCATCTATTTTACAAAACCTCCCGTCGGTCAGAAAGTCGGCATCGCCTTCTCCGGCGGCTTGTGATACCTCTCGCCGCGCTGTGTGGATGAAACTCAAAGCGCGCTGC
CTTATGCCCTACACTGCCAACCTTGGCCAGCCGACGAAGACGATTACAAACCCATTCCTCCAAAAGCAATGGAATACGCTGCGGAAAACGCCCGCTGATCGACTGCCCGCACAACTGCG
ACACGAAGGCATCGCCGCATCCAAATGCGGCGCTTCCACGTTTCCACCGCGGCATCGCCTATTTCACACACCGCCTTGGCGCGCGCTGAGCGCGCACCATGCTGTTCGCCCATG
AAAGAAGACGATGTGAATATCTGGGCGCAGCGCAGCACTACAAAGGCAACGACATCGAGCGTTTCTACCGCTACGCTTGTCTACCAATTCGCCGCTGAAAATCTACAAACCTTGGCTCG
ACCAGCAATTTATCGACGAACTCGGCGCGCTCAGGAAATGAGCGAATTTCTGATGCGCAACGGCTTCAACTACAAAATGTCGCTTGAAAAGCGCTTCCACCGATTCCAATATGCTCGG
CGGACCCACGAAGCCAAAGACTTGAATTTTGAATCTCGGCGCATCAAATCGTTAAGCCATCATGSGCGTTCCTTGGGACGAAAACGTCGAAATTTGAACCCGGAAGAGTCAGCGTG
CGCTTTGAAGAAGCGCTGCCGCTTGAATTTGAACGCGCAAGAAATACCGCGACCCCGTGAATCTTCTCGAAGCCAAACGTCATCGGCGCGCCACCGCTTGGGTATGAGCGCAACAAATCG
AAAACCGCATCATCGCAAGCCAAATCGCGCGCATCTACGAAGCCCGCGCATGCGCATTTGTTCCACATCGCTTACGAACGCTTGGTTACCGGCATCCCAACAGAGACACCATCGAACATA
CCGATCTAACCGGCTCGCGCTCGGACGTTTGTCTACCAAGCGCGTGGTTTCAGACGCAAGCCTTGATGTTGCGGAAACCGCCCAACGCTGGGTGCGCAAGCGCTTACCGCGCAATG
ACCTCGAACTGCGCGCGCGCAACGACTACTGATTTCTGAACCCGAATCGCCCACTGACCTACCAACCCGAACGCTGAGTATGGAAGAAATCGAAGGTGCGGCTTACACCGCTCG
ACCGCATCGGACAGCTCAGATGCGCAACCTCGACATCACCGACACCCGCGCAAACTGGGTATTTATTCGCAAGCGGTTTCTCTCGCTGGGCGAAGGCTCGGTATTGCCGAGTTGGG
CAATAAGCAA

SEQ ID 364

MNQNTTILQNLFPVQKVGIAFSGGLDTSALILMMLKALPYATNLIQPDDEDDYNAIPKAMEYGAEMARLIDCRAQLAHEGLAIIQCGAFHVTGGIAYFNTPLGRAVTGTMVLSAM
KEDDVNIWGDSTYKNDIERFYRYGLLTNPALKIKYPLWDQFIDELGGRHEMSEFLIANGFYKMSVEKAYSTDSMHLGATHEAKDLFLNSGIKIVKIMGVAFWDENVETIEPEEVS
RPEZGVPVALNGKEYADPVELFLANRIGRRHGLMSDIENRIIEAKSRGIYEAQMGALFHIATYERLVTGTHNEDETFIEQYRINGLRLGLLYQGRWFDQALMLRETAQRWVAKAVTGEV
TLELRGNDYSILNTSPHLYTQPERLSMEKVBGAATPLDRIGQLTMRNLIDITTRAKLGIYSQGLLSLGBGSVLPQLGNKQ

SEQ ID 365

ATGAAAGCACCCGAACCTTATTGCCCGCCGCGGATTTGAAAGAAATGCGCGCCGCTACGATTACGGCGCAGATGCCGTTTACGCGCGCAGCCCGCTTACTCCCTCGCGCGCCGCAACA
ACGAATTTGCCAAACTCGACGCTCTCGAGCAAGGCATTAAAGAAGCGCAGCAACGCAACAAAAAATTCCTTTTGACCGTCAACACCTGCCGCGCAANTTCCAAACTCAAACCTTCGTTGC
CGACATGGAGCGCTGATTGCCATGAAACCCGACGCGCTGATTATGGCGGATCCGGGTTGATTATGACCGTGCAGGAAATGGCGGAAATGCCGATCCATCTGTCCGTACAGCGCAAC
ACCACCAACTACTGGGCGTGAAATTTTGGCAGAACATTGGTGTGAACGATCATCTCTGTCACGCGAATTTGGGATGGAAGAAATGCCGAAATCCCGCAAGAAATGCCCGCATCGAAC
TCGAAGTCTTTCATCCAGCGCGCATTTGTCATCGCTACTCAGCGCGCTGCGTGTGTCGGGCTATTTCACACCCCGCATCCCAACCAAGGCACCTGCACCAACTCTCGCGTTGGGACTA
CAAAGTCCAACGCCACGGAAGCGAGGCGAGCGATGCCAGCTTCTGCAAGGTTTCAACTTTGAAAAGCCCAAGAAAGCAACCAAACTTTGAAGGCATCAACGGTCAAAGACG
CATCCCTACGCGCAAAAGTTTCTGATTGAAGAAATCCAAACCGCCGCGAGATGATGCCGATTATGGAAGACGAACACGCGCACTATCATGAATCCAAAGATCTTCCGCGTATCG
AAGTCGTGCAAAAACCTCGCCAAATCGGTGTGGACAGCCTCAAAGTCGAAGGCGGTACCAAGTCTCTACTACGTCGCGCGCGTGCAGCTTACCGCAAGCGATTACAGGATCGCGT
CGCAGGCGCTCGGTTGATTACAGCTGTGTAGCGAACTCGAAGGCTTTCACACCGAGGCTACACAGCGGCTTCTCGAACGCCACCAACTCAGGATTTCAAACCTACCTCAGCGGC
CATTCACCGCCCAACAAAGCCAAATACGTCGAGACGTTACCGAAATCGACGAAATGGCTGGGCGGACCATCGAAGTTAAAACCCGCTTCCCGCTCGCGGATTCGCTCGAAATCATCCAC
CGAGCGCAACCAACCATCAAATGGAACAAATGACCCGCAAGGCAACCTGTGCGATGTTGCCCGGGCAACGGCATTCAGGTCAAATCCCAATATGACAGGCAAGAAAAAGCCCT
CATCGCACGCGTGTGAACCCC

SEQ ID 366

MKAPELLPAGGLERMRAAYDYGDADYAGSPRYSIRARNNEFAKLDVLEBQIKEAHERNKKFPLVNTLPHNSKLKTFVADMEPLIAMKPDALIMADPLIMTVREXWPEMPIHLVQAN
TNYWGVKPNQNGIVERIILSRELGMEEIAEIRQCPDIELEVFHIGALCIAYSGRLLSGYFNHRDPNQCTCTNSCRWDYKVENATESEAGDAQLLQGFNFKAQEANQNFEGINGQR
HPYADKVFLLIESNRPEMPMEDEHGTIYIMNSKDLRGIEVVEKLAKI GVDLSLKVGRKTSLYYVARVAQSYRKAIDHDAVAGRPFDYSLLSELEGLANRGYTSGLERHQTDQYQNTLSG
HSTAKQSQYVGHVTEIDENGWATIEVKNRFAVGDSLRIIHPSCNQTIKLBQMTKRGQVVDVAPNGIIVQKI PNMQGEKALIAVLNP

SEQ ID 367

TTGTGCGACATATCGGCTTCGCGGGCTGCCATATATGGATGTGCAAAAACAATATCCCTTTGAAACCGTCGCGGTATGCGTCTGCCGAACCATATTCAGGCATTGGACGCTGCCCGCG
ACGATGCGGATTTATCCCTACTCGCGCGCTGATTAAACCAAAATTCCTCCGATATTTCCCTCATACTAAAACTTAGGGCTGTACTAGATTATCCC

SEQ ID 368

LSDISASRAAYMDVQKQYFPFVAVCVLPNHIIHAIWTLPDDADYSLRLRLIKTKFSAYSPHTKNLGAVLDYP

SEQ ID 369

ATGGTTTGGTTCATGAAAAATCCTCGATAGCTTGAATAATCAAAGCCATTATCTTATAAATAGAAAAATATGTCAGCCATCATGCGCTCTGAACGGGTATTCGCGCTTTACGGCGGTA
TT

SEQ ID 370

MVLVHEKILDSLKNQSHYLINRRYQPSRLNGYSVSGGI

SEQ ID 371

ATGAACGCGTTCAACCTCATCATCGGAGACGAAATCTTACACGGCAGCGCGCAAGACAAGCATTTGCGCTTTTAAATCCCTGCTCGAATCCAAAGGCTGAAGCTCAATCAGGTGC
AATATCTGCCCGACGAACCGATTGCTGGTCAGGCACTGCGCGCAGCTTTTACAGCGCATACCGACGTTGTTTACCGCGGCACTGCGCGCCACGCGCCGACGCGCCCAAC
CGCAGCGCTGCTTTGGATTTCGCGCTGCTCGCGCATCTGAGAGCGCAAGTTTATCGAAGGCATAACCGGAAACGCGGCAAGCGCTCGATTGCGCGCAACGCGCCACGCTGAAA
ATGGCGGATTTCGCGAGGCGCAGAGCTTGTGCCAACCCGTTCAACAACATCGCGGATTTCATCCGCGCATTTATTTCTTCCCGGCTTCTGTGATGGCGCACCGCATGCGCG
AATGGGTTTGGAAACTTATTATGCGCGCGCTTCAACCAACCGAACCGCGCAGCGCGGTATGTTGTTGAGCAGCCGAATCGCGCATTACCGGATTTATAGACATATTCAGCA
AACTTATCCCGCGCTGCTGCTACAGCTGCCAGCGTGGTGGACGATTTCAGACGGCAGCAGGTCAAACCGCATTTAGTTCCGATCAAGCGAAGGAGAGCGCTCAACCTT
TTGACCGCGCGTGGCGGAAGTGTGACAGCTTGGACGAGTGGGAGCAGAGCTGAAAATCGGTTAAAC

SEQ ID 372

MNAFLNLIIGDETHLSGRQDKHFAFKSLLESKGLKLVQVYLFDEPDLLVRQLRRSFSDGIPPTVTTGGIGATPDDRTQTAAAAALDLPVVRHPEAAKFIETITRKRKPLDSPEHAQRK
MADFPEGAELVNPFPNNIAGFSIREHYFPFGFVMAHPMAEWLETTYAGRNQTERGSRSVYVFBQFESRITPIIEHIBQTYPGVRSYSLPSVGNWTHSDGTQVKPHIEFGIKAEGBAVNL
LDAANAELHSLDGLGAELKNRVN

SEQ ID 373

ATGCAATACCGAATCAGAAGAGAAAACGAAGCAGCCGAGCAAAAAATCGCGGGGAAACCTTATGGGAGCGGACATTATGCGCGAAGTGTGCTGTCCGCTATCGGACAGCGCAGGG
AGCGGATGTGAAAAACATCTGGCGCGCTCAGCACCTTGATTCTGGTTGCCCTGATTGCAAGCATTTCCGAAAAGACGAAGCCGATTCAGTTTGGCGGCAACACGCGCATACCGG

AGTCGTCAACCTGTACGGCAAAATCGGCAACGGCGTAGAAGACCAGGTCAAAAACTCAAAGACGGGATGGAGCCGCTACAAAAACCCGAGGCAAAAGCCATCGTCATCCGCGCCAAC
AGCCCCGGCGGTTCGCGCGTCTCCACACCCGCTTTTGAAGAAATACCGCGTCTGAAGGCGCAGCACCCCGGCATCCCGTTTATCTCGTGCCAGAGGATATGTCGCGGTCCGCGTCT
ACTACATCGCGCGCGCGCGGCAAAATCTATGCGGACCCGCTCCAGCATCTGCGGACGATCGCGGTATTCGCGCAGCAGTTCGACCGGACCGCGCTGATGGAATAAATCGCGGTAAACG
CAGGGTTAAATTCGCGGCGAGCAAAAGGCATGGCGATCCGTTTTCGCCGAAACGCCGGAACAGTCGAAATCTGGGAAGAAATGTGACCGGCATACACGGGAATTTATCAAGCC
GTCAAAACCGGACCGCGCGCGCGCTCAAAATCCGACAAATATCCGACGTGTTCAGCGGTGCGGTATCACAGGCGCGGACCGCTGAAAGTCGGGCTGGTGGACGACTCGGCAATATTT
ACAGCGTGGCGGAGACGTGTCAAAGCTCCGATGTGGTGGATTACACTCCGAGGACGATTTCGCGCAGAAATCTTGGGCGACGCTTCGGAGCAGAACTCAAGCAAGCGTTTCGGAAGC
TCTCGAGCCGCTCCG

SEQ ID 374

MYRIRRENEAPEAKNAGETLWERDTHREVLISAYRDRRRERMMKNIWRAVSTLLILVALIAGIFRKDEAALQLAGNTPHTAVVNLVYKIGNGVEDQVKKLKDMGEAAYKNPQAKAIVIRAN
SPGGSFVVSNTAFERIRRLKAQHPGIPVYLVAEDMCASGCTYIAAADKIYADPSSIVSGISVIGSSFDATLMEKIGVKRVRKLAGSNKMGDPPSPETPEQSKIWEMLTGIGEFIRA
VKTGRGRLKFRQYDVPFSGRVTGADALKVGLVDGLNITYSVARDVVKAPDVVDYTPKLDPRILGRFRGAEKASVSEALQAVR

SEQ ID 375

ATGCACAAAACCTCCCGGGGACAACTGCTTTTCGGGCTTTAAGTGACCGTAAATAGTAACGCGGCTGACTAGTGGCAGCATACTGGGAGGTGAGTGTTTTGTGTATATTTTATTT
CTGGTATTCCTTAGAAATACTG

SEQ ID 376

MHKTSGQPAFCGFKCTVNSNAADLVAAYWGGECFCVYFYSIGIPLELL

SEQ ID 377

ATGTTTGTATGGCAAGTAGAAGCAGATGAAAGTATTTTGGCGGACAAACGCAAGGTAAATGCGGTGCGGTGCTGCCGGAAGTCCAGTATTCAGGCTCTCAAACGAAATGCGCAAGG
TTTCTCTTTCGCGTCCGTATGTACGTTTCGTAACTTCGAAGACTTCTTGAACCTTCCCGCGGTTCGCTTCTGTATACCCCTCTGTAGATAAGGGGGGGAAGATTGGAAGCGGTGCGC
GGCTCTTCCGCGTCCGTGGCGCGCTCCGTATCACGCCGGAACCTCTTGTATCTCTTGTATCTCCCATGTGCGAATCTCTCAAACCGGGCAAAAAAGCCCTGTACTGTAGTA
AAG

SEQ ID 378

MPDGEVEADESYFGQKRGKCGRAAGKVAVFRLLKRNKGVSAVRVYRVFTFEDFLNPARRFPGCTPLLDKGGEDSKRLPASCRPSARPSSRRQPPLSSLAYLPCANPQKRAKSPVTCR
K

SEQ ID 379

GTGAAACCTGACAGCATTTGTTATACGATTGTTATCGTCGCTATGATGTTATGGATGACAGGCGAATTTAGCCATTTCCGTATCAATCACAGCACACATTTTCCGGAACGACAAAACCATTA
TTAATGGAATTTGGAACTTTTGGAAACCGGCAAAACCTCATTTACGCAAGTTTGAAGCGCATTTCCCAAAGAGCATTTTGAAGCGTATTTAAAGGAGTCCGAACCGCGTTTAAACACAGTGA
GATAAAGTCTCTGTTCCATTT

SEQ ID 380

VKPDIVTDCYRRYDVLDAGEFSHPRIHNSHFAERQNHINGIGNFWNRAKRLKFDGIPKEHFPYLBECERFNNSEIKVLVFP

SEQ ID 381

ATGATTATTCAAAATGAATTTAATTTATATCTAGTAATATGCTTCTGAAGGTTTGTATCTGAAAAGTATGTTCTGATCTCTAACGATACATCTTTAATACCTTATATTCAGCCAC
ATAATTTTCATCTGTTGTTTGAAGATTTATGGAACAGAGGGGAGAGTAGCTTATATATTTAGAAATTCATCTGCTGATTTAAATCTTATCCCATTCGTAGTAATGGAGAAATGGGA
AGCTTATTTGATGCTTAATGATGTAAACAGGAAATCTAGCGTTATGTTTATTAATTTAGATAATATAGAAAACCATGAATTTTTAATAGTTTGAAGAGTGGCTTGAATTAGCAATTAAG
GATACTTG

SEQ ID 382

MIQNEFNLYPSNMLPEGFCYPEKYVRI SNTSLPIYIQPHNFHWFENYGTGEAEVAYIFRNSILPDLNLIPFASNGEWEAYFDGNDVTGNPRVIVINLDNIENHEFFNSFEWLELAIX
DIW

SEQ ID 383

ATGTCCACCGCGCGCTGTGGAACGGCGGTTTCGCCAGCCAGCAATGGGAATCAGGAGGATAAAACAAAATGCTCCGGCGAGGAATATTTCTGTCGATCCGATGATGAAGCCCTGTTGC
GTAATGSTATTTGTATGATGCTTAGATTGACCGTCGGAAATGCTTGTGGGACAAATGCGCGCGGTTTCGTGCAATGTTGCGGAATAGGCGGTGATGTTGCGCAAAACCGGTGT
GGTGCACCGCTTCGCGCGTTCACAGGGTCTGACGACGGATACCGCGACACCGCCCATCAGCACGCGCAGGAAATTCGACAGGCTGCCGCGCGCGGCAATCTGTCCGCCCTTCATGTG
CGACAGTGTGATGGTGGTCAGCGGAGGAAGAATCGCAACGCCCTACCCCTTGCCAAACTGCGGCCAGATGACGTTGCCGATATCCATGTCGGCATAAAAAATCAGTGCGCCAATAAAAA
GTGAAGCCAAAGTTCAGGAAGCTGCGGTTACGAGCAGCGCATATCGATTTTATTTGCCGAACCTGCCGATTAACGAGATAGGAAGACGCGGGAGATGCGCAGCGGCGCGCAGCAGCC
CTGCCACGCGGAGGTATAGCCCAAGTTGGTCTGCAACACTAACCGGACGAGGTCAGCGTCCCATATACACCATGAAACCCAGAGGTGGCAATTAACGCGCGGTAAATTCGGATC
TTTAAACAGCGGATAAATCGACAATCGGATATTTTCTCCCAATTCCTCAAAATAAATACGACAAGCACACCGCGGTTATGCCAAGGTAATGATTTCTCCAGAGCGCAACAGTCA
AGTCTCTTACCCCTGTCCAGCATCATCTGTAACGCGCGATACCGACCATCATCAGCTCAGCGGACATAGTCTGCGCGGTTCTGACGCTTCCGCTTTCGCGGTGTTTCAAATGTTTCC
ATGTAATCATGCGGATATGATCCGATGGGATATTAATGAAGAAATCCAAACCCAAATGCCAGTTTCCGGAAATCCAAACCGCGGATATCGCGCCGAGGACAGGGCGGACACGAGCGT
CATTCGCCCAATGCCAGTGCAGATCCGTTTTCGGGGCGGATAGGATGCCATTAACAGGCTTTGCGACAGGGGAATCAACGCGCCCGCGATAAAGCCCTGCAAAATGCGGAAACAAAC
AGCGATGAGGTTGGCGCGGATGCCGACAGCAGATCGGATGACGAAACCGCGCGCGCGGTAACCAATTTGACCTCGCGGATACGTTTTCGCAAAAGCCCGTACCGCGCACGG
AAACGCGGTTTGCACGGAAGAAAGAGTGTGACCCAGTCCCTGCGTGGTTGCCGACCGAGGTTGCCGGAATGACGGGACGCGGACGTTGGCGATGTTGATCTAAACCTCCAT
AAATACGGAAGCCCAAGACAGCGTAACCCAGCCCAATGCCGACCTTAAGCGGTGGAATATCCATTTGTCTCCGTTTCAGACGGCAT

SEQ ID 384

MSTAAAVERRFRQFANGNQDDKQNAAGEEYFVRSDEALLRWIGIVDDA*SLTVGNALIGQRRRRFVQCCGIGRNVFGKTRVVQRFAPFPQGADDGYADTAHQHAQRIQAAGGNNLSALRV
RQCDGGQRQEEHGNAYPLPKLRPDDVADIVHGIKISAPIKSEKGGQEGGYEQAHIDFLAEPAD*RR*EDGEDADGRGSKPCPRGGIAQVGLQH*ROQGORPHIHETQRGNYADGKIPI
FKQR*IDNRIFPSQFPMKIRQAHRGYAQGNDFSRGEFVKFLTPVQHHL*RADTDHQRQPDIVGRRSDGCRFAVFMFPCNPCRYPDGDLINEENPTPMPVSGNPTAEYRPEDRGDNDG
HCLQCCQHPFCGRIGCH*QALRQGNRPRGDKALQNAENNRQLKVRDAAQPRCDETTGGGGGQFDLADTFQKQKARQHRHNGVCHGKRSDDPRFLRCRTEVAGNDGDGVDGRI*NLH
KYGKPRQRNPRQCRILKRWIHCVLRFRRH

SEQ ID 385

TTGGCAGGCTCCAGCATCAGGCGCGCGCGGAGATGAGGATTTTTATGTCGGATGTCCTTGTTCGTGTTGGGAAATCATTCGCATTGTACAGTAAGATTCAACAAAATCCCGTCTG
AAAACGGGGTTCCGACGGCATTGTGGCTCAGGGGTTCAACACGCGTGCGA

SEQ ID 386

LACQHQGGGEYEDFLCRNSLFAVGNHCHCTVRFNKMPSENGVTRTALNLRGSTRVR

SEQ ID 387

ATGAAGATAACACACTGCAAAATTAAGAAAGAAAGTACAGAAAGAACCGCTCCGTTCTTTGTACCCGAAGTTACCGCCGCTTCTGCCCGCGATATTTGGGTATCCATCCCGATTCCGCGG
CACTGTTTACCCGTAAATTCGACCGGTACCAACCATCGTTTGGCTTGGCTGCGGATGAGGTTTTCGAGGCGCCCGCGCGCGCGGAGCTGTTTCCGCGGACGGCGGTAAAGGCAG
ACGCGTTCGCGCGCGGAGGAAAGCGGTTGCTTCCGATTCGGAACGCAACGGCGCGGCTTACCTGTTCCGCGGACATGCGGAGCTGAAACGTTTACCCCTCGCGCTCAAAAAG
AAAATCATGCGCGGATGTTTATGCGGATAGCCCGGCGAGCGCGGCAAGTTGACGCGCGGCGGTTTACCCGTTGCCGATCAACCGTTTCAAGGAATTTGACAGCGCTCGGAACC

ACATTAACGGCATTGGGAACCTTTTGAATCAGGCAAAACGCGCTTTCGAAAAATACAACGGAATCGATCGTAAACCTTTCCCGCCGTTGTTGAGGGAATGCGAATTCGACTTAACTTCGG
CACACCGTCCCGGACAGTAAAAATCTCGCGGATCGGTGTGGAATT

SEQ ID 388

MXITHCKLKKEVQKEPLRSFVPEVTARSAADILGIHPSAALFYRKIRTVNHRLLAADEVFEPAGPGGSCFGRGRKGRGRGAAGKAVVPGIPKRNGRAYTVAADNAEPETLPPAVIK
KIMPDGIVYADSPGSRGLDAGGFTRCRINRSKEFADRRNHINGIGNFWNQAKRALRKYNGIDRKPPPLLRCEFRNLNPGTSPRQLKILRDRCGI

SEQ ID 389

ATGAATGAACACAACCTGTTAATTTCTGTTTAAAGACAATGTTTCAATTAAGTGAATATACTGAAATGGTTGATGGGCTTATGAAAAATTCAATCTGAAACAGTTGTAGAAATTACGG
AAAATCAAATTTATGAATATCAAAATCGTGATTTATGGGGCTTGTCTGAAATTAACGATAATTTGTTATTTGGACCAAGTGAGGGGATTTGCTAATAGATAAGGAAAGTATTTTGGC
TGTAAGAGAAAAATTACAAAATTCAGATTTTCTACAGAGCCCTTAGTGAAAAATATTATTATGTAATGCTATATAAAAAATGAAAAACAGTAATTTTTCATTTT

SEQ ID 390

MNEHLLIFCLKDNVSISETTEMVDWAYENIQSEFVVEITENQIIIEYQNRGLWGLVSRITDNLWLPFSEGDWLDKESILAVKEKLQNSDPSTEPLVKNIIHVLEYAIKNEKTVIFHF

SEQ ID 391

GTGGGCATCAATGCCAATCCTAATCTGTGCTGATGAAGCAGGAAAACCTGATATGGGAAAACGACCCCGATAAAAATTTGGTGGGCTAACCGTATGGATGATATTCGCGGCATCATCCAAGGTG
CGGTTAATCCTTTTAAACGGGTTTCAAGGAGTAGGGATTGGGGCAATTACAGACAGTCCGGTAAGCCCGGTACAGATACAGCCGCTCAGCAGACTCTACAAGGTATTAATGATTAGG
AAAATTAAGTCCGGAAGCACAACCTGCTGTGCGGAGCCTATTACAGGACAGTCTTTGCGGTAAAGACGCGCATTAATTCGCCAGACAATGGGCTGATGCCATCCGAATATAACAGCA
ACAGCCCAAACTGCCCTTGCCGTAGCAGAGGCCCGCAGGTACGGTTTGGCCCGGTAAAAAGTAGAACTTAACCCGACCAATGGGATTGGGTTAAAAATACCGGCTATGAAAAACCTGCTG
CCCGACCTATGAGACTGTTGACGGGGAATGGCAGGTGGGAATAAACCATTAACTCTTACCAACAGCGCCGTGAAAAAGAAAAAAGTTTAAAGAGTTTAGTAGCAACTGGAG
TTCAGCAAGTTTGTATTAGTGCACAAAACCTAATCCCAATGCACCTGGTATTAACTCTGATAAAGTTAAACTCGATACACTAGTTTAGATGAAAAATTAACAATTATAAAGAT
AACGAAAAACAATTTTGAATCCATGATAATTACGAAAAACAGTATCTTGATTCAAATGGTAATGCTGTGAAAAACCGGTAATTTACAAGGTAAAGCAAGCAAAAGATTATTACAACAAC
AAACTCATATCAGGAACCTTAGACAAA

SEQ ID 392

VGINANPNCADAEAGKLIWENDPDKNWWANRMDIRGIIQGA VNPFLTFGQGVGIGAITDSAVSPVTTAAQOQLQGINDLGKLSPEAQLAVASLLQDSAFVAVKDGINSARQWADAHFNITA
TAQTALAVAEAGTVWRGKVELNPTKWDVKNVTGYEKPAARPMQTVDEMGAGNPKIKSLPNSAAEKRKQSPKFPSSNWSSAFDSVHKTLTPNAPGILSPDKVTRYTSLDGKITI IKD
NENNYFRIHDSNRKQYLDNNGNAVKTNGLQKQAKDYLLQQQTHIRNLDK

SEQ ID 393

TTGACAAGCAAAATAAAATTATTATGAATATAATCAATTACACAGGTGATGACATTATTATTTCTTAAACAAGAGAAGAGCTTCAATTAATTCGGTTCCCTTGTATTGAAATTTATGCAG
GTGTTTGCATAGACTGAGAAGAAATTTGAGATTGTGTCAGGAATTCGCAATCTCTCAATTAGTGCAAGAGCTAGAACAACATTTAATTGAAGCATATAATCTAATGGATACATCTAAC

SEQ ID 394

LTSKNKILMNIINYTGDDIIISLTREKQLRLSLVIRIYAGVCIDAREFEIVSGIRNPQLVQLEQLHLEAYNLMDTSN

SEQ ID 395

ATGATTAAATTCGATTTAAAAAGCATAAAATTTATATGATATTGATTTTGAATAATTTACCCCGGAAATTCAGATAAATTTTCATAGATGGATAGATTTCGATATCGGAATCGAAGGAGAAC
AAGGCTCATCTATTTTTCACCTTTGCATTTGTTCTCTCAATGGATTTCCTCATCTGTAATAAGAAGGTTTTCCTTGGTCTAATGCATTAATATTAGAACAGTTTGATCATAAGATTAT
TAAAGTGAAATTTGATAAAATTTAGAATATTGCTCAAAAGAACTTTGGGATTTCAGACTTTCAAACCTATTACGATTTTTCCTTGGGAATTCGAAGATTACAATCCAAACACA

SEQ ID 396

MIKLDLKSINLYDIDFEKTPPEIPDNFHRWIDLIDIGIEBQSSIFSLCICSPKWI SHHCNKEGFFWSMALILEQFDHKI IKSEIDKILEYCSKETWDLTSLNLLRFPSPWEPEDYNPNT

SEQ ID 397

GTGCAGATGGCACAAGCGTATATCGTCTCCAACATCAAAATCAACACCCCTGAATCACTTAACCCAAACGGGAGTGCAAGCTAATTTGTTACTAGAAAGTTGATGAAAAACCT

SEQ ID 398

VQMAQGYIVLQLNQTPILNLTQRECKLILLLVLMKFP

SEQ ID 399

TTGTCCGATACAAATAAATATCCGACCTACATTTCTGCGCAGCAAACTTTACAGGGTATTCAGGATTTAGGAAATTTAAGTCCCGCAGCACAACCTTCCGGCTGCAACCGCATACAGACA
GTGCTTTTCCGGTAAAAGACGCGCATCAATTCGCCAGACAATGGGCTGATGCCCATCCGAACATTACAGCTACTGCCCAAACTGCCCTTCCGCTAGCAGAGGCGGCGAGTACGGTTTGGGG
CGGTAAAAAGTAGAACTTAACCCCGGCAAAATGGGATTGGGTTAAAAATACCGGCTATAAAACACCTGCTGTTCCGACCATGCATCTTTGGATGGGAGATGGCCGGTGGGAATAGACCG
CTTAATCTATAACGTCGAAGGAAAAAGCTAATGCTGCAACCTATCTTAAGTTGGTTAATCAGCTAATAGAGCAAACTTAAATAACATTCGCGCTCAAGATTCAAGGTTAGCAAGTGTCTG
TAAAGAGATTGGAACCAATACAAACCAATAAAAGGGGGAATTAATTTGGTATTGGTTCTGCAACTCGTCAAGAGGCTGAACAGTTAGGAAAAATTTGGGTTGGAGACGGGGCTAAGCC
AGTTAGTAGTCCATCTTGTCAAGGATGTATGTTAAGTGCAGATGGCACAAGGCTATATCGTCTCCAACCTACAAATCAAAACCCCTGAATCACTTAACCAACGGGAGTGCAAGCTAAT
TTGTTACTAGAAAGTTGATGAAAAACCTTAACATAATGGACATTTGAATATAAAA

SEQ ID 400

LSDTNKYPYIISAQOQLQGIHDLGNLSPAAQLAAATALQDSAFVAVKDGINSARQWADAHFNITATAQTALAVAEAGTVWGGKVELNPAKWDVKNVTGYKTPAVTMTHTLDGEMAGGNRP
PKSITSKGRANAATYPKLVNQNLNIAAQDSRLASAVKDWKTIQPNKKGEINFGIGSATRQEAQLGKIWVGDAKPVSPSCQGCMLSDAGTRLYRPTTKSNTPESLNPITGVQAN
FVTRSDGKTLNGLHLNIK

SEQ ID 401

TTGTATCCGACAAAAATATTGACGCGCTATCGTTCCGAGATGCCGCTGTGGAAAAATGTCGGATTGAGAAATCCGATCTACGGCTGC

SEQ ID 402

LYPTKIFDPIVSEMPLENVGFENPIYGC

SEQ ID 403

ATGAATATACTATCCATAAATAATCAAACTCAACTATTTCTACTAAGTGAAGTTTGTGTTTACGAGCTATCTTGAATGAGATATATGCGGGCGTATGTTAGATTCAAGAGAAT
TTGAAATGTATCTGGTGTAGAAAAATGAGTAGATAATTTACAACAACAGTTTGTGGAATTTATAAAAAATGACAACT

SEQ ID 404

MNLSINQNSTISLTQDEVFLRAILNEIYAGVCDVSREFENVSGVRKEVDNLQQQFAGIYKMTT

SEQ ID 405

GTGGGCATCAATGCCAATCCTAATCTGTGCGGATGAAGCAGGAAAACCTGATATGGGAAGACGACCCCGATAAAAAATTTGGCGGGCTAACCGTATGGATGATATTCCCGGCATCGTCCAAGGTG
CGGTTAATCCTTTTAAACGGGTTTCAAGGGGTAGGGAATGGGGCAATTACAGACAGTCCGGTAAGCCCGGTACAGATACAGCCGCTCAGCAGACTCTACAAGGTATTAATGATTTAGG
AAAATTAAGTCCGGAACAGTACAACTTGTGCGCGAGGCTATTACAGGACAGTCCCTTTGCGGTAAAAGACGCGCATCAATTCGCCAAACAAATGGGCTGATGCCATCCGAACATTACAGCT
ACTGCCCAAACTGCCCTTCCGCTAGCAGAGGCTGCAGGTACGGTTTGGGGCGGTAAAAAGTAGAACTTAACCCGCGCAAAATGGGATTGGGTTAAAAATACCGGCTATAAAACACCTGCTG
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AGAACAAATTAAGTAGTGGGATGCTTATAACAAGCATGTATAGACAAACAGAAATTCAGGATTTAAATATCAATTCACCAGCAGATTTGCTCGGCATATTGAAAAATTTGTTAGCCAT

CCAACAAATATGAAAGAGTTACCTCGCGGTAGAACTGCGTATTTGGGATGATAAAACAGGACAATAGTTATCCGAGATAAAAAATCTGACGATGGAGGTACAGCATTTAGACCAACATCAG
GTAAAAAATATTATGATGATTTA

SEQ ID 406

VGINAPNCADAEAGKLIWEDDPKNWRANRMDIRGIVQAVNPFLTGPQGVGIGAITDSAVSPVTTAAQQTLOGINDLGLSPEALAAASLLQDSAPAVKDGINSKQWADAHNPNTA
TAQTALAVAEAGTVWGGKVELNPAKWDVWNTGYKTPAVRTMHTLDGEMAGGNRPKSIITSNKADASTQPSLQAQLIGBQISSGHAYNKHVIRQQEFTDLNINSADPARIENIVSH
PYNKELPRGRTAYWDDKTGTIVIRDKNSDDGTAFRPTSGKYYDDL

SEQ ID 407

GTGTTATCTTCATATTTTCGAGGTAACATATCTGCTAATCTGGTACAGACCAAAATTAATTTGATGGCTTTTATGATCCCGATTTGCGAAAAATGCCGTCTGAAAGCTTTGTGACGCTTT
CAGACGGCATTTTGATCATCAAG

SEQ ID 408

VLSSYPEGNISANLVQTIKLHAFNIPDLKRCRLKVFVRLSDGILLIK

SEQ ID 409

GGGCGCGGATTCGCCGAGGATTTTCATCGACCGTCCGATCGACTTCGACACAGTCGGTACTTTCCATTTCCGGCAATGCCGACCGCGGCTTTTGAACAGCGCGGCTGGCGGGAAGTA
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GCGCCGAATCAGCGAAAACGCGCTGCCGCTACCTGCGGAAACCTGCCACCTGCGCGGATPAAACAAATTTGTTTCCGCTACAAATCGGACACCGCTCGGACGGCTGTCGATTTTCAT
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CGCGTCCGAAGATCTTTCGCGAAAGCGGCTTAACCGCGCGCTGCGCTGAGACACTGCGCTACGCGCGTGTGCGAGCTCTTCGCGGACACCGCACCGGATTCGCCAAAGCGGACCG
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CAGCGCGCTTTGCGTTTGACTTTCGCTGTTTGAAGTTTGTCTGCTGTGCGCTTCCATAAGATTGGGTTCCGAATTTCTGATTTTCAT

SEQ ID 410

GRGLPEDFIDRPIDFRVPVTPHFRQCTRRP*NRACCGSLHFNHRQTDQRMPPVHFAVQHDITDGDALHFNFPVRCVLRNQRKRAARTCRKPCHPAAINNLFVAVQIGHQLGRSDFH
MPQLRLFKIHIHPHQRHHRQRACRHLPLHRTLRHLTVRRADLRPKVQPRIFQPADCLNLRFLAQRNLSAQSRACRRFRQSRNLRRLRLHRCRTGVCQLFGGHRTRFRQSGP
AA*IILRARQIRTAQGNLRLPRLSGGILPAVLAHRLNLVFCPLVSQHIIVIQHQAHPFHGIRIVQNLPHRAALLRRNLNHAAGNLSVFRFLVLP*KKRRSGCGGKREBQRQCR
QAAPADLRVLKPCFVCRFHKIGFRIS*PH

SEQ ID 411

TTGCATGATTTCCGCGCGGTGTCGCGCGGATGCCGTGTCGCGTTTTTAAAGCGCGCGCGGATGGCAGGCTGCCAGCATCAGGCGCGCGGAGATGATGAGGATTTTTTATGTCG
GATGTCCTTGTGTTGCTGTGGAAATCATTGCCATTTACAG

SEQ ID 412

LHDSAPGVADAVCAFLSARPDWQAASIRAAESMRIFYGCPCLLWELIAIVQ

SEQ ID 413

ATGAAATTAATGATTTGAAGGAATTAGTTAAATAGTCTCGATAAAGATGAGTTGTATATTATCAAGCAATTGTAGGAGAAATTTATTCAGGCGTATGCGGTGATGTAGAGATT
TTGAGATAATTCATGGTGTGAAAAAATAAGTCTTCTTTTGGATAAAGAACTTAAAAAATATATGATACTTGGGATAAATGT

SEQ ID 414

MKLIDFEGNLVKISLDKDELYIIQAIVGEIYSGVCVDCRDFEIHGVEKNKVLILLDKELKKIYDTWDC

SEQ ID 415

ATGAGATTAAATTAATAATTTATGATGTTCTGACTTTGATTTGGAAGATTTCACAAAGCAAGTTAGAAAAATTTTGTATATTTTGACATTATCAATAGTTTGTGAAAGTAATG
GTGCTGATTATTTTATGTTTATATATATAGCACCGAATGGTACTTTCAAATATACATAGACCGATGTCATTAAAAAACTCAATTGTTACAAACCGTTTAAATATTGAACACATATTA
ATPGATAAATGATATATGGAATATGTAATTCACGCTCGAAGATACTATATCAAAATTTGGCAAAATATTTGACTGGGAATTTGACGATTATATCTAAATATACCAAGAC

SEQ ID 416

MRLKLNKDYCSDFDLEPPQDKLENFCILLFLSIGFDESNGADYFVYIYSTEWLLSNHRPMSLKNSTVTRNFNIEHLKLLINDILEICNSTSEDKSISNLAKYFLWEPDDYNLNIQD

SEQ ID 417

ATGGCACTCGACAATATCGGCCCAACAGAAAAAATCACAATTTGCAACTACAGGTATTCAAGCAAAATTTGAAACTTATACCTATTGATTCAAAATGAAAAAGAAATAAAAATAAAA
TGGACATT

SEQ ID 418

MALDNIHQQKKHNLQLQVFKIILKILLIQMKKEIKLMDI

SEQ ID 419

TTGCTGCAAAATCCCATTTAGTCATGCGAACGGTTTGGATGCCGCTTTGCGCGATGATATCGAGGCAAAACACTACGAACCGGGTGCGAAATACCATCTGTTTGGTAATGCTCGGGCAGTG
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CATCCCGCAGACGGATATGACGGGCTCAAGCGCGCGTTATCCGGAACCAAGGGGCAAGGATATATACAGCTACCATATCAAGGAACCTCAACCAAAACAAAGATAAACACTGTTTC
CGCAAGCCCCCTTTTTCAGACCGCTGGCTAAAGAAAAATGCCGCTGCCGCTTCCGTTTCTCAGCGCTGCGGATGAAGCAGGAAACTGATATGGGAAACGACCCCGATAAAAAATTTGGCG
GGCTAACCGTATGGATGATTTTCGCGGATCTGCAAGGTGCGGTTAATCTTTTAAACGGTTTTCAGGGGTAGGGATTGGGCAATTACAGACAGTCCGCTAAGCCCGCTACAGAT
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SEQ ID 420

LLQIPISHANGLDARLRDMQAKHYEPGGKYHLFGNARGSVKNRVCVQTFDATAVGPILPITHERTGFEGVIGYETHFSGHGHEVHSPFDNHSKSTSDPSGGVDGGFTVYQLHRTGSEI
HPADGYDGPQGGGYPEPQCARDIYSYHIKGTSTKINTVPPQAFSDRWLKNAGAAAGSLFRADAGKLIWENDPDKNWRANRMDIRGIVQAVNPFLTGPQGVGIGAITDSAVSPVTD
TAAQQTLOGINDLGLSPEALAAASLLQDSAPAVKDGINSKQWADAHNPNTATATQALAVAEAGTVWGGKVELNPAKWDVWNTGYKTPAARHMQTVDEMAGGNRPKSIITSGKA
NAATYPKLVNQLNEQNLNLAQDPRLSLAHEGKNPFIPTATYEEADRLKIVWEGARQTSGGGWSLSDGTQRYRPPTEKRSQFATTGQANFETTTIDSEKRNKIKGNHLNR

SEQ ID 421

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SEQ ID 422

LIHFAITACCGKQNEFAYSKIHDVCSGNI VAANPH

SEQ ID 423

ATGCGGGCACGGTCTGATACCTATTCTTTTTCAGTTTATTATTATCCGCTCGGGACACTGACAGGTATTCATCGCATGGCGGAGGCAACGCTTCGCGGTGCAACAAGAACTTG
TGGCGGCTTCTGCGAGAGCTGCGTTAAAGACATGGATTTACAGGCATTACACGGACGAAAGTTGCGATTGTACATTCGAATATGGCGGACCAAGGTTTCAGGCAGTTTGACAGGGGTG
CTACTCCATTGATGACCTGATTCGCGGCGAATACATAAAGACGCTTCCGCTCGCGACCGATTACCTTATCCGCTTACGAAACCCGCTGAAACAACATCAGGCGGTTTGACGGGTTTA
ACCATTCTTTATCTACACTTAATGCCCCGTCACCTCTCGCGCACCCAAATCAGACGGTAGCGGAAGTAGGAGCAGTCTGGGCTTAAATATTTGGCGGGATGGGGATTATCGAAATGAAACCT
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CGTATTTCGGAACGATACGCAACAGAACCGAAATGCACCTATACAAATGCGGAAACACTGAAAGCCCAACAACTGGAATATTTGCGAGTAGACAGAACCAATAAAAAATGCTCATCAAA
CCCAAAACCAATGCGTTTGAAGTGCCTATAAAGAAATACGCAATTTGTTGATGGGCGGTATAAAGTAAGCAAGGAATCAAAACGACGGAAGGATTGATGTCGATTTCCTCGATATCC
AACCATACGCAATCATACGGTAACTCCGCCCCATCCGTAGAGGCTGATAACAGTTCATGAGGGTATGATACAGCATGAAGCAGTCCGCAACATAGACAAGGCAACCT

SEQ ID 424

HRARLLIPILSVFILSACOTLIGIPSHGGKRFVBEQELVAASARAANKMDLQALHGRKVALYIATMGDQSGSLTGGRYSIDALIRGEYINSPAVRTDYTYPRYETTAETTSGLTGL
TTSLSLWAPALSRQSDSGSSSLGLNIGMGDYRNETLTTPRDTAFILSHLVQTVFPLRGIDVVPANADTVFINIDVPGTIRNRTEMHLYNAETFLKAQTKLEYFAVDRTNKKLLIK
PKTNAFEAAIKENYALMHGPKYKVGKIKPTGELMVFSDIQPYGNHTGNSAPSVEADNSHBEGYGSDEAVRQHQQP

SEQ ID 425

TTGATGATTGACATAGGGTCGCGAGATATAGTCGATATGGGCTTCAGACAGCCATTATTATATGAGATTATAGTGATTAATTTACAATT

SEQ ID 426

LMIDHRVGRYSRINASDSHLLYGDYSGNLQF

SEQ ID 427

TTGGAATCAGGATTCCTCAGCTTCGCGCGCGGCTACCGGTGCAACCGCAGGAATCTAGTTACACGGCAAGCGCAACCGCATTGGCAATCCGATCCGAGGCTCGCAACAG
CCCTAATCAATGCCGCCGCAATTCAGCAGACCGCGGCAACTCGCGGGCGCAGTGTACCGGCTTCACAGCTACTTTGGCAAGCAATCGTCGAAGCGGCAATACGACTGTCA
GGCAGGTTCTTCCAGTCCGCGGCTCATGCGGCCAATGCTGCTCGT

SEQ ID 428

LESIPVSPGGVPVANGRLNLTQAAANGIGKSDSEACEHALINAARKFQQTAGKLGGRSVTGFHSYFGKQSLQGGYDQAGSFHVRVAMRANVVR

SEQ ID 429

ATGGTCAATCATCAATCAGCAGTGGACCACTGTGCTTCTGCTTCCGCGGTAATGACCGCTTGTAGCGAGCTTGTGTTGGCGATGCCGAAGACGAGATATGAGCTTGGCTTCGCGGCG
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ATCAGGTCGCCATCATGCCCATGTAGTCGGCAGTGGCGCGGTCCATGCTGCTGCTTGTGTCAGATACGCGCGGAAATGTTACCGCGCGGACCAAGGATACCGACTTGCACACCCATT
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SEQ ID 430

MVNHQSAVDQCAFVAGNDAFERALPGDAEDDIELFAABEGKGRVHDFEVPFIQGFVKSNGFVACGGRVFFVCGVHAVDVGGFEHVVAVHFAAQCGGSVGREERTTGTGGENHDFAF
QILNGFRITGVSFSDLHRQCGLYARFDAQGFKVFECQGVHGRHHAHVVGSAVHAACLCRYAENVTAADNDTDLHHTFHDGPNFADSLNNGIVDAERIGTHQGFAGEFQ

SEQ ID 431

ATGACACAGCAATCAATAACAACGCGTATTACTGAAACTCTCCGCGCAATCCCTGATGGGTTCGATCCGTTCCGCAATCAATCAGATACCATTTGTTCAAACTGTCCGCGAAATGCGG
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GACCGTATGAACGCTTGGCACTCAAGACGCAATTTGAAACCTTGGGCATCAAGCGCGCTACAATCCGCACTGTCTATGACAGCAATCGCTGAACTTACGCGCGCTCTAAAGCCATT
CAATATTTGAAGAAGGCAAGTCGTGATTTTCCGCGCGGTACCGGTAATCCGTTCTTACGACCGACACTGCGCGCGCTTCCGCGCGCGGAAATGAAGTCGACGTGATGCTCAAG
CCACCAACGTCGACCGCGTGTACACCGCAGACCCGAAAAAGACCCGTCGCCACACGCTACGAAACCATTAATTTTGAAGCAAGCCTTGAAATAAAACCTCAAGATCATGGACGCGACCGC
CTTTGCCCTTCCGCGAAGCGAAGCTCAATATCTGCTGCTTTCGGCATCGCAACAAAGGCTCGCTCAACCGCTCATACCGCGAAGACGAGGCACTGTGCCACTGCT

SEQ ID 432

MTQQLKYRVLKLSGESLMSDPPGINHDTIVQTVGEIAETVKMGVQVGVIVGGNIFRGVSAQAGSMRATADYMGMMATVMNALALKDAFETLGIKARVQSALSMQQAETIYARFKAI
QYLEEGKWVIPAAGTGNFFTTDTAAALRGAEMNCVMLKATNVDGVYADPKKPSATRYETITFDEALNKNLKVMDATAPALCRERKLNIVVPGIAKQGSILKRVITGEDBOTLVHC

SEQ ID 433

TTGCTGTCTCATGGGATACCTTGCTTTCTTGAATGTCGTCGCTCGGAGTTGGGACGCTCGAATTTCAATGCTCGGATTACAATGATATGGTGTGCTTCTATTATGTTTGTGTTTCAG
ACGGCTTTTATATTCGCTGCT

SEQ ID 434

LICHGIPCFLECRRELGRINPKNSDNDMVCRSIIVLFSGLYIRSS

SEQ ID 435

GTGGAATCCTTTCCGTAATTTCCCAAAATCTAGGAGATTCAAAATGGCAGAAATTAATGCAAAAATGGTTGCCGACCTGCGCGCCCTACCGGCTGGGTATGATGGAATGCAAAAAG
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CAACGGTAATGTCGCGCATGCTGCAAGTAACTGCGAAACCGACTTCGTTGCTAAAGACCGCGCTTCTGTAAGATTTGCCAACTTCGTTGCGCAAACTGCTGCCGAGAAAAACCGGCT
TCTGTTGAAGAACTGAGCAACTGCTTGAATCAGAACGCAAGCCATCATGCTAAATTTGGGCGAGAACATGCTGTCGCGCGCTTCCAAGTATTGACACTGCCAACCAACTGGTTGCT
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AGAAAGCCGTTGTGACTACGCGAGCGAAGTAGCCGACCGCCAAAGT

SEQ ID 436

VENPFRISQKSRFPKAEITAKMVADLRAATGLMMECKKALVBAENFDKAEILIRIKSGAKAGLAGRTAABGVLAVALINGVGALEVNCEPDFVAKDAGFVEFANFVAKTAAEKKPA
SVEELSELVESERKAILAKLGENMSVRRFQVIDTANQLVAYIHGALATEGVLVEYKGSSEIDVARKIGHIIVAAKPCVSEAEVDAETVEKERHIYEQALASGKPADIAAKMVBGRIRKFLA
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SEQ ID 437

ATGCTCTAAATTAATCTGCTGATGATGAAGCCGGTGTTCACCTTCCGTCACCAACCCGCTTCTGGAACCCGAAATGGCTCAATACATTTTCGCGCGCGCAACAAATCCATATCG
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TCGTTATCGATACCGGCTACCAAAAGGTACTTTGGTTGAGGCTGAAAACTGGGCATCCCGGTTATCGCCGTAGTCGATACCAACACAGCCAGACGGCGTGAATACTGTCATCCCGG
CAACGAGACTTCGCGCAAGCCATCCGCTGACTGCGGAGCATCGCGAGCGAGTTTGGAGGGCAAAACCAAGCGCTGCAAGAAACCGTAGCCGTCGCCAAGAAACCGCTGCGGAG

SEQ ID 438

MSQITWRQMEAGVHFGHQTRFWNPKMAQYIPGARNKIHVNLKTLPMFQEAQZAVRRLVANKGTVLVFGTKRQARDIIRBEATRAGMPFVDRHNLGGNLVNYKTVKQSTIKRLEETAAAL
ENAAESGFSKKEILEMQRDVEKLESLGGIKNMKGLPDAIFVIDTGYQKGLTVEAKLGPVLAUVVDNNSPDGVKYVIFGNDDSAKAIRLYCRGIADAVLEGNQALQETVAAAQETAAB

SEQ ID 439

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TCTTCCAGCGGTTTGTAGGATTGCTTAAACGGTTTGTAGTTGGTCAGCATACGCCCAACAGCGGTGTCGACGAAAGGCATACCGCGCGGGTCTCTTCGCGGATGATGTCGCT
GCCTGGCGTTTGGTACCTACGAACAATACCGTACCTTTGTTGGCAACGACGAGCTACGGCTCTTTCGCCCTCTTGGAAACATCGCGAGGGTTTTCAGTTTACGATATGGATTTTGT
TGGCGCGCCGAAAAATGATTTAGAGCCATTTTCGGGTTCCAGAAACGGGTTTGGTGACCGAAGTGAACACCGGCTCAATCATCTGACGCATAGTAATTTGAGACATGTTATTTCTCTGAAA
GGGTTAAAGAGCACACATTCATCGCA

SEQ ID 440

LGSGYGLQRLVFAFQNCVGDAVAQADGPGGVVAGDDVFHVAWVVGIDYDNGDAQFFSLNQSTFLVAGIDNENRVQAQFHVDTAQRAFQFFNVALHFQNFPAETAPGSIFFQCGCF
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GLKSTHSA

SEQ ID 441

ATGTGGCAGCATCGTCCCATCGGCTATCTTTTGTGTCCGTTATGATATCCGCCGCGCAGCGAGTATTGCGCGCGCTTTGATTATTTGGTTTTTGGGTGGTTCTGCCACCGTGTTCA
CGGTCTTCGCCGTAACCGTCCGCCCGCAACCGCTGATGGGCGACGAGAACAGGCAGAAATCCGAACAGCAGCGCCCAACCGCAAAAGACAGCGGCACAAACCC

SEQ ID 442

MHHIVAIGLYLVAVMYSAAQPSIARALTYLVFVVVLPVTFVAVTVRRNRRLMGQEQAESEQQRAQRQDSGTRP

SEQ ID 443

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ACAGCGGCACAAACCTGAATCCCTTTTCAGAGCGCATCTTATCCGCTATAATCCGTCAGTTTTCATTTTCGAAACACACTATTTT

SEQ ID 444

LLTFKQDAHVHRRHRLSFCRYVFRRAEYCARFDLPGFLGSSAHRVHGLRNRNPPQPDPGAAGTGRIRTAARTTAKRQRHKTLPNPSDGLISAITRQFSISETHYF

SEQ ID 445

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GCACGACCTGCGCTGACGGTTTGTATCGGAAGCGGGGATATTGTGTTTT

SEQ ID 446

LCASCLNVNKIVIATFYRNPSEMRNEEKRALRRELGRSSQMGDRVRAAAVKINRLKRYIKRGRKIGVYFPMGKELRLGGFVRAAQKRAKLYLPVIEPHTFRMWFPTVPERGME
RERKGRRAKLVHPQFAGRKIRVHGLSVLLVPLVGLDREGYRLQAGGYDATLSANKYRLQARTVGVGFACQLVDRLPREAHDLPDGFVSEAGILCF

SEQ ID 447

AGTCAGTATTTAGATGCAATATTCAAAAAACAACGCTTCAGTGCCAAAACGAAATATATTTCTGTTATATATGACATGGCAAAACCGCGCGCCGCAACAT

SEQ ID 448

SQYFRNIQKTHQVAKLIKIVFYI*HGKHRRPHH

SEQ ID 449

ATGCCGCTCGAACCGCTAAAAACACAATATCCCGCTTCCGATACAAAAACCGTCCAGCGGAGGTCGTGCGCTCCGCTGGGAGGCTGTCCACCAACTGGCAGGCAAGGCCACGCCCAAG
GTTTTCGCTCGAAACGGTATTTTCATCGCGAAAGCGTCGATCGTAATAGCGCGCTGCTGCCCCAAACGGTAGCTTCGCGGTCTATGCGGACAGCGGAGCAGCAATACCGACAAC
CGTCAGCGCGGATTTTCGCGCTGCAAACTGAGGGACATCGAGCTTCGCCCTACCGCGCTTGGCTTCCGCTTCGCTTCCGCTTACGAGTACGGCTTAAACACATCTCGCGGTGTGCGG
TTCGATATAAGCGAGATGAGTATTTTCGCGCGCGCTTTTCGCGCGCGGCAAAAGCGCGCAAAACGCAATTCCTTTCGCGCAATACACGCGGATTTTCGAGCGCGCTTGATATAA
CGTTTTCAGCAGCGGTTGATTTTACCGCGCGCGCGCGCGCGCACGTCGCCGCCATTTTCGCAACGCGCGCGCAATTCGCGCGCGAGGCGGCTTTTCTCGTTCTCATTTTCAGAG
GCTTTTCAGGATTCGCGTAGAATGTTCGATTTAACGATTTTGTTAACATTCAACAGGACGACACATAATGTCACATCGTGCATCGGCTATCTTTTGTTCGCGTTATGATTTCCG
CGCGCAGCGGATTTTCGCGCGCTT

SEQ ID 450

MPSERLKTQYPRFYKTVQRQVRLAWEPVHQLAGKAHGFRLQTVFHRKRRIVIAACLPTQVFAVYADXRDEQYRQTVHADFPCKLRDMQLRPTALAPPHSAFRIRRKPHPPVR
FDIRQIEFCAFLRRADKAQQTFLAHRPIHADFTALDITFEQAVDPYRRRRPHVPLRLTPAQFAAQGAFFLVPHFRFPRIAVECCDNDYFVNIQTGRTCCGTSPPSAIFLLPLCIP
PRSRVLRAI

SEQ ID 451

GTGTTTTCAGCGTTTCAGACGCAATTTTCGGGCGGAAATGCCGCTGAAGCGGGAATATTTGGGAGAAAAGGATGTCGGAAGGATAATCTGCCGCTTTTGTCAFTGGGCGCGGTACCGTTC
GAACCGTTGGATGTGATCA

SEQ ID 452

VFLAVQTAFAEMPSGGILGEKDVGLWNTAGFVIGRETVRTVGCAS

SEQ ID 453

ATGATTTTGAACAGGTGTTTATCCGTTTCGCCGTCGCGATGCCCATACCATGTGAATCCGATATCCAAACGCGGAATCTCGGTTCAAAA

SEQ ID 454

MLQQVFIIRPRADAAYHVNPISKRGICGSK

SEQ ID 455

TTGATGTGATCATGAACCGGTTTCGCGAGGCGGTTTCGATGGGAGGTTTGAAGCTGGGGTAACCTCGCGGCCCATCCGATAGGTTGGCAGACATATTCGGACAGCATTTGG
CAACGCGTTTCGCGTTTCGCGTTTGTGATGAAGAGCGGACAGGTTGTCGGGACACCGGCTATTATCATTTGAACCGCAGATTCGCGTTTGGATATCGGATTCACATGTTATGCGG
ATCGGCACGCGGAAACGGAATAACACCTGTGCAAAATCATGCTGTGGATTACGATTTGATGTTTGGTTTGTCTGTTGGCGGATGGCGCAGGATATTCGAACCTTCCTTCGCA

CGTGCCATCGAACCGGTGGGCGCGGAAAAAGACGGCGTCTGCGTATGCATATGCTCCGTAAAGACGGCAGTGTGCGGATACGGTTGTGTACAGTATGCTGAGGGAAGATTGGTGCAAAA
ACAGGGAATCTGACGGCGAGGTGGCAGGGTATGGCGTGCAGGTG

SEQ ID 456

LDVHHETGLREAVDCGEVWKLGVTSAPHPDRVADYIGTALATRLAFVDEADRVVGTAYYHFEPQIPRLDIGFTWYAASARRKRINTCKIMLLDYAFDVLVCCCAWRTDILNLASQ
RAIERLGAEKDGLVRMHLRKDGSRDFTVYSMLREDWCKNRELLTGLRAGYGVQV

SEQ ID 457

TTGTGACATATCGCGTTAAAGTTTPTTAAATTTGAGAFACTGCCTCACACCTGCACGCATACCTGCGCAACCTGCCGGTCAGGATTTCCCTGTTTTGCAACCAATCTTCCCTCAGCATA
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TGCGCCATCCCGCGCAACAGCAAAACCAAAACATCAATGCGTAATCCAACAGCATGATTTGCAACAGGTGTTATCCGTTTCCGGCGTCCGATGCCGATACCATGTGAATCCGATATC
CAACGCGGAATCTGCGGTTCAAAATGATAATACGCCGTTGTCCCGACCACTGTCGCCCTCTTCATCGACAACCGCAACGCAACGCGGTGCCAATGCTGTCCCGATATAGTCTGCC
ACCTATCCGGATGGGGCGGAGCTTACCCAGCTTCCAACTCCCATCGCAACCGCTCGCGCAACCGCTTTCATGATGCACATCAACGGTTGCAACCGTACGCCGCCAA

SEQ ID 458

LSAYRVKFPKFWYASHLHAIPQAPAGQDFPVFAPIFPQHTVHNRIATVFTZHMHTQHAVFPFRAQPFDTGLRGKVQNIAPSRATANQNIKCVIQHDFATGVYPPPPCRCPICPSDI
QTRNLRFKMLIRRCPDHVRFLIDNRKRQTRCQCPDIVCHPIRMGRGRYPOLPNLPIANRLAQTRFMHIIQRFEPYAAQ

SEQ ID 459

GTGAATGTAGTGGATTTTACTGGGAAATGCAAGTTTTCTGTGCCGCCCAAGCCGGGAAGTGGCAACAAAAATAAAATAGTTATTATCTATATATCAAAATTTTAATAGACA
AAAAATCAAAATGTTTATATAT

SEQ ID 460

VNVVDTGKCKVFLSPAKPGNCEKKNKNSYLSIYIKFLIDKSKLFIY

SEQ ID 461

GTGCTCGGACACACACATTGCCGGTTTCCCTGCTTTTGGGATTAGGCGTTGTAGTACGGCAATAACCATAGGGCAGAAGATGCTGTTTTTAGGAGTAAACCATGCG

SEQ ID 462

VLGHTFLPVSPAFAIQAFVVRQITIRAEADACFLVNHG

SEQ ID 463

ATGGCTGAAGCGACAGACGTTGTCTTGGTGGGCGCGGCATTATGAGCGCGACTTTGGGCTTTTGTCTCAAGAACTCGAACCGTCTTGGGAAATCACCTGATTGAACGCTTGGAGATG
TGGCGTTGGAATCGTCAAAACCGCTGGAACAACCGCGGACGCGGCATTTCGCGCTGTGCGAATTGAACATATGCGCGCTGGGTGGGACGCGGTCATCAATCCGGCGCGCGCTGAATAT
TGCGCAACAGTTTCATGTGACGCGCAGTTTGGGCGGACGCTGGTTCGCGGAAGGCAAGTTGGAAGACAATTCCTTCATCAATGCCGTGCCGATATGCTTTGGTGTGAACGAAGACAC
TGCGCTTACCTGCAAAACCGCTATGATGTGTTTAAACGCGAAGACTTTTGAATAATGGAATTTCCACCGATCGGAACAAAATTTCCGATTTGGGCTCCGCTGATTATGCGCGCGCGG
ACGAAACCAACCGCTCGCGCCCAACTATTCGCGGAGCGACGATGTCGATTTGCGACGCTGACGCCAGATGTTGAAATATTTGCAAGGCAAGGCGTAAAAACCGAGTTCAACCG
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AAAACCAAGAGAACGCTTTGCCCTCCCTGCTGGAATACTACCCGAGGCAAAACCCGAGACTGGGAATCATCACCGCAGGCAACCGCTTCAAAATCATTAAGAGACTCCGAAAG
CGCGCTGTGTCAGTTTGGTACGGAGATGTCGCGCACGCGGCTCGCTCGCGCACTGTCGGGAGCGTCCGCGCGCATCGACCGCTGTGCGCTGATGATCGCGCTGATGACCA
ATGCTTCCCGAGCGCGCGCTTGGGAGGTCGTGAAAGAGCTGTAACCGGTACCGCATCAAGTTGAACGAAACCCCTGAAAGGGCGGATGAATATATCGCTATACCGCGAA
GTGTTGGATAT

SEQ ID 464

MAEATDVVLVGGGINSATLGVLLKELEPSWEITPLIERLEDVALESSNAWNAGTGHSALELNYAFLGADGVINPARALNIAEQFHVSQFWATLVBAGKLEDNSFINAVPMHSLVMNEH
CRYLQKRYDVFTQKLFENMEFSTDRNKISDWAPLIMRGRDENQPVAAANYSAEGTDVDFRLTRQMVKYLQKGVKTEFNRHVEDIKRESGAWVLKATDENPDWQLTLRLTRFLGAGG
GALTLQKSGIPBGKYGGLPVSGLFFRNSNPETAQHNKAVYQASVGAAPMSVPHLDRNVDKRLHMPGYAGFRSNFLKQGSFMDLPLSHMDNLYPHLRAGWANNPLTKYLLGELR
RTKERRFASLLEYTPEANPDWELITAGQRVQIIRKDSKGVLFQGTETVAHAGDSLALLGASFGASTAVPLMTRIMHQCFPERAPSWEGRLKELVPGYGIKLENPERADEIYATK
VLDT

SEQ ID 465

ATGGCAACACCGCGCGCCGACCATGCCGCTCTGAAGAAAATACACAAATACCGCGCTTATATTAACATCGCGCGCGCGTTCGAAACCTCCACAC

SEQ ID 466

MANTAARTMPSENYNTTAAAYITIAAPWFENLPH

SEQ ID 467

ATGACCAATTCATTTTCTAACCAGCGCGGTGTCCTCTACTGGGTAAAGGTATCGCCGCGCTTCTATTGCGCCATCTCGAATCGCGCGCTTGAACGTTACCATGCTCAAGCTTG
ATCCCTATATCAACGTCGATCCCGCACGATGAGCCGTTCCAAACAGCGGCAAGTGTTCGTAACGACGCGCGGAAACCGAACCCTGACTTGGGACACTACGAACGTTTCATCGATTC
CAGCATGACCCGCGCGCAACAGCTTCAGCACGGGTGAGGTGACGAAACGTTATCGCCAAAGAACGCGCGCGACTATCTCGCGGTACGCTTCAAGTCATCCCGCACATTAACGACGAA
ATCAACGACGATCCACGAAGCGCGCGGGTTACGATGTGGGATTTGTCGAAATCGCGGTACGCTCGCGACATCGAATCGCTGCGCTTTTGGAGCCATCCCGAGATGCAAGCC
AGTTGGGACGCAACACACCTGTTGCCCACTTGAGCTACGTTCCCTACATCGCGCGCGGAGGAAATCAAAACCAAGCGACCCAGCACACCGTGAAAGAAATGTTGAGCATCGGCTT
GCAACCCGACATCTGATTTGCCGTATGGACAGGAAATGCCGCGAGACGACGCGCAAAATCGCTTGTTCGCAACGTGGAAGAGCGCGGATTTGTCGCGAGCTACGATGTGGACAG
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GCAGGTTTGGTCATCGCGCGGTATCCCGGACGCGAAGCTTGTGCAAAACATCGAATGCGCAACCATCTTGGTTCTTCCGCTGCGAGTTCAATCCGAGTTACGTTCAACCGC
GCAAGGGCATCTTGTGTTACCGCGTTTGTCAAGCGCGTGAACAAATAAAAGCC

SEQ ID 468

MTKFIPTVGGVSSLGKGLAAASIAAILESRLNVTHLKLDPYINVDPGTMSPPQHGVEFVTDGAEITDLGHYERFIDSTMTRNSFSTGVYENVLAKERRGDYLGTVQVIPHITDE
IKRRIHEGAAGYDVAIVEIGGTGDISSLPLLEAIRQMSQLGRNWTLPALHSVVPYIAAAGEIKTKPYQHTVKEMLSIGLQPDILICRMDRMPADERRKIALPCNVEERATVGSYVDS
IYECPEMLHDQIDNIITEQLQNLVQADLTAWKLIHAKVNPKEHTVKLIAMVGKYVDLPESYKSLIHALKHAGIHTETDVQITFVDSIESIEKHKGDVSVLKHMDAILVPGFGSGRVSBEKI
AAVRYARENNVPIGICLGMQIALI BYARDVAGLKGANSTFDLKAAPVVALIDENQTDAGSVETREDSEADLGTMRLGAQEVELKAGSLAVKIYSGSHIRERHRYEVNNYVSALEQ
AGLVIGGVSAGRERLVEITELPNHPWFACQHPHEFTSNPRKGHPLFTAFVKAALNNKA

SEQ ID 470

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SEQ ID 476

SEQ ID 477

SEQ ID 478

SEQ ID 479

SEQ ID 480

SEQ ID 481

SEQ ID 482

SEQ ID 483

SEQ ID 484

SEQ ID 485

TTGCCACAGCTCGCGCATTTTTCGATTCTCTGGGGGTTTGATGATGATGCCGTTTCATAATGCTTCCTTGGATTGGGGTGTCCTGCCGTGCCGGGTCAAAGAGGTTGTGCGAATACTCTTTATGGGGTTTGGCGGGCGTGTTTTCGGGGTGTCGGTTTGGTATGGTTTCTTCTTGGGCGTTTCTTTTCTTTGGGTGTTTCTTTGGGCTGCCGCTGTTTTTCGGGTGTTTCTTTTCGGGTTCGGAGTGGGGGGCGTTTGTGGGCAGTACGGGGGTTCTTTGAGTGTGTTTTCAGCTTGTGTTCGGGTGCCCGTTAAACGAAATCGGGCTGCCCGGGCGCAATCCGAAGGGCGCGGTTTGACCCGTTTCTTGGGTGCCGACGGGACGGCAGTCCGCTGCCGCTTCTCTGTGCCGTCCGGCTGTGCCGGTTCCGATGAGGCGCGCTGGTGTGTGTCGGGTGGCGGGCATCTGTCTCGACGCCGCTTTGGCAGCCGAGAAATCTCGGTTTCCGGGGGCTGTGGTGTGTCGCCGTTCGGTTTGAATGTCTGCAGCATGCCCTACTGCCAATGCGCGATGGCGGTGACACAGATGAGCAATACGGGCGCTACAGAGTTTGGGGTGACCTGACAGGAGTTTGTTCGGTTTGTTCATTTGTATGTGCTTTGGGTGTGCGGCAATGCGCTCTGAAGCGGTTGACAGCGGCAATGCCGAGTCAGCGTTGGAGCTAGTTTGTGTAGAGGGTAATGACTTTTGTACCGCGACGCTGGTGCTGACTTTTGGGTAATCTGCGCTCTCTTCG

GGGGTGAGGATGCCCATACCTAGGTTACATTGCCGTAGGTAATGATTTTGACGCGCGCTGTGTAGCGGGCTGATGCCAGCAGCGTGGCGCGGACTTTGGACGTGTTCAGGTGTCGC
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SEQ ID 486

LPSSRIFSISSGVLMMPFIMLPNIAGVPAVPGQKRLSRLISLWLAGVFPVGSGLVWPSLGVSPSLGSLGACFSGVSPRSGWGAFFVSGTGVSLSVFSACVPVFNESAARAASEBGRGL
TRFFLAGAGDGSPLFSSVPSGCCAGSDEAAWNCSGWAASCPAPFPGSQNSVSRGLSVCCGSVMRVLSPFGLNVLMTPTANAFMAVIQMSNTARIRSLVSLKGLFGFFAILIVLLGCRAMP
SEGGSDGLAESALDVVLVEGNDPLYADGGADFLGNLRLFFGGEDAHNVGYIAVGNDFDARLCSGADAQQRGADPGRVPSVAGDVARSARQGGDGNVYVAFGLFGTCNLTDLELPAFGGD
LSEQQQVAVVADGDLGRVAFGLVLAQVGTGGGFTQQRHNVVIGLRAGGSADVDFCADGGPADDCAEAAABGKAEDGNGADGVWFGPHRGLPFLGVSDGIALRHAV

SEQ ID 487

ATGCTGCAATGCTGATGAACGACGCAAAATCTGGCCTGCGGCAACGGCGGTTCCGCTGCCGACGCGCAACACTTCGCCGCCGAAATGACCGGGCGTTTGGAGAAAGAACCGATCGAAC
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CGGCAATTCACCTCCGCAATTCGCCAACGTCATCGAAGCGCTCAAAGCGCACACGACGCGATATGCACGTCATCGCCCTGACCGCGCGCAAGGCGGCAAAATCGCGCCATGCTC
AAGACACCGACGTTCTGCTCAACGTCGCCATCCGCGCACCGCGCCGATTCAGGAAACACATCTGCTGATACGCGCATGTGCGACTGTATGACTCGCTACTGCTGGAAGGAATG

SEQ ID 488

MLQCLMNDGKILACNGGSAADAQHFAEMTGRPEKERMELAAVALTDTSTALTAIGNDYGFHVFQKQVRALGRAGDVLVGLISTSGNSANVIEAVKAAHERDMHVIALTGRDGGKIAANL
KDTDLVNLVPHRFARIQENHILLIHAMCDICDSVLLBGM

SEQ ID 489

ATGCGCTTAAACCAACAGGGTACGCGAGGGGAAGATCGCGCACTTGCGCTTCCTCCAATCCCAAGGCTGCACGCTGCTTGGCCGCAACTGGCACTGCGCTACGGCGAAATCGACCTGA
TTGTCAAAAACCGCGCGCATGATTTCTGTTGTAAGTAAATAACCGCAAAAACCAACGGTTTCGGCGCGCGCGCATACAGCAATTTCTCGCTCCAAATTTATGAAACTGCAACGAAGGTAGTA
GTATTATCTGCAACAGAACAGGCTGACAAACGTACCGTGCCCGCTCGATGCGGTACTTATCGAAGGAAACCGCGCGCGGAGTGGAATAAGAAATATTACAGGT

SEQ ID 490

MRJNHKQGTAGDAALAFQSGCTLLARNWHCAYGEIDLIVKNGMILFVEVKYRKNQRFGGAAYSISPSKLLKLQRSVEYTLQONRLTNVPCRLDAVLIENRPFEMIKNITG

SEQ ID 491

TTGTGGTTTAAAGCCATAATCGGTTTAACTTTATAATGCTGCTGTTTTTTCAGACGCACTTTTTTATGTTTTCAGAAACACTTCAGAAAGCCTCCGACAGCGTCTGCGGAGGACATTTATAG
TGGTTGCCACGCCCATCGGCAATTTGCGAGACATATTACCTGCGCGCTTTGGCGGTATTGCAAAAGGCGGACATCATTTGTCGCGAAGACACGCGCTTACTGCGCAGCTTTTGAAGCGTA
CGGCATTACGGCAGGTGTTGTCAGTGTGCGGCAACACAGAGCGGAGATGCGGACAGGTAATCGGTTTCCTTTCAGACGCGCTGTTGTCGCGCAGGTTTCGATGCGGGTACGCGG
GCCGTGTGCGACCGCGCGCGAACTTCGCCCGCGCGTGCAGGAGGAGGTTCAAAGTTCGTTCCCGCTGTCGGCGCAAGCGCGTAAATGCGCGCGTTGAGTGTGCGCGGTGTCGCGAAT
CGGATTTTATTTCAACGGTTTGTACCGCGAAATCGCGCGAAGTGAAGAAATGTTTTCGCAAAATGGGTGCGCGCGCATTTCTGCTGCTATGTTGAAACCGCGCGCAAGTTCGCGG
AACGCTTGCAGATGTCGCGAATGTTTCCCGGAACGCGCTGATGCTGCGCGCGGAAATTCAGCAAGGAGGTTGAAACGTTCTTAAGCGCGCAGGTTGGGGAATTCAGACGCGATTCGCG
CGGACGCGCAACCAATCGCGCGGAGATGTTGTTGCTTATCCGCGCAGGATGAAACACAGGAGGCTTTCGCGAGTCTGCGCAAAATGCGATGAAATCTTTCGCGCGGAGCTGC
CGACCAAGCAGCGCGCGGAGCTTTCGCGCAAGATTACAGGTGAGGCGCAAAAGGCTTTGTACGATTTGCGCACTGCTGCGGAAAAACAA

SEQ ID 492

LWFKRIIGLFTINSVFQTAFFMQHLQKASDSVVGGLYVVTPIGNLADITLRLALVLQKADIICABDTRVTAQLLSAYGIQRLVSVREHNERQADKVIQFLSDGLVVAQVSDAGTP
AVCDPGRKLARVRREAGFKVFPVVGASAVMAALSVAAGVASEDFYFNGFVPPKSGERRKLFARWVRAAPVVMFETPHRIGATLADMAELFPERRLMAREITKTFETFLSGTVGRIQTALA
ADGNQSRGENVLVLYPAQDERHEGLSBSAQAMKILAEELPTKQAEELAAKITEGEGKALYDLALSWMK

SEQ ID 493

ATGTCGCCAACCAAGAGCTGCAAGGCACTCTCTTTTGGGTAAATCAAAAACCAATATCCGACCGGCTACGCGCTGAAATTCGGAAGCATTCGACAAACCAATCCGACAAAG
ACTATTTCTGCAAAATCTGCTGCGCCGAATTCACAGCTCTGCGCGATGACCGCGGCGAGCTTCGCCACCATCGTCATCCGCTATATCCGCAATCAAAATGTTGGAAGCAAAATC
CCTGAACTCTACCTCTTCAGCTTCGCAACACGCGGATTTTCATGAAGACTGCGTCAACATCATGAAAGACCTCATCGCCCTGATGGATCCGAAATACATCGAATGTTTCGCGGAG
TTCACACGCGCGCGGCGCATCGCGTTTATCCGTTTGCCAACTACGCGCAAGCAGGACAGAGTTTGAAGCATTTGGCACGCAACCGCTGTTTCGAGCAGCAGCGACAA

SEQ ID 494

MSRNNEELQGISLLGNQRTQYPTGYAPEILPDKHPNDYFVKVPCPEFTSLCPMTGQPDFATITVIRYIPIHKMVESKSLKLYLFSFRNHGDFHEDCVNIIMKDLIALMDPKYIEVFG
FTRPGGIIVHPPANYGKAGTEFEALARKRLFENDAQ

SEQ ID 495

TTGTGCTTTAAACTTTCCCGAGTCGCGGTGAGTTTGAAGCTTAAACCGCGAGCATTTATTACTTCAGCGGACAGATATCCGCTACTACGCTCGATTCAACACCTGTGAAACCACTA
ATTATGGTTTCTCACTGTCTGATCAATCCAATGGAACGAGCTGTTACGACGCGGTGAGATATCCGTTACGATATACCAAAATGACCGCTCAGGAATGGAATGCGAGTGTGATGCTG
TGACAAACACCGCTGCGCAATATCTATAAGGCTGGAGCGGATTTGTCGTTTGGCGCGCACTGAATCAGGCTTGGCATGTGCGTTACGACATTAATTCGCGCTACCGGTGTCGCC
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CAATCTTATTCGAAACACCGGAATGCGAGATGCAAAATATCGATAAGGCCGGAATCCGTTGTTGAGCTGACAGGCGCTGGAATGTGGACAAAATAGCGTCTTTTGTCTGAGGGC
TGAATATGTTGGCTCGCTGGGTTATGCGAAAGCAAACTGTCGCGCGACAAACGCTGCTGTCCACACGCGCGGAAAGTATTGCGGTGTCGACTACGAAGCCGAGCGGAAAGATG
GGGTGTGTTTCGCGC

SEQ ID 496

LSFKTFASRRREFENLRDDYYFSQGISRTSSIQHPVKTTNYGFSLSLQIQMNDVSSRADIRYDHTMTQELNABCHADKTPPAANTYKWSGFPVGLAAQLNQAMHVGYDITSGYRVP
NASEVYFTYNHGSGNWLPSNLKAERSTHTLSLQGRSEKGLDANLYQNNYRNLSEBQKLTITSDVGCTQMNYYYGMCNPNYSEKPEWQMNIDKARIRGLELGRNLVNDKIASFPVEG
WKLPGSLGAKSKLSGDNLSLSTQPKVIAGVDYERAKNGVCSFA

SEQ ID 497

ATGGAAGAAATCTGGTTAGAAAGCTACGAGAAGGCGTCAGTCCGAAATCGACATCACGCAATACAATTCGCTCAGCGACGTATTCCGCCAAAGCGTGGAAAAATTTGCCCGCTGCGCG
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CCCGCGGTGTGCTGCAACCCCTTAAACATCGAATCATACAGCGGCAGCATCGGTTTCCCGTCCCGTCCACGAAGTCAAGTGCAGCGCAACCGCAAGAGTCCCGTGGGCGAGC
CGGCGGAATPGTGGGTAAAGGCCCGCAAGTGATGCAAGGCTACTGGAACCGCCCGAAGAAACCGCAAGCCATAGACGCGTGGCGCTTTTGGAAACCGCGGATATTGCCGTGATGGA
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SEQ ID 498

MEKIWLESYKGVSAEIDITQYNSVSDVFRQSVKPARLPAPQNMGRITLYAETGKLATDFASYLQNVLELPRGERVALMMPNVLYQYPIALFGILQAGLVAVNTNPLYTPREHLQKDSG
ATATLVLENFANTLELVLERTQIKHVIVASVGENFGLLKGSLINFIIIRIKMVPYRIRRETVPQTALKEGAKHVFPVALNREDTALLQYTGTTGVARGAVLSHGNICANHLQAKEHI
KNQLREGKETVIAALPLHYIFALTIVNLMIFANAGSKIVLIANPRDMRGFIGELKKQVRNVFIGVNTLFNAMVNRDPFAEVDPSGLRLTLGGMATQKVAEKWKKITGTPIVEAYGLTEAS
PGVCCNPLNIESYSGSIGLVPVSTEVLELDANGKEVPVGPGLWVKGPQVMQGYWNRPEETAKAIDACGLETGDIAMDEKGRLLKLVDRKDLVVVSGFVNPNEIEFIAHHEKVMVEV
ACIGVPEKGTGEALKVFPVVKDPSLTREELTAFCTGLTAYKVPKDI EPRDELKPSNVGKILRRELRSAGK

SEQ ID 499

ATGCGCTCGAAACATCTTCAGACGGCATTATAAAATCTGTTACCTTTTCAGATGAGTAATGTACACCCCTATACAATTTTGTCTACCATGCACCATAAATCCACGGCTAAAGATAATT
GGGTTTATCTTTTATTCAGAAACATCCAGATACGGATCAGGGCTATACTATAGGCTTATATTTACACGATTCTCATTCATCAAGGCGGAAACCGCAAAATCTGAAACACATATC
GATCGAATTG

SEQ ID 500

HPSENIPRRHYKICSPFQMSNVHPYITPATMEHKSTAKDNWVYSFIQKQSRVSVITIGLILHDSHSAENRTNTEYLSIDL

SEQ ID 501

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SEQ ID 502

IKFNKIKRLREYICVTVHLHIVNKRK*K*Q

SEQ ID 503

ATGAACACAAACCACTGCGGTTTACGACCGCTTGACACGCGCGCTGCACTGGCTGACCGTTGCGGCTTCATCGGCATTCTGACACCATTTGCTGTGGACAATTTACGAAGAGCGCG
AATGGCGGGCGAGCTGTTCGGCTGCACAAATCTTTCGCTTCTCATGCTGACGCTGATTCGATTCGCGATTCGCTGTGGCGGTTGCCAACCGCGCCCAAGCGTCCGCAAGCGACAGCA
GGCGGCGAGCGGACAGGACCGGCTTCTGTATCTGCTCATGCTTTCGCTTCCGCTTATCGGCAATGATCGGCAATACGCTGGCGGAGCGCGCGCTTGAAGATGTTCCGGCTTGAAGTAATG
CAGGGTTGCCGGAATAATCGAGTGGATGCAAACTTGGGCAACAGCTTCCACGCAATTTGGCTGGCTGCTGTTTGGCGCGCTGCTGCGGACAGCTGCCATGCTGCTGCTCCACCGTG
TTCAAGGCAAGAGCTGCTGTACCGCATGACGGGCGGTGCTCGT

SEQ ID 504

MNTNQPAYVDPLTRALHMLTAVAGFIGILATIVLWITYEEAEWAGSLFGLRKSFGFIMLTIVIALRIVMAVANRAKRPQSDSKAAAAGHGILYLLMLAVFVIMIRQYGGGRGPKLVFVGEVH
QGSPEKLEWMANLGNTPHGNLWLLFAAVGVHVMVVRVQGDVLYRHTGRV

SEQ ID 505

TTGCCCGCAAGATTACAGTGGAGGCAAAAGGCTTTGTACGATTGGCACTGTCTGTGAAAAACAAATGATGCCGGATGGACCGGACCATAGTGGCAACGGAATCAACGGACACGCCCC
GTATCGCGGTACAGCAGCTCTTTCCTTGAACAGGTGGACGACGACCATGGCGAGCTGTCCGACGACGCGGCAACAGCAGCGACGCCAAATGCGGTGGAACGCTGTTGCCAAGTTTG
CCATCCACTCGATTTTTCCGGCGAACCTGCAITACTTCAACCGCGAACACTTTCACGGGCGCGCTCCGCCACCGTATTGGCGGATCATGCCGATAACGGGAACGGCAAGCATGAGCAG
ATACAGATGCGCTGTCTGCGCTGCGGCTTGTCTGCTTTCGCGGACGCTGGCGCGCTTGGCAACCGGCCACACGATGCGCAATGCAATCACCGTCAGCATGAGGAAACCGAAAGAT
TTGTGCGAGCGCAACAGGCTGCCCGCCATTCGCCCTCTTCGTAATTTGCCACAGGACAATGGTGTGAGAATGCCGATGAAGCGCGCAACGGTCAGCGAGTGCAGCGCGCTGTCAACG
GGTCTGTAACGGCAGCTTGTGTTGTTCATAAAAAATCTTTATCATATGTAAACGTTTGAACGGACATTCCTCGCGGTGGAATGTCAAAAAGCGCGATTGTACAAAGAAAGTTGGAC
ATATTGTTGTTGTCAGGCTGAGAATTTGCTTAAAAATTCATTAAGATGGGCAAGCAAAATAGTTTCTCGCGGTATATTGAATACCGCTTATACCTTATAATGTCGGCAGAAAAATCTGTTT
AGACGCGCATCAAAACATATGGCAATCCGCTGAAACCCATTAAAAACCAACAAACAGAGCATT

SEQ ID 506

LPRLQVRAKRLCTIWHCRGKTNDAGWTGTIVRTESTDTPRHAVQHVFALNTVDDDHGDVSDDGKQQAQIAVERVAQVCHPLDFFRRTLHYFNAEHFQRAASATVLADHADNMGNGKHEQ
IQNAVSCRCLAVALTGLGAVGNRPDAQCNHROHEETERFVQAEQAARFRLFVNCQDNGQNADEAGNQPVQARQCRVNVNRLVCHVKKILICNGLNGHVSQKGAIVPKKLD
IFCLQAEOLLKSLRWABQIVSPRYIEIPLIFVYVGRKSVQTAASKHAIKRLPYLKPTNKSI

SEQ ID 507

ATGAATTCATCGACGAAGCAAAATCGAAGTCCGCGAGGCAAAAGGCGTAAATGGCGCAACCAAGTTTCCCGCGCAAAATTCGTATCCCGCGCGCGCGCGGACGGTGGCGACGGCGGCA
AAGCGCGAGCGCTGTGGCGAAGCCGACGAAACACCAACCCCTGTCGAATACCGCTTCTGTAACCGTACCAAGCAAAACCGGCGAAAGGCCACGGTTCGACCGCTACGCGC
AGTGTGCGGACGACATPGCTCAAAATGCGCGTCCGCGACCCCTATCCGCGACCTCGACACCGCAAGAAATCGTTCGCGACCTCACCTACCGACGACGCGCTGCTGCGCAAAAGGCGGCG
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CAGCTGTGCTGATTGGCACCCCTTCGACGAAACCGTCAATCCCGCGCAAGAGCACTCGCCATCATCAACGAATTACGCAATACGACGAAGAACTTTACGGCAACCGCGCTGGCTGGTGC
TGAACAACTCGATATGCTCGACGAAGAAGAGCCGCGCGCAACAGCGCGCTTCTCGAAGCGGTGCGCTGGGACTACCCGCAACCTGATACCGGTTTCCAAATTCGACATGAAACCCCG
CGCGCTTCTTCAAAATCAGCGCGCTGACACATCAAGGACGCGAGGATGTGTACACAAATCAACCAATACCTGCGCGAGAAAAACGATTCGAGGCTGAAAGAGCGGAGCGGAGAAAGCA
CGGCAAAATGTGAATTTATCGAACAGCAGCTTAAACGGGATCTGGCGGTGTTAAGCCGAG

SEQ ID 508

MKPIDAEKIEVAAGKGGNGATSFRRREKVPFRGGPDGGDGGKGGSVWAEADENTNLVIEYRFVKRYQAKNGEKHGSDRYGAGADDIVLKMFPVGTILRLDLDTEIVADLTTHYQVRCLAKGG
KGLGNIHFSSVNRAPKQSTPGEGETRSLQLEKVLADVGLGMPNAGKSLTITAVSAARPKIANYPFTTLPNLGVVRIDENHSFVMDIPGLIEGABAGAGLGHRLKHLRSLTGLLL
HVDLAPDETVPNPAEALAIINELRKYDEELYGKPRWLVLNKLMLDEEARARTAAFLAVGWNDYEPDDRFPQDMETPRLPQISALTHQGTQELVHQINQYLAKKRIEAEKAEAKA
AANVEILBQQPKTDTGVFKPE

SEQ ID 509

ATGTACAAACCAATAGATTATTTTTCAGGCATTGGCGGAATACGCTAGGCTTTGAAAAATACGGGTGCACCAATGTATTCTCATCGGAATGGGACAAATATGCCGACAAAGTGTATGAAG
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GGGATTGAAGATACGCGCGGAACATGTTTTCATATTTGCCGAATCTGAAACCAACAGCGCGAAGGCTTTTCTTCTGGAACCGTTAAGCGGCTGACTACGACGCAATTCGGGCGAG
ACTTTCCGTATTATTTAGAAACCTTAAACAGCTTGGTTATACGCTTTATTTAAGGTTTAAATACTTTGGATTTCGGATTGCGGCAAAACCGGAGAGAAATTTATATTTGGGTTTTT
CAGACAACTCCCTTTTACTTTCGGAACCCATAAACCAATATCGGCCATTTGGCGCACTGCTGGAACAGATCGAGATGTGGAACCAAGCTATTTTATCAGATACCTTGAACAAAA
ACGTTTGGCAGCCTTAAAAAAGCTCCGCGCCACCCATCAATTTGGCATGAAAAATTTGGCGGGAATGTTTCCGCACTTCCATATTCCTGTGCTTAAAGGCGCGGGGAAGTTACAAATTAT
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TATCCGTCTCTGTAAGAGCCATCGCGGAAATATGCTCGCTTCTTTCGCGCAAGGTGCAACAAAAAGGCAATTTGGAATTTATTTGAGGCGAGG

SEQ ID 510

MYKTFIDLFSGIGIRLGFKEYGCTNVFSSWDKXARQVYEANPGEKPPGDIINGIDPSDIPDHDILLAGFPQPPSIAGKGLGPEDTGTGLFFNIAELIKTKPKAPLLENVKRI/THDSGR
TPRIILETLKQIGYIVYFKVLVFLDFLPGKRRERYIVGFSNIPFYFPEPINQYRPLGELLENDRDVEPSYFLSDTLKQKRLAALXKAPPTPSIWHENIGGNVSALFYSALRAGGSYNY
LVVNGVRRLTGREMLRQGGFPDDFEINIPYSQVRKVAGNSVSVFVIEIAENMLASLSGKVEQRGQLDLEAG

SEQ ID 511

ATGACCGCTTGAAGAACAACAGCCAAGAAGCATTTGACGGCATTTACAAAAATCCCGTGTCCACCTTTATAAACCACTTCAAAATTCAGAAATTTTATATCATGACCGTGTATATAAAC
AGTTGGATTTTAAATTTAGATACCTTACCGCAACCAATTAACACGCTGGAGGATGAATCTGCCGTCGGTTTTAGGGCGGATTTCTACTTCATCTGCAGAAATTCAGAAATATATCTGTT
TGAAAAAATGCAATACCGCTGAAAAATAGCGGTATTTGGGAACATTAACAGACAGTCGACGCGCGGGTGAATCTGACATTTATAAACAGTPTTCAATCGTTTTCCCAATGAGC
GAAGCATTTGCTTATGTCGCAATACAGACAGATACCTTCCAACTGTCTGAATTTCTAAATTTATTTTGGCTCGAGCCGGGATTTGAAAAGAGGTATAGACAAGATATATGAATCTGTTG
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GCCGAAAAATGAGCATTTAAAACTTCTGCAAAATCCATCGTGTAGGCGTAACCAATGCTGCCGATAGAGGTTGGATATGTGTTCTAACTTCGGATTCGCATACAGGTCAACATCTC
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AAGCCGAATTTCAAAACATCTGTAACCTGAGGATGATTTGATAAGTTGGTACGAAAAAGCATTGAGAGGCCAATATCCGATTGCGAGAACGGTTGTGGAAAAATATTAACACTGAAATTTATGCG
TGAATTTCTGCGGTATATGAGCAATGAATTTTATAGATTTCCGCCAAAAATCCGCGATATGACATTACTGTTACTCATTTT

SEQ ID 512

MTLEEQAKLEALDGLIKSRVHLKPIQIAELIYHDCIKQLDFLNLDTYRQSKRWDEICRRFLGRISTSSAKFQDNLFEKNAIPPEKLAVLGLTNRQSDGGVESTIYKQFFNRPQMS
EALAYVGNTRYSFQLSEFLNLFLEPLKRSIDKIYEIVVYALFDALVSELGITVSIDFPKENLFLWEEYQDFAEKIITMPKNEHLKLPKIHVRVGTNAADRLDMNSNPLAIQVKHL
SLDELAEDIVSSISADRIIVICKAEQSVIVSLTQIGWKSRIQNTVTEDDLISWYKALRGQYPIAEALLENIKTEIMREFFPAVNEANEPLDFAQNRGYDITVYHF

SEQ ID 513

TTGACCGGTAAAGGTGTGTAGATGGCGGTATATTCATCAAGTAAGTTTAGAAATGAGTAACAGTAATGTATATCCGCGATTTTGGGCGAAATC

SEQ ID 514

LTGKGVVDGGHIIHQVLSMNSNVI SAILGEI

SEQ ID 515

GTGCGTATGTACGTCGCGCATGACCGTTTACGACTATTGCCACTTAGGCCATGCCCGTGTGATGGTGGTGTTCGACATGATTGCCCGTGTGTGCGCGAGTGGCGTTATCCGCTCACTT
ATGTGCGCAACATCACGACATCGACGACAAATCATCGCCCGTGCCTGAAACCGCGGAAACCATCGCGGAACTGAACGCGCGTTTCATTCAGGCGATGCAAGAGTGGCGATGCTTT
GGCGGTGTTGCGTCCGACATCGAGCGGAAGGCGACGGAACCATCCGCAATGATTTGCCATGATTGAGACCTGATTTCAAACCGCAAGGCATATCTCGCCGCAACGGCGACGTTTAC
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CGCGCGCGCGGATTTGCACTTCCCGACCATGAAATGAAATCGCCCAAGCGTGGTCCGACGCGTACACCTGCGGTATGACACCGCGCAACCCACCGTCAAGTATTTGCC
AGCCACGTCAAAATCTGCTGCAACACCGCTTATCCGTTGAGCGGCAAAAAATGTCAAATCGTGGGCACTTCTTTACTATCCGCGAAGTATGAAACAAATAGACCCCGAAGTGT
TGGCTTTCTTCATCTCGCGCCCATACCGCAGCCGTTGAATCTACTCCGACGCGCATTTGGACGACGCGAAAGCGCGTGCACCCGCTGTACACCACTTGAAAAACACACCGCGCG
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AAAACCAATGACGCAACCTCGCGCGCTGCTGAAAGCTTTGGCGGCGCATCATCGGCTGTCGCAACGCAACCGATGATGATTTCTTCAAGCGCGCGCATTTTCAGACGCGCTTCCAAAG
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CGGCACGACTTGGCGCGCGGT

SEQ ID 516

VRMYVCGMTYVYDCHLGHARVMVVFDMIAWLRRCGYPLTYVRNITDIDDKIARAENGETIGELNARFIQAMHEDADALGVLRPDIEPRAPENIPQMIAMIEITLIQNGKAYPAANGDVY
YAVREFAAYGQLSGKSLDLRAGERVEVDGPKRDLDFVLWKAAGKAGAPAWESPWNGRPFWHIECSAMSENLFPGDTTIDHGGADLQPHHENEIAQSVGASGHTCGHDAQTHHGQSLA
SHVKYTWLENGFIRVDGEMKSLGNFFTIREVLYQYDPEVVRFFILRAHYRSPLYNSDAHLDDAKGALITRLTTLKNTFAAEFLDENANGYTRRFYAMNDDFGVEAVLVELAGEVN
KTNDLAHLAGCLKALGGIIGLLQRNPIEFLOQGAUSDGLSNEETIEDLIARRKQARADKNMAESDRIDLLNEHKIILEDASAGGTTWRRG

SEQ ID 517

AAAACTAAGGAAACCTATGTCCCGCAACAGAGAGCTGCAAGGCATCTCTTTTGGGTAAATCAAAAAACCAATATCCGACCGGCTACGCGCTGAAATTTCTGGAAGCATTCGACA
ACAAACATCCCGCAACAGACTATTTGCTCAAAATTCGTCTGCCCGAATTCACAGCCCTTGCCTGATGACCGGCGAGCCGACTTCGCGACCATCGTCATCCGCTATATCCCGCACAACAA
ANTGGTGGAAAGCAATCCCTGAAATCTTACCTCTTCAGCTTCGCAACACCGCGATTTTCATGAAGACTGCGTCAACATCATCATGAAGACCTCATCCGCTGATGGATCCGAAATAC
ATCGAAGTGTTCGCGGAGTTTCAACCGCGCGCGCATCGCGTTTATCCGTTTGCACAACTACGCGCAAGCAGGACAGAGTTTGAAGCATTTGGCACGCAACCGCTGTTTCGACGACGAG
CACAA

SEQ ID 518

KN*GNPMSRNNELQGISLLGNQKTYPTGYAPEILEAFDNKHPDNDYFVKFVCEPTSLCPMTGQDPFATIVIRYIPIHKMVESKSLKLYLFSFRNHGDFHEDVNIIMKDLIALMDPKY
IEVFGEFTPRGGIAVHPFANYGKAGTEFEALARKRLFEHDAQ

SEQ ID 519

TTGTGCTCTTTGAAGCGGACTTCGATTATCAGAAAAACCAAGTGGCGCGGTAAACAAAGGCTCGTTCCCGATGGATTATTCACCTGGACGCGCAACTATAAATCAGAAGGATTGG
GACGAAATATACAAACCGCAGCATGGACACCGATTCAACCGTTTTACTTTTGGTATGGACAGCAACCGTTGCAACTGGGCGGCAACATCGTTTGTGCTT

SEQ ID 520

LSSLKADFQKTKVAAVNNKGSFPMDYSTWTRNYKSEGFGRNIQPHGHPIQTFYFAYGQPTVATGRPTSLVV

SEQ ID 521

ATGCCAATAGCGTGCAATCCGTCGGGATTTTTCATATCCGCAGACAAATCAGCCTCTGCGCTTTGAGTTCCTGCAACGACAGCAATGTCTGCGCCGATGCGCGATGTATTCGTAAAAA
CTTTTGTGAGCGCGGAGCGGATCCGTTGACGTTGGCGGAAATGATTTTAAGCATATAAAAAATAGATTCTCACAATGTTCCCATACAAAGCGGCAACCGGTCGCGCGCGGATTT
CCCATTCGCTCTGCTGCTG

SEQ ID 522

MPIAVHPVRIPIHIGRQISLLRFEPLHADNVNRCAGDVFKTFFVGGADAVDVGNDPKHNKNKFSQCSHTQSTRCARYPPFPAC

SEQ ID 523

ATGCACGGCTATTGGCATTGCGCGGAGAGCGCGTTACAGCGGTGTGGCGGTGTACAGCAAAACGCAAAACCGACAAATGTGCAAAATCGGCATGGGCATTGAGGAATTCGACCGGAGAGGCG
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CGAAGCGATGAAAAACGAGGCGCGACATCGTCTGCGCGGACTGGAACATCGCCCAACCAACATCGACCTGAAAAATTTGAAAGGCAATCAGAAAAATTCGGGCTCTGCGCGAA
GAGCGGAGTGGATAGGCAAGTCATCCATACGCTGGGCTGGAGCGACATGTGGCGCACGCTTATCCCGATGTGCGGGTTATACATGTTGGAGCAACCGCGGCGAGGCTATGCGAAAG
ATGTCGGTGGCGCATGCAATTATCAGATGTTACGCGCAACTTGCAGCAAGCGGTGTCGCAACGCTTTATAAGATGAAAAATTTCTGGATCACGCCCTTTAGTTGTGAGATATGA
CTATGCTCCGAA

SEQ ID 524

MHGYWHCAEKRGYSGVAVYSKRRPDNVQIGMGIKRFDRGRFVRCDPGRIGVISLVLPSGSSAEERQVKYRFLDAFYPLLEAMKNEGRDIVVCGDANTAHQNTIDLKNWKGNQKNSGFLPE-
 EREWICKVILPTLGTDMWRTLLYDPDPPGYTWSNRGOAYAKDVGWRIDYQWVTPPELAAKAVSAHVYKDEKPSDEAPLIVVEYDYAAE

SEQ ID 525

TTGTGGAGTATGACTATGCTGCCGAATAAGGTTTGGGTAATATGATTTGGAATGTGGACGAAAAACAGGAATAGGCGGGCATGGGTGTGCTGCGGTTTATCTCGCCATATTTGGTGT
GGGCGGTGTTTATGTGTGTCGGGATGCAAGGCTGGCTTGCGCCGACCAAGGCAAAACCGGATATGGGCGTTGGTGTGGCTGCTGATTTGTCTGCCCTGCCCTGCTGATTTGCGGCCAAATGTTT
GGGTGGAAAGCGCTGGCGCGGGGTGTAATATTTTGTCTGCCTGACCGCTCTGCCCATATTGACGCTACCCGCTTCTGCTGCTCATGCGCTTTAACCCTCGGAGCACTGCTCAA

SEQ ID 526

LNHSMTFLPNKVLGKYDWNVDGKTFGIGAAWVAFLPLVWAVFMLSRLMOGLAPTKANPIWALVWLLICLPCLLIAAKCLGKGGWRRVNNIFVCLFVCAILSVPASLLIAFTLRDLK

SEQ ID 527

TTGAGCAGGTCCCGGAGGTAAAGCGGATGAGCAGCGAAGCGGGTACGCTCAATATGGCGCAGACGGTCAGGCAGACAAAATATTACCACCCGCGCCAGCCTTTCCAACCCAAACATT
TGGCCGCAATCAGCAGGCAGGCAGACAAATCAGACCCACACCAACGCCATATCGGGTTTGCTTGCTGGCGCAGCGAGCCTTGCAATCCGGACAAACATAAACACGGCCCAACACAA
TATGGCGAGGATAAACCGCAGCGACAACCCATGCCGCGCTATTCTGTGTTTTCCGTCCATATCCAATCATATTTACCCAAAACCTTATTCGGCAGCATAGTCATATCCACAAC

SEQ ID 528

LSRSRRVKAMSSEAGTLNMAQTVRQTKIFTRRRQPFQPKHLAAISRQGRQISSHTNAHIGFALVGASQPCIRDNINTAHTNMGRINAATTHAAPIPVFPSTFQSYLPKTLFGSIVILEN

SEQ ID 529

ATGGAAGATTTCAGACTTGAGGATTTGACCGTGTGGCTGATACCGGATGCGGATGAAGCGGAAATGTGGATAGACCGTGGGGCGGTCACTTATCCCGTGTGTCAGATGTCGGAAGCGTTCG
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CCGCGCCGACATCTGACGCGAAGAAAGCTGCCGCGTATCATCTCGTATCTCCGCGTCCCGATATTTTCCGACGATGCGGAAACACACTTTCACAAOCGCTCCGCTGTCTTTCGCGTGCC
GCATTGTGTGGTGTTCGGAACACGGCGGCTGCGCAGCGTGTGGCGCAAAAAACAGGCGGATTTGTGGAACGCCCGCTGTGTGTTTCCCGCATTCGGGCGATTTGAACGGTATGCTCGCGG
GCTGGCAGTGGGTATGAAGCTGATGCAGGAAATGTGCTGGCG

SEQ ID 530

MSSEFEDITLHLIRDAEAEWIDRAWVSYFVVQMSASANGSTEAWQSALQTAFERIQGRHIAVVARAGAAFLANWLYRADILTOKKLAGITLVSPPDIFPDDAEHTFORVRCPCRA
ALVSEHGCVPHGMAQKQADLHNRALLVSPHSGSLNGLGGWAGMKLMQEHLLA

SEQ ID 531

GTGTTTCGGACACCACCAATGCGGGCAGCGGCAAGGACAGCGGACGCGTTGGAAAGTGTGTTCCGCATCGTCGGGAAAAATATCGGGACGCGGAGATACGAGAAATGATACCGGCGAGTTTCTTC
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SEQ ID 532

VFGHHQCGTARTADALESVFRIVGKNIOTFRYENDTGEFLLRQDVGAQVPROEGRARAACVNDGMPALVYFPCRLKRALPRFAAACVGRFHGLHNGITDRPTVYPHFRIRIAYQPQRQI
LKLETFHCPRLFEQVPEKGDEBQSGYAYQADGQADKNIHPPAPPTQTTFGRNQAGQTNQOPHORFYRVCIGRRKALHPRQHKHRPHQYQDKRSDNFCRAYSCFSVHIPIITQNL
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SEQ ID 533

ATGAAAGTAGGTTTCGTCGGCTGGCGCGGTATGGTCGGTTTCGGTTTGTAGTCAGCGTATGAAAGAAGAAAACGACTTCGCCACATTCGCCGAAGCGTTTTCTTTACCTCTCCAAACGTG
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CTTCCAAGCCCTGCGCGACAGCGGCTGGAACGGCTACTGGATTGACGCGCGCTCTCACTCGCGCATGAAGACGACGCGATTTATCGCCCTGCACCCGCAACGTCATCGACAC
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CAAAGTGTCCGATTTCCTCCGACGCGAAGACTATCCGAAAGCCAACTTCTGGCGTACCGCTCGCGCGGACCGCTGATTTCGGTGAATTGACGTGGAATTTGGGCAACGCGCAAGTCAAAGAAGAA
TGGAAAGGCGGGGTGGAAACCAACAAATCTCGACACGACGGCAATTCGACCGCTATCGACGCGCTGTGGTTCGCGATTCGGCGGATTCGCTGCCACAGCCAAGCCATCACTCTGAAGT
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CGGACCGCTGTCTGCTCTGTGGACGATCCGCAAACTGGGCATGGCGGCGAATATCATAGCGGCTTCACCGTGGCGGACCACTTTTGTGGGTGGCGAGCGGAACCGATGCGCGCGGTG
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SEQ ID 534

MKVGVGVWRGVGVSVLQRMKEENDFAHTPEAFFPTSSNVGGAAPDFGQAAKTLILDANDVAKLAKMDITVTCQGGDYTKSVFQALRDSGNHGVWIDAASSLAKDDAIIALDPVNRNVIDN
 GLKNGVKNYIGGNCVTSLLMALGGLFONDLEVWATSMTYQAASGAGAKNMRILSGMATHAQVADELADPSSAILDIDRKVSDFLRSEDYPKANFVGPLAGSLIPWIDVDLGNWQSKEE
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 LRTVLGSL

SEQ ID 535

ATGAAACCATTAACACATGCTTCTATTGCGCGCTGGTGGGAGTATTTTCGGCAATCCGGCTCTTGGCAGCGGATGAAGCTGCAACCGAAACACACCCCTTAAAGCAGAGATAAAAGAAG
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ACCAAAACCTGCAAGGCATGATTGTGCTGTGGACGACAGACAATTCGGCGTGATGATGAAAAACGGTTACAGCAGCGCGACCGGCGAATGACCAAAATACACTCGGTTTCGGTGTGAGCAA
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CGATT

SEQ ID 536

MRPLHMLPIALVGSIPGNVPLAADAETATTPVKAETKEVRVKDQLNAPATVVRVNLDRIQEHIRDNKDLVRYSTDVGLSDSGRHQKGFPAVRGVGVRGVGSIDGVSLPDSEENSLYAR
YGNFNSRSLSIDPELVRNIEIAKGADSFNTGSGALGGGVNYQTLQGHDLILLDDRQFGVMKNGYSSRNREWTNLTGPGVSNDRVDAALLYSQRGHETESAGERGYPVEGAGSGANTRGS
RGITPPDSKHKYHNLGKIAIYINDKHRIGASFNGOOGHNYTI

SEQ ID 537

TTGTTCTTAAACAGATGGAATTCCTACCGCCCTACTGCTGCAAACGCCAATCCCAAAAAGAAAATTTCGATAAAGAACTTTACATTTTCCCAATACGGCGT

SEQ ID 538

LPLNRWNSTALLQTPPIPKRKFDELYIFPIRR

SEQ ID 539

ATGGAAGAAAAAAGACTACACCGACGCGGTATCCGACAAACCGCAACGGGAGGAATGAAGTCGGAATTGCGCGCAGGCGACCGGATCTTGGCGCGTGTGAACCAATGTTTA
CCTTTTGTATTTGTGTGGTCCGCTTGTGCGGATGATGCTTCCGCGTCAAAAATGAAGCAGGATGCGCGCGGTGAGGAAATATCGGGCTGCTTTGGGCGATGATCTCTTTGGGT
CGGATGCGCGGCGATTTGGCGTACACCGTCATCCAAATCTACTATATGAGCAGGAGCGGCGAGTCATTTGGTAAAGAAATCATGAGAAATCCGCGTGTGAAAACCGACGCGCGCAATCCG
GGTTTGTGCGGACGGTTTGTGTACGCAAAATCGCGTGTGCGTTTGTGTGCGATTTATCCGCGCTTATCGGTCTTGCAGTAGGTGAAAACCGGGAACCGCATCAACCTGCTGGCAT
TCCTTGGCAACTTTGTCTGCTCTTTATGGTCAACCGGACCGCGGACGCTTTACGACATATGGCGGATACGGTTGTGCTCAAGCTGCCAAA

SEQ ID 540

MEERNDYTDVSDNRNGQEIEVGIAGAGDRILALNLQFLFTLLVFPVGLIAFAVKNRIGRIGREITFGLLGMTSPFVGLAGILAYTVIQTYYMSRDGQSLGKKIMRIEVLKTDGRNP
GFVGTVLVREIAWSVLVAIAAVIGLAVGENGENAINLLAFLANFVLLFMVKRDRRTLYDILADTVVVKLPK

SEQ ID 541

GTGGCGCAACGGCAACAGGACAATCTGCACAGCCTTGCCTGGCGGTGTTTGTGCGAGGCGACCTTGCCTGGCGGAGTTATGTGCGCAACAGAAAACCGCTGCCAAAATGCGGCA
TCAAGTCGCTGTGTCGTAAGACTGCCCGAATCAACATCGCAGGAAGAACTGCTGGCATTTGGTCGACCGCTGGAATGCCGATCCGAAGTGGACGGTATTTCTGGTTACGCTTCCACTGCGGAA
GCACCTCGACAGCAAGCGATCTTGAACGTATTTGCGCGGATAAGGACGTGGACGGCTTCCATCTTACAATGTCGCGACCGTGGCGGTCAAAAATCGCGTGTATGCGCCGCTGTACGCCC
AAGGGCTGTATGACGCTTTTGGAGGCTTACGCGATTTGATCCGAAGGGGAAAAAAGCGGTGCTGTGCGCGCGTCGAAATATTGTGCGCGCGCGCGAGGCGTGGAAATTGCTGCTGGCGCGCG
CAACGGTAAACGCTTGTCCACAGTGCACCGAAAATCTTCCGATGAAGTTGCCCGCGCGATATTTGTGCGCGCGTGGGCAATCCGAACTTTGTCAAAGGCGGGTGGATCAAAACCGG
CGCGGTGCTTATCGATGCGGCAACACCGTTTGGACGACGCGACCTGTGCGCGGACGTGGAATTTGAAACGCAAAAGAACGGCGCGGATGATTACCGCGCTTCCGCGCGCGTGGT
CCGATGACGATTGCCACATTAATGGAACACTTTGCACGACGCTTCCGTCACGATGCT

SEQ ID 542

VAQRQDNHLPFLAVVLVGGDPAGAVVVRNKTACQKGIKSLSYELPESTSQEELLALVDRLNADSEVDGILVQLPLKHLDSQAILERISPDKDVDFHPYVNRGLAVKPLMRPCTP
KGVMTLLEAYGIDPKGKAVVVGASNI VGRPOALELLARATVTVCHSATENLADEVAAADILVVGVI PNFKGGMKPGAVVIDVGINRLDDGSLCGDVEFTAKERAAMITPVPVGVG
PMTIATMENTLHAASLHDA

SEQ ID 543

GTGTTTTCGGAACCTCTTTACCGTTGATCAGTTGTCCGACATATCCGTCCTTTTGTAAACAGGTAGAAAATGCTGAAAATTATCGCATTTCCGTTGTTTTCACAGCAGAATGCCG
AAAATAAATTTGCCCGGAAA

SEQ ID 544

VFLRNFTVDQLCRHIRPFVKQVENAENYRIFRLFLQNAENKFAPK

SEQ ID 545

ATGCCGAAAATAAATTTGCCCGGAAAATAACCGCTGTTGGACGGATTAAATATTTTCAAAATCAAAAACTATATTTTCATCTTGGTGTTTTGAATAAATGTTGACGATCTT
TCCTGAACCTGTATATTCGCTTCTCAAGTCGGGGCG

SEQ ID 546

MPKINLPKIRLFGRIKYFFKSKNYIFHLGVLKINVDASPPELYIPLQVGA

SEQ ID 547

TTGATGTTGACGCTTGGCTGTCTCCGATTTGAATCGAAAATCTGTCCGCGGAGGCGTTGGCGCGCGCTTGGCGTGTGTCGCGCGCGCGCTGTTTACCAACGGCTGTTTCGACA
TCTTCCACAGGGGGCAGCTTACTTATCTGGCGCAGGCGGCTTGGCAGGGGCGCGTGGTGTGCGGTGAATACCGATGCTTGGTGGCGGTGTTGGCAAGGGCGGCGACCGCGCGGT
TAATCCTTTGGAGAACCGTGGCGCGCTTGGCGCGCGGTTGGAAGTGTGGATTGTTTACTTGGTTTGAACGAGGATACGCGCGCGCGTGGATTGAGCGGCTCAAGCGGAGGTTGTTGTC
AAGGGCGCGGATTTGGTGTGTTGATAAGATTGCTGGTGGCGCGGAAACGCTGGCAGCGCGCGCTCAGGTGTTTCAATTCCTTCTGTCATCAGACTTCGACACGAAGACTTTGGCAAAA
TCCGTGCGCGCAGAGGGCGGAAA

SEQ ID 548

LMDAWSVPDFESKICPPALALRALLPRPLVFTNGCFDILHRGHVTVLAQARSAGAAVLALMTDASVRLRGKGRDPVNPLENRAA VAAALESVDLVTFWDEDTPAALIEAVKPEVLV
KGGDMVVKIVGAETLARGGVFSIPFLHQTSPTTKLAKIRAEAGK

SEQ ID 549

ATGACGCTTTGAAGCCTTCGATTTGGCGGTGTTGGCGGAGCTTGGCGACGTTTGGCGCAACACGTATCGCAATTGGCGGTGAGGCGGACATGAAGCGCAGCAGCTCAACGCTTTT
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AGGGGGCGGCGAGGGCGGAAGTGTGCGACCGCTTGGCGGAGTGCCTGATGTTTCACTTTCGCTTGGCGGTGTTGACCGCGCAGTATGATTTGGGTTCGCTGTGCGCTGTTGCGGCACTTG
CGTCCGCGCGCGCTTTGGGGTGTGTTGGTTTGGAAACGCAATCAAGTGGCCAAACGATTTGGTGTGCGGACCGGACAAATTTGGCGCGCATTTGATTGAACAGTCAAGGCGGGCGGTAA
AACGTTTGGCGTGTGCTGATCGCATCAATTTGCTGCTGCCAAGGAAGTGGAAACGCGCTTCCGTGCACTGCTGTTTTCAGACGGCATCGCGCGGGGCAATGCCGATGCCCGCTA
TTGCTGAAACATGCTTGGCAACTGGCGCGGTGTTGGAACAATATCGGAAGAAGGTTTCCGCCATTTTAAATGAGTATGAACGGCCACCGCGACCAACCGCAAGCGGTATTTG
TGTGCGCGCAGCGCGAAACCGTGTGCGAAGGCAAGGTTAAAGCGGTGGACGAGCGGCTTCTGCATTTGGAACCGCAGAGGCGGACAGCGGTGTCAGCGCGGAAATCAGCTCGG
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AACAGCTCGCGCGGAAAATCGAGTGGCTGCCGTCTCCGCAACGCTTTGGCAGTACGCAACCACTACCGCCACCGGAAAGAACCGGTTCGACCGCTTGAACGCTTGGCGAGCGG
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GAATCGCTCGCGTTCGAACCGCCAACTCAACGCGCGCGCGGCAACGTTTACCTTTCCCGACACACGCGCAACCGGTGCGCAAGCGGATGATGGAACGCGGTTCGCGCGGATGAA
TGATGATGACGCGCGCTTTGAAAGAAAAGAACGCGCGCGGCAAGCTGTCGATGTCATCATTTACCGCGCGCGCGCGGCGGAAAGTCCGCGGAGCCCTGCGCGCTGCATTTTGGCGGAAA
TACCGTGGCGGTGCGGCAACCTCTGTCATCCAGGCGTGTGAACCTGATTCGCGCGGAAAGCGGGGAATCGGAACCGT

SEQ ID 550

MTVLKPSHMYLAELADGLPQHVSQLAREADMKPQQLNGFWQNPAPHIRGLLRQHDGYWRLVRLAVFDAGLELRLGERSGFQALKHECASSNDEILELARIAPDKAHTKICVTHLQSKG
RGRQGRKWSHRLGECIMFSPFNADRPQVELGSLSPVAALACRRALGCLGLETIQKPNLNVGDRKLGILLIETVRAGGKTAVVVGIGINFLPKVEVENAASVQSLFQYASRRGNADA
LLETLAELGAVLEQYAEGBFAPFLNEYETANRDEKAVILLRLDGETVCESTVKGVDGRVGLHLETAGGEQTVVSGEISLRPNRSVSVPRKPDSEFLLEGGNSRLKNAWVENGFATV
GSAFYRDLSPIGAWEAKDGNVRI VGCVCGESKKAQVKEQLARKIEWLPSSAQALGIRNHYRHPFEBHSDRWFWALGSRFRSRNACVVSVCATVFFVDALTDGCHYLGSTIMPFGHMK
ESLAVRTANLNRPAKRYPPPTTGNVAVSGMMDAVCGS IMMHGRLKEKNGAGRPVDVITGGGAARVAELPPAPLAENTVVRVADNLVIHGLNLIAAGGSEBHA

SEQ ID 551

ATGAAGATAACACACTGCAAAATTAAGAAAGAACTACAGAAAGAACCGCTCCGTTCTTTTGTACCGGAAGTTACCGCGCTTTCGCGCGGATATTTGGGTATCCATCCCGATTCCGGCGG
CACTGTTTACCGTAAATTCGCGCGGTTCGCAACCATCGTTTGGCTTGGCTGCGGATGGGGTTTCGAGGGCCCGCGCGCGCGCGGCGGAGCTGTTTCGCGGACGCGGCTAAAGGCA
ACGCGGTGCGCGCGCGCAGGAAAGCGGTGCTTTCGCGCATTCGAAACGCAACGGCGCGGCTATACCGTTCGCGCGGACAAATCCGAGCTTGAACGTTGCCCTTCCGCTCAAAAAG

AAATCATGCCGACGGTATGTTTATGCCGATAGCCCGGCGAGCCGCGCAAGTCGACGCGGGCGGTTTACCCTGTCGCGATCAACCGTTCGAGGAATTCAGACCGTCGGAAC
ACATTAACGCGATTGGGAACCTTTTGAATCAGGCAAAACGGCTTCGCGAAATACACGGAATCGATCGTAACCTTTCCCGCGTGTGTGAGGAATGCAATTCGACTTAACCTCGG
CACACCGTCCCGCAGCTAAAAATCTCGCGGATCGGTGTGAATT

SEQ ID 552

MKITHCKLKKEVQKEPLRSFVPEVTARSADILGIHPDSALFYRKIRTVANHLALAADGVFEGPAGPGSGCFGRKRRGRGAAGKAVVFGIPKRNGRAYTVAADNAEPETLPPAVKH
KIMPDGIVYADSPGSRGKSDAGGFTFRINRSEFADRRNHINGI GNFNWAQRALAKYNGIDRRKPPPLLRBCEPRLNFGTFSRQLKILDRCGI

SEQ ID 553

GTGTTAAATCCCGCTTTAAAAACCCCGTTTCAAGCCATCTCGGTATGAATACGACATCAAACTTCCAATATCATCGTCGGGCTTTCCGGCGGTGCGATTCTTCGTAACCGCGG
CCCTGCTCAAGCAGCAGGTTTATCAAGTCGCGGTGTGTTTCATGAGAACTGGGAAACGACGACAACGACGAATATTCAGCATCAAAAGGATTCGTCGATGCGCATCGCGTTCGCGA
TATTGTCGGCATCGACATCGACATCGTTAATTCGCGCGCAATATAAGACAAAGTTTTCGTTTATTTCTTCAGGAATACAGTCGCGGGCGCACGCGGAATCCGATGTGTTGTCAT
GCCGAAATCAAAATTCAAATGCTTTTGGACTACGCGTATGGGACAGGCGCGGATACCATTCGACCGGACACTATGCGCGCAAGAAGCCGCAACGCGGTGCTATTCGTCGCAAGGTT
TGGATCGAAACAAAGACCAAGCTATTTCTTACCGCTCAAGCTTTTCAACTCGAACGCGGATTTTCCGTGCGCGGTTTGGAAACCCGAGTGGCGCGCTTCCCGCGGAAAT
TAAFTTCCGACTCGCGCTAAAAAGACAGTACCGCATCTGTTTCATCGCGAGCGTCCGTTCGCGGATTTCTGCAAAATACCTTCCGACCGCAACGCGGCAAAATGTCAGCGCGGAA
GGGAAACCATTCGCGCAACGTCGCGGTGATGTTTACACATTTGGTCAGCGCAAGGATTTGGGATTCGCGCGCGCGCGGCAACCGTGTGTTTTCGCGCTAAAGATTTGACGAAAAAG
AACTCATCGTCGTAACAGGACAGGACATCCGCTGCTCTATACCGCAGCTTGTGATGAACGATTGAGTTTCACGCTGCGCGAACGTCGGAAGCGAGGACGCTATACCTGCAAAACCGG
TTACCGTATGCGCGACCGCGCTTCCGAAATGTCGCTATTTGGATGATGAAACCGCGAGCTGTGTTGACGAAACCGCAATGGGCGGTTCACGCGGTCAGTCGCGCGTCTGTCAGCAGCTC
GACATCTGTTTGGCGCGCGCATCATCCAAACGACGCAAAACCGCTCATCATCAGCGA

SEQ ID 554

VLKSAFNRRFQAILRNMNTSNTSWIIVLSGGVDSVTAALLKQGYQVRGVFMQNWENDNDDEYCSIKQDSFDAIAVADIVGIDIDIVNFAAQYKDKVPAYFLQESAGRTFNPVLCN
AEIKFKCLDYAVGQADTIATGHYARKEARNGVHYLLKGLDRNKDSYFLYRLKPFQLERAIFPLGLEKPEVRRLAAEFNLPTAAKNDSTGICFIGERPFREFLQKYLPTDNGKHVTP
GKTIGEHVGLMFYTLQRRGLGIGGAGEPFWAANDLTKNELIVVQGHDPPLLYTRSLVNDLSFTLPERPKAGRYTCKTRYRHADAPCELCYLLDDETAELVDFEPQWAVTPGQSAVLYDV
DICLGGGIIQTDRPVIITR

SEQ ID 555

TTGCCCGCAAGCGCGGGAATCGGAACACGCTTAAAAATATGCCCTTTTTCACACGGGCGGCATCCGTCCGAATCTGTCCGATTCGCGCGCGACAGACTGCGCGCGCGCGCGGCG
GGGTTTCAACATTCAGGAAATTCATGAATGGCTCTTACCCCTTTTGGCGTACTCAATATTCGCGTATTCGCGCGCACGCTGGGCTATAAATGGCGCTTAAAGCGCGCGCGCGCT
GCCGAAAACCGCGCGCTCGAAAACACGCGCCCGCAACGCGCGCGCGCGCAATGCGCGCATCCGTGGAGGATACGCGCGCACTGCTCAAAACCGCGCGCATCTTACGCGAAGAACAG
CGGAGCAGTTGCGCTTGAAGAAAGAACGCGAACAGAAAACCTGAGGAGAAAACAGCGTGAAGAAAACCGCGCGGAAAACCTCGCGCGCGGAAAGCGCAGGCGGAACGTGAAA
ACGCGCGCGCGGATGCTTATGCGCGCGCGCAGGCTTACGATGGACGAGAGCACTACCAACCGCATCAAAAGGCTTTTGGGCAAAATGTCGCACTGTCGCAAGGTTTCAACCCCATACCGTTTGAC
ACGCAACCGCAAGGCAAACTGCGCAAAACCTTACCGCTGCTGCTGCGCTTTCGCGGATGCGGAAATCAGGCGCGGAGCTGCTGCCAAAGGTTTCAACCCCATACCGTTTGAC
GGCGATTGAGTTTGGGTGTCGCGAACGCGGAAAACGCGCCGCTGCAAAACCGCACTTCCGATGCGCGGATTCGCGCGCGCGCATATTTGTCGAACACTTTCGCGAAGCGGACAGCG
AGGACGATTCCTTACGCTGTGCGGTATGACGCTTTGTTTACGCGCGTGAATGCGCGGATCGGACGAAATCCGTAAATACGCTCCCTATACGCGAACTGAACCTCAAGCTTTCGAA
A

SEQ ID 556

LPPKAGNRNPLFKYAFQHGAAASVRIQFSAARQTAARAGGVSNIEELIMKWLFTLLAVLNIAVFGTVGYKLAVKAAGGVENRAVENTPPATPAAGNAAASVEDTAALLKPGDILSEBQ
AEQLRLKKEABQKLRKEKQREKARREKLAEEKAQERENGADALCAQASLTDEDDYHRIKGLGKNSHVASRSVEKETAKAPADKTYRVVLPVSADAENQAELSARGFNPIPF
GALSIVGNSRENAQALQNLADAGPGGAHIVEFAEDRQDLSVSRMTVLFTGVNADADEIRKITSLYGLKLNKSCX

SEQ ID 557

ATGTATGTCCTGATATATCGGACTCCAAGTGTGAAAGTGAATTTGTAGGGAATACAGTGTTAATGGTTCGGAACGACGCGCTCCGAGTGGTTTGTATTATACGCTAATAATAATTA
TCAATAAAAATTAATAATAATCGGATTTTTTG

SEQ ID 558

MYVSMPSPSVKNCEGIQCLMVRNRLPSGFDYTLIIIIINKNLKINADFL

SEQ ID 559

TTGTTCAACACGCGAGGCTTCTTTCCGACAGGACAGAACCCCGCTCATGCTGCCGACCCCGATTTGTCGCGCGCAATGAAAGTTTGGCGACCCAAATCACAACATCGCGGACAGG
TTAATTTGTTTATTTTCATCGCATTACAAAAATCCGATTTATTTTAAATTTTAT

SEQ ID 560

LPKHGRLLSDRHEAPFHACRPRFVRNRESLPTQITNIGGQVNLFIHRIKTNPHLFLNFI

SEQ ID 561

TTGAACAACCGTCGATTTGGTCGCGACAGGTTGCCATTGCGGGGTGTTGAGCGCGGATTCGGGATGCAAAAGCGGTGAACCGTTGCGGATGAAGGCTTACGGATGCCCGAGGTAT
TTTTAATGTATTCAACGCAAAACTCCCTTCTATTGCGGTACTTAGGCTTGCAGCAGGCTCGCGCGCGGGAGTCCGGGTGTTTGTGTTGCGGTGTCGGGCGCGCGGCAAGG
TTTTCCGCGCGGTTTCCCTGTTCTCAGCAAAAGCGGTGATGCGGGGAATGCGGTTTCCCGTTTGGGCGCGGATGCGCTC

SEQ ID 562

LNNRPIWCGGCGSGVFERGFGDAKAVKPLRMKAYCPEVLNVFKRNSLLLPYLGLAQAPARRGVVFRWLRCRGRGQFPAGFPVPHDKAVMPGNGLPVMGRDAB

SEQ ID 563

TTGGCATTCGCGGAAATATTGAAAAGCGCGCAAAATGCCGTCTGAAGGCTTCAGACGGCATCGCGGCCCCAAACGCGCAACCGCCATTCGCCGCGCATCAGGCTTTGTCGTGAGGAAC
AGGGAACCGCGCGGAAACCTTGCAGCGCGCGCGCGGACACCGCAACCAAGCAACACCGGACTCCCGGCGCGCAGGCTGCTGCGCAAGCCCTAAGTACGGCAATAGAAGGAGTTTGT
CGTT

SEQ ID 564

LAFGLILKKAAMPSEGRFRHRGPKRANRHPASRLCREEQNRPENLAARPDATNETPGLPGAQAAQALSTAEBSFV

SEQ ID 565

ATGCTCACCTGTACGCGGAACTTTCCCTTCGCGCTGCTGCTCGGACGCGCGCTACCGACCCCTGAAATCCTCAAAACATCCGTCCGAACCGCGCGCGCGGATGATTACCGTCT
CGCTGCGCGCACGCGGATTCGCGCGCGGAGGCGCAGGTCAGGGTTTGGTTCGCTGCTTCAAGAAACCGCGCTTCCGTCTTCCGCAACGCGCAGGCTGCGCAAGCGTGCAGGAACCGGT
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ATTAAAGACGGCTTCAAGTGTGCTTATTGCAACGAAAGCTGATTGCTGCGCGCGCTGCTGATGCGCGCTGTCAGGCGTGTATGCCGTGGCGCGGCTCCCATCGGCAAGGTTTGG
GGCGGTTACCGCTATGCGCTCAAAATCTTGCAGCAAGCGCTGCGGACGCGCTGATTATCGACGCGGCTTGGGTTTCCCTTCCCAAGCGGCAAGTGTGGAATGGGTTTGA
CGCGGATTTGTAAACACCGCGCTTTCCCGCAGCGCGGACCCGCTCAACATGCGCGCGCTTTCGCACTGCGGTCGAATCCGCGAGGCTGGCATTTGAGCGCGCGCGCTGCAAGCGCGA
ACCAAGCCCAAGCGCAGCGGACGTCGGAACCGTTTGGCATTCGCGGAAATAT

SEQ ID 566

MTLYGETPFSRLILGTAAYPTPEILKQSVRTARPAMITVSLRRTGCGGEAHQGFWSLLQETGVPVLPNTAGCQSVQEAVTQAQMAREVPEFDWIKLELIGDDDTLQPDVPLVVEAEIL
IKDGFKVLPHYCTEDLIACRRLLDAGCQALNFWAAPTIGTGLAVHAYALKILRRLPDPLIIDAGLGLPSQAAQVMEWGFVGLLNTAVSRSGDPVMMARAFALAVESGRLLAFRAGPVEAR
TRAQASTPTVVGQPFWESEAET

SEQ ID 567

ATGTACGCATTGACGCCGACAGCAACAGAGGCACTCTCCGGCTGGTCTTTTCCATATCTCATCATCGCCGCCAGCAACTATCTGGTGCACTGCCCTTCCGGATTTCGGCATCC
ACACCATTGGGGCGGCTTTTCCCTTCCCTTCATCTTCTCGCCACCGACCTGACCGTCCGCAATTTGGTTCGCACTTGGCGCGGCGATTATCTTTGGGTGATGTTCCCGCGCTTTT
GCTTTCATACGCTCTTTCCGTTTGTTCACACCGGCACTTGGACGGGCTTGGCGCGCTGTCCTCAATTCACACCTTTGTGCGACGCAATCGCGCTGGCAAGTTTTCGCCCTACCGCTC
GGACAAATCTTGATATTTTCGTATTCGACAAATTACGCCGTCTGAAAGCGTGGTGGATTGCCCGGCGCATCAACCGTCATCGGCAATGCACCTGGACACGTTAGTATTTTTCGCGTGT
CCTTTTACGCAAGCAGGATGAATTTATGGCGGCAACTGGCAGGCGCATCGCTTTGTGCGATTACCTGTTCAAACTTACCGTTCGACCCCTCTCTTCTCGCCGCGCTACGGCGTGATCT
GAATCTGCTGACGAAAAAAGTGAACGCCCTGCAAAACCAACAGCGGCAAGACGCCCGGCTGCGCTGCAAAATCCG

SEQ ID 568

MYALTAQQQKALFRLVLFILIIAASNYLVQFPFRIFGHTTWGAFSPFFIFLATDLTVRIFGSHLARRIIFWVMFPALLLSYVSVLFPHNGSWTGLGALSQFTTFVGRIALASFAAYAL
GQILDIFVFDKLRRLKAWNLAPAASTVIGNALDPLVFPFAVAFYASSDEFMAANQGLAFVDVLFKLTVCTLFPLPAYGVILNLI/TKKLTALQTKQADRFPVPSLQNP

SEQ ID 569

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AACGCTTAAGGCGGATACCAACGCGGTTACGACAGCGTGATTAACCTCGTATGTCTGTCTCAACCGTTTGTGAGCAAGAAATACATCAAAATTTTGAACTGCAATCCGTGTTCCTA
CAAGCGGTGTGATCATATCTATAAAGACCCGAGTTGAACAAAGCCATTTCGAGCTTGAATACATGCGCGGATACGATGCCGTAAACGCAAGACTTTGAAAGACTTGGGCGAAGAGCTTAC
AAATTCGACAAAGAAATGCCACAGAAACCGGCAACAAAGCCGTCGGCTGCTTTATGCGCGGAGGATCAATTTGGGCGCGGCAATTTTGTTCAAACACGCGCAAAAGCTGGATTACA
CCGGCGAAGCAGCGCGCGCCACTCGCTCCGCTACCGGACGGCGCGGCAACACTGGCGCGCTTCTGTCGAGCACTTGAATGCCCTGAACTTAACTCCGGAAGCAGAGCAGAGCCAT
TCAAGCGCGCAGGAAGCGTTTGTCTTCTATAAAGTGATTCTGCGTGAAACCTTCGGTTTCCCGGAAGGAACAGAGCCCGCAAGGATGATGCCGACAGACAT

SEQ ID 570

MLLYVFCMRASLDFPARTASLSLTKGELMSETEQALTFAPKRLKADPTAVHSDVNLVMSVQPFVSKENYIKFLKLQSVFHKAVDHIYKDPKLNKAISELEYMARYDAVTDLDLGEFPY
KPKELPHETGNKAVGNLYCAEGSNLGAFLFKHAQKLDYTGEGARHLAPHPDGRGKHRAVFEHLNALNLTPEARBAIQGAQRAFAFYKVLRETFFGLPBGTEAPEGMMPRH

SEQ ID 571

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CGTTCATGAAATCCCAACGACGAAGCCAAACAGACTTTTGTCTGTCGGAAGCAGCCCGTTGCGGACCGCGTGAAGTGCATACCCACATCAACGACACCGCGTATGCGTATGCG
CGAAGTCAAGGCGCGCTGCTTTGGAGGCGAAATCCGTTCACGAACTCAAAACCGGCACTATCACGTGATGTTTATGGGTTTGAAGAAACCACTGAAGAGGGCGACAAGATTCCCGTT
ACCTCGAAATTTAAAGCCCAAGCGCAACCGTCCAAGTCAAAACCGCGCGGATGTCGCAANTGAACACCGGTATCACCAACCGGCAAGCGCATCAGCAC

SEQ ID 572

MKKLLAAVMMAGLAGAVSAAGVHVEDGWARTTVEGMRMGAPMKIPNDEAKQDFLLVSGSPVADREVEVHTHINDNGVMRMREVKGVPLEAKSVTELKPGSYHVMFGLKKQLKEGDKIPV
TLKFKNAKAQTVQLEVKTAAPSAMNHGHHGEARHQ

SEQ ID 573

TTGTGCGAGCGGATGCGCTGAAAGCGCGCGCTGCTTTGGGTTTTCAGAGGCATTACGCGCCGACGACGCGGCGGACGATGTCGATTTTGTGTTTTCGTGTAAGCGTTTCCG
TATACCGCGCTTTGGGATGAAACCGGTGTTGACCGCCACGCGCAAGGGTTTTCGCGCGCGTTTGGGCGATGAGGTCGCAACGCTTGTGCGG

SEQ ID 574

LSDAMPSESRRRPFVSDGIQPPPTGRTMSILSFSCKRTVSVAFLQMKTVLTATAGFCGAVMMRSATLVP

SEQ ID 575

ATGAACATCATCTTAAACGGCGGACCCGCGCAACTTCACGSCACAAGCGTTGCGGACCTCATCGCCCAACCGCGCGCAAAACCGCTTTCGCGTGGCGGTCAACACCGTTTTCATCCCA
AAGCGCGTATACGGAACCGTTTACACGAAACGACAAATCGACATCGTCCGCCCGCTGCTCGGCGG

SEQ ID 576

MNIIANGPABLHGTSVADLIAQTAQPKPFAVAVNTVFI PKGAYTETVLHENDKIDIIVRPVVG

SEQ ID 577

ATGTGGCATATCATCAAAATCCGTCATTCCCGCTCAGGCGGGAATCCGCCGGAACCTTGAGAAACCATATTGAAAAACAGTTTCCGAAATTTCAAAATGGAATCCCGCTGCGCGGGA
ATGACGCGCAACCGCGGTGCGTATCAAAAAATAAG

SEQ ID 578

MWIIKFRHSRSGGNPPENLRNHLKNSFRI SKMSRLRGNDGNRPVAYQKIX

SEQ ID 579

ATGACCTTCCCGCCCTAAAAATCCCTACTTAAATTTACGCGCTGCTTCCACCGCGGATGGGTGGGGCGCATGGTCAAGCAGGTGCGGACAGGTGCAACTGCGCTGTAAACCTTGC
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TCTCGGCGAGGAAGATGACACCGCGGACCTTTCGCGCATCGCGCGCGGCTTTCGCTTGGGTTTGGTACGCACTTCCGTCGCGCAACTCGACCGCGCGCTTGTGTACACCGCGG
TACATCGCGAGCGCGGATTTTCCAGACCAAGCAAAATGCCACCGCGCGGCAAGGCTTGGACAAATTCGCGCAATATGTGGAACAGGCTCGCGGCAAGCGCGCTGCGCGCATCG
GCGGCGATCGATTGAACAACGCGCGGAGCGGTGCTGCGCACCGGCTTCTCTACTCGCGCGCTCGCGCGCTAACCGGAAGCGGCAATCCCGAAGCGGTGTTAAAGCGTTTCAGGCTTT
GTGGGATGA

SEQ ID 580

MTFPLKSLKLYAVVPTADWVGRMVKAGADTVQLRCKTLHGNEKREIARCVAAQGSRTQLPINDHWREATEAGAYGVHLQREMDTADLAAIAAGLRLGLSTHVAELDRALFVHPG
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SEQ ID 581

ATGACCGTATCGCGCTCTCGGAGGCGGCTTTTCGGAAGGCTGACCGCATTCGAGCTTGCAGAAACAGGTTATCAGATTGAATTTTTCGACAAGGCCACCGCCCAAGCGCAACACGCGG
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CAGCTCAGGATGATGACAGGAAACGCGAGCTGATTTGTGCGGACGCGGAGGCAAGCCATTATCCAGCGAGTTCGTCGCCCATCTCAACCGCGCGCGGTAGCGGATGACGAAATCGTC
CGTTGGCGCGCGATGAAATCGCGGACGCGAACCGCAACTCGCGGAGCTTTTTCAGAGCGCATCTACTCGCGACGGAAGCGGACCTCGACCGCGGCAATATTTGTCTGCACTTTCGCG
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CCAATCCCGGAGCACACCGACCTTTCGCGCGGATACGCGGAGTGGCGGCTTACACGCGCGGAAATCAGCTTAACCGCGCGCTGCGCTGTCGACCGCGCTATCGCTCTAC
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CGGCTTTCGCGGAGCGGACATCTCGAAATCGCGCGGCGCTGCGCGCGGCTCAACCAACCAACCGGAAATTCGCTACAGCGCGGAGCGCGCTCATCGAAATCAACGCGCTTTT
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AGACAAGAT

SEQ ID 582

MTRIAVLGGGLSGRLTALQLAEQYQIELFDKGTQGEHAAAYVAAAMLAPAAEAVEATPEVIRLGRQSIPLWRGIRCLNLTLMQENGSLIVHGDQKPLSSEFVRHLKRGGVADDEV
RNRDELAEREPQLGGRPSDGIYLPTEGQLDGRQILSALADALDELNVPCHEHECAPDLQAYDVIDCRGYGAKTANNQSPHSTSLRGIRGEVARVYTPETILNRPVRLHLHPRIPLY
IAPKNEHVPIGATQIESRQAPASVRSGLLELSALYAVHPAPGEADILEIAAGLRPTLNHNPEIRYSRERRLIETINGLFRHGFMI SPAVTA AAVRLAVALFDGKDAPERDEESGLAYIG
RQD

SEQ ID 583

ATGATTATTACAAAATCGGGGTTTATCAAAATAGGCTTGTCCGCCGAGGGGCGAGCCGCTCAAAAATATTTTTCGCCGACACCAAGGGTTTGTTCATACTGCCGAACCTGCCGGTTTTC
CATCC

SEQ ID 584

MIITYKIGVLSNRLVGRGSRSKNIPAGHQGFVHTAEPAGFAS

SEQ ID 585

ATGGAACTTCCTCTACGCGGCAGAAAAAAGGCAAAAGCGGCATCAGCGCGTCATCAACGCATTCCGCTATTTCGATAGACGGCATCGCGCGCCCTACCGTTACGAAGTGGCATTC
GTCAGGTTTTCGCGTGAACCGCGCTGCTGCTGTCGCGGCATTTTTTGGGTTTCGAAACCGCGCTCCGCTGCCGTGATTATCCGCTCTTTTGTGTCGCTCATGTGCGAACTGTTCAA
CACCGCGTCGAAACCGCGCTCGATCATCTTCGACCCGAAAAACACGAGCTGCGCAACCGCGCAAGATGACAGGTTTCGCCGACAACTGGTTGCCATGCTGATGTGCGCGCGGTTTCG
CTGTCGCCCTGTTCGG

SEQ ID 586

MEPSSYAAERKKGSGIRRVINAPGYSIDGIAAYRYEVAFRQVLNALLVCAAFVWSETAVRLLPIIASFVSVIVELFWTAVEAAVDHTSTKHELAKRAKDAGSAAQLVANMLAAVH
LSALFG

SEQ ID 587

GTGCTGATTTCGCAATCGATACCGCCGCGCGAACCAACAGCCGATGCGCGCGAAGATGAAGGAGAGGAGGCAITGCCGACATA

SEQ ID 588

VLISAIDTAAPNQTSPMAEDGGEALPDI

SEQ ID 589

TTGGGCTGGCAGCGCGTCTGGCGGCCCTGCTTTTGGGTGTCATCCGTCGCGCGCGCGCTGTTTTTTCGCCGCGCGTATATCGCGCGACTGACCGGACGAGCTCGATGGAAGTGTGCGCC
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CCTGCTGCCGCTGGCGCGGACTACACGCGCAAGCAGCGCGCGCTTTTCGCGCAACCTGACGGCAACGCTCGCTTATACGCTGACGGCGTCTGATGTATGCTTTGGGTTTGGCGCG
GGCTCTGTTTACCGGAGAACCGACGTGGCGAAATCTGTTGGCGCGCGGCTTTGGGCAATACGGCGCATTTTCGCGAGTCTGCTCTCCACCGTTACCAACAGCTTTTCGATACCTATTTC
GCCGCGCGAGTTCGAACAACATTTTCGCCGCGTTTTTCGCGAAATACCGTCTGCTGTCGCGGTTTTACCTGATCGCGCAGGTGCTTGCCTCATGCTGCCCGTTACCGAATATAAACTTTC
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AGGCTTCATCTCTACCGCTTCTGCTCTGCTCGGTTCGGAAGCAGCATCGTCTGACCGCCCGTAATGCTGCGCTGCCATTGCCACCGTATCGGTACCGCTTTTCTTAAAAAA
ACCCAATCTTTACAAAGGAACCGTCA

SEQ ID 590

LQWRQLAALLLGHAVGGALFFAAAYIGALTGRSSMESVRLSFGKCGSVLFSVANMLQLAGWTAVMTYVGATVSSALGKVLMDGESFVWALANGALIVLWLVFGARRTGGLKTVSMLLHL
LAVLWLSVEVFPASSGTNAAPVSDGNTFGTAVELSAVMLPSWLPLAADYTRQARRPFAATLTATLATTTCGMYALGLAALFTGETDVAKILLGAGLITGILAVLSTVTTTFLDTYS
AGASANNISARFAEIPVAVGVTTLIGTVLAVMLPVTEYKNFLLLIGSVFAPMAAVLIADFPVLKRREIEBGFDFAGLVLMLAGFILYRFLSSGWESSIGLTPAVMSAVAIATVSVRLPFAK
TQSLQRNFS

SEQ ID 591

ATCCGCTATATCAAGCCCTGATTTTTTATGCGCGACACTATGCATCCGACCTATTCGCCGCTACAGCGCGCGCTGCTCGAAGCCAAACCGCTTTCCCGGAACTGCTCGCCAAAGCC
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GCGGACAGGTGGACATCACCAGCGGAAATTTGCTTTCGCGCGCTCGAAGCGTGGTGGTGGAGGCGCGAGGCTGCAATACCCGTCAGAGGCGGACCATATCGGCAACCGCGCGG
AGTGTGTAACACGTTTCGATGATAGCGAACGATACCGCGCTCGACAGCGGTGTCGCGGTGTCGCGCAAGAGGCGAGCGTCCCGCTGCGCGTGGGCGAGCGACCTGCGTATCGAT
GCCGGCTGACCGTTCGCGCGCAGCGCAATC

SEQ ID 592

HPYRQAPDFLCADTMHTPTSAVQARILLEANRLSPELLAKSLCIIGAHHVDYADTYQRTAYESWHEEGIVKSGSFQIDQGVGVRAVSGDKTAFAYADSLCIDINSARAVRAIGAAGKK
VSAKMPSETRGKPVCSASDPIAGLDSAAKVALLNKVEALAKAADPRIVQVHAGLTCEYDMVYLARLDGKHAADIRPMVRLNVTVIARQGERRECGGAGGGGRYDLAYPDETLVBQFVDAV
KQALTNLESRPAPAGETTVVLGNWPGVLLHEAVGHLEGDVFNKGTVSFGRIGERVAAGKVTVVDQGLDLAGRRGSLNIDEGNETRRTVLI EDGILVGMQDETNRALGTQSTGNRR
QSYASVPMRHTWTFMENGSTYEPERILASIDKGIYAVNFGGQVDITSGRFVFGASEAWWVEGRLQYPVKGATLIINGPEVLKHMIGNDTALDSGVGVCKRQSVFVGVGQPTLRID
AGLTVGSAI

SEQ ID 593

ATGCCGCTGTAACAACTTTTCAGACGGCATCGTCCCGGATTCGCGCTCAGATTGCGCTGCGCGCGCAGCGTTCAGCCCGCATCGATACGAGGGTCGGTTCGCCACCGCGAGCGGGACGCTC
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GCAGCGTCCGCTTCCACCCACCGCTTCGACGCGCGGAGAACTTTCCCGCTGGTGTATCCACTGTCGCCCGCGAAGTTGACGGGTAAATGCCCTTTGTCGATGGAAGCGAT
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CGGCCAACGTTGCCAAAACGACGCTCATCTCGCGCGGAGCGCAGGACGGATTCGATTGCTCAGGCTTGTTCGAGCGCGCATCGACAACTCGCGCAACAGGTTTTCGAA
TAAGCAAGTCTGAGCGTCTTCGCCCGCGCGCGCGCGCGCTTTCGCGCGCTTCGCTCTGTTGCGGATGACCGTAACGTTTCAGGCGCACCATCGCGCGGATGTCGCGCGGTTTTCGCG
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GGAATCGAGGCCGGCAATGGGTCGGATGCGAACAACCGGCTTGGCGGCGCTTTCAGACGGCATTTTGGCGGACACCTTGGCGCTGCCGCCCAATCGGCGGAGCGCGGGCGGAA
CGGTTTATCGAATCGATGCACAGGCTGTGGCGGTAGGCAAGCGGCTTTTGTGCGCCGAAACGGCGCGCACGCCACACCTGATCGATTGGAAGCTGCCCGATTGACGATGCCCTCTT
CCAAATGCCAGCTTTCATAAGCGGTGCGCTGGCAGTAGATATCGCATAATCGACGTGGTGGCACCAGATGACACAGGCTTTTGGCGAGCAGTTCGGGGAAAGCGGTTGGCTTCGAG
CAGCCGCGCTGTACGGCGGAATAGGTGGATGCATAGTGTGCGGCA

SEQ ID 594

MPSENLSGIVPDSASDCAADGQPGIDTQGRLEPHADGDLFFFAHADTAVERGIVAYHRNVQHFQAVADNGRAFDDGLQPAAFHPHPRGRAEDKFPAGDVHLSAAEVDGVNLDVGRD
DFFRLVAAPHKGVGHTRHRRDGGVALAAAVAGRLRTRQAGVGVFLHIADQDAVFNQYGAACFVAFVVDVERTAPAGNIALIDGNAPGGDAFADPAGKDAGPLAVELAFQTVSDRFVQQA
RPTVAQNDGHLGRRRTFEIGQLFDGIDKLPHQGFIEISQVVASAARAALFAAFALFGDDGNVQAHHRADVGGVFVAVQTGEVNHIVFAGQTHHLHDARIGGGDCPFHVQQRDPGG
GTEAGNVGVCRTNRLAARFRHRFGHLLAACRPNRADGAGTGVYRIDAAQAVGVGKGGFVARNGAHAHTLIDLEAARFDDALFQMPAFISGALAVDIGIIDVVRTDDAQAFGEQFGKAVGFE
QPRLYGGIGRMHVSVA

SEQ ID 595

ATGCCGCTCGAAAGGTTTTAGACGGCATCGCCTTATCTTTTTCCGATGTTTGATATTCCTAAGCATCTTTAATCATTACTTACAAGTTTCATTAATAACCGCCTTTTCGTTAAGCTGA
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CGGTGTAACGGCATACCGCATCCGCCCTTCTACGCATTGGCGCGCGCTTATATCGAGCTGTGCGCAATACGCCCTGCTGATCCAAATTTGTTTCTATATACGGCTCTGCGGAAAT
GGCATCAAGTAGGACGGTTCACCTCGCGCTAATCGCGCTGGTTTCTTGGCGCAAGCTTATATGGCGGAAGCTGTGCGCGCGGCATCTCGCGTCCCAAAGGGCAGGTGCGAGCG
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TCGTGACACGGTGGCATTCGGAATTTGTTATTTGTTACCAAGACGTCATCGGTATGAGCTACAAAACCAA

SEQ ID 596

HPSESRFSGIALFFPHFDIPKHSLSYKFIKIPFVKLISDELALPNRCRTQIRRCGKADAGIVLRRCFVAVRPARRRNGIHPHPLAIGARLYRAVAQYAPADPIVFPILRSABN
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SEQ ID 597

ATGAACCTGGCTTATTTAATCGATGCCGTACCCAAATTCGCGCATGCGGCAAGCTGACGCTGGAATTTGTCGTTTACGGCGTTGTTTGTCTGTTGTCGGCTTCGCCCTGCCCTGG
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GCAATCGGTTTGAAGCGCTTCAAGTGTTCGCTATGTGCAATTCGCCGAGGTTTGGCGGTGCGCGTCCCGCATCGCGCAAAATATATTGTTTTAATGAAAGAACATCGGTCGTCA
GCACGGTGGCATTCGGAATTTGTTATTTGTTACCAAGACGTCATCGGTATGAGCTACAAAACCAATGAAGCTTGTCTGCTGTTTGGCGCTTATTTGATATCTGCTGCTGTTTCT
TTGTTGGCGCGCGGATTTGAAACCGCGTACGGAGTGGCAATATGCGCT

SEQ ID 598

MMWPLYLDAVFKPADAARKLLELSVYGVVLSLFLGLPVAVVTAYRIRPFYALARAYIELSRNPLLIQLFFLYYGLPKMGIRKMDGFTCGVIALVFLGASYNABAVRAGILAVPKQVQAGK
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SEQ ID 599

TTGGCGCAAGGCTGCTCTTAAACGGCACAAATTTCTTTAATCTCTGTTGCGGCTTCTTGCCTATTTGGGCAAGCTGTGCGCTTGGTTTGGCTTGGCGCAACCGGCTTGTCCGCTTTGTGCG
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GGCAGCAAAATATTGAAACTCGTGTGACGACGAGCCCAATGCTTCAATTTGGGTTTACGGCGTGAATTTTATGCTGTATTTCTCTGTTGCTGCGCGCTATCTACTGCGCGCAAACT
TGAACAAAAATGGGAACAC

SEQ ID 600

LGBGLLTAQISLISVAACVLGTLFGLVLRNRNLRVVRGFLYLETIRIVPILVWLFGLYPLSVWTHIGGFWVCVWVPSLWGVAMGDLVRGALESIEKHQVESGLAPGLSRGQVFR
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SEQ ID 601

TTGCAACACTGCCGGAACGGATAAATCCGGATTCCACCCACTTCGTATTCGCCGAAAGCGGAATCCGGTGGCTTGGGGTTCACTCATTTCCGATAAATCTCGCCGATTTGTATTT
CTAGATTCCCGCTTTCCGCGGAA

SEQ ID 602

LQTLPERINPDSHPLRHSRESGNPVRWGSVIDKLLPHCISRFSLRE

SEQ ID 603

TTGCATCTGATTGGGTGTATCGCTTTTTCCTTTAATATCCGCCATTTATATTTGCCACTTTCGCGATGAAGCCGTTTGGCGAAATATCCCCACAGCTTTCGCGCAACTGCGCGG
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SEQ ID 604

LHPDMVYRFPSPIMPPIFATFPMKPPAENIPHSLEGNCRDEALPHTVDCPECGCRDVPQLDKGEAARPCRCGHKLFVSGSHFSGPPAYAAASLILMAFAYSMTYIEVGIPGAASVLS
LPEMRLMWFDYGFLEAVMPLVFGAPVFLILLCLYVYALIRKQAYPALRLAFRVMVRLRQAMMVDVFPVSTLVAYIKLSSVAKVRPGAPAFYLMFALSVMILRTSVSVQHWVYPIGR
LNGNNAVOTASEGRTCSSRLYFRDSESPCGVCAELVRRRPSLSISSAF/TAADVLYFPANILPIMISSNPAAETANFIPSGIAYMDEGRDILAAVIPSASILVPLKIAAMSVLIA
AARFALPAGAKLSHLYRTAAGVRWSMIDIFVIIILMCSFHYYAARVPGSAAVYPLVILVILMLSAYYFDPRLLDKRAADGIAFNETEKYD

SEQ ID 605

TTGTGCGCGCAAGCTGCACTTTTGGCGGCTTTGGCGAGCTGCTGTTTTTGGCTGCAAGTATGATCGACGGCGGCTTCGACGGCGGTGTTGAACAGTTCGACAATGACCGCACAAAGAC
CGGATAATCAACGGCAGGCGGACGGCGGTTTCGGAACCCAAAAAATGCGCGCACACAGCAGCGGTTTCAGCCACAAACCTGACGGAATGCCACTTCGTAACGGTAGGCGCGCGGCA
TGCCGCTATCGAATAGCGGAATGCGTTGATGACGCGCTGATGCGCTTTTGCCTTTTTTCTGCGCGTATGAGGGAAGGTTCCATCGGTATCTTTCAAAATGCTCTCAATATATGCG
GTC

SEQ ID 606

LCGRTCIFGAFGQLVFFGRSMIDGGFDGGVEQFDNDRHKRRDNQRQADGGFGNPKKCAHQQRVQPONLTECHFVTVGGGDVYRIAECVDDAPDAAFAPFFFCRVGGGRFHRYPPKMSSTIYA
V

SEQ ID 607

TTGAACAAAATGGGAACACTGACATGGCTTTACTGAGCATCCGCAAGCTGCACAAAANTACGGCAGCGTAACCGCCATCCAATCCTTAGACTTGGACTTGGAAAAAGGCGGAAGTCATCG
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AACCCACGAAATAGGTCGTCGCAAGAAATGTCCGACCGCATCTGCTTTATGACACAAGGCGGCATCTCGAATCGTCCGACCCGCAAACTTTTTCGCGACCAAAAAGCGCAACGGCC
CGCAACTTTCGCGAGGTATGGACTAC

SEQ ID 608

LNKNGNTDMALLSTIRKLHQYGSVTAIQSLDLDLEKGEVTVLLGPSPGGKSTLLRCVNGLEPHQGGSIIVMDGVGEPKDVSRQTAHQKVGMMVFPQSYELPAHMTVTIENILLGPVKVQNRDRA
EAEQAQAGKLLERVGLLDLRKNAYPEILSGGQKQRIATVRALCLNPVEVILLDRITAALDPEMVRVLEVVLELAREGMSMLIVTHMGFARKVADRIVFMDRGGIVESSDPETPTFSAPKSERA
ROFLAGDY

SEQ ID 609

ATGTTTGCTTGGGATGTTTCAACACACAGGACGACACATAAAGCACTGCCCTATGAAATGCCGTCTGAAAAGGGTTCCGACGGTTTTCGGG

SEQ ID 610

MFANDVSTHRTTHKALPYEAPSEKGS DGLR

SEQ ID 611

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CCGAA

SEQ ID 612

MKLNAKIKALLASAAIAVLGTACGGSSGSDAQSSQSSGAATVAAIKKGVIRIGVFGDKPPFGYVDANGKQGGFVIEAKDLAKDLLGSPDKVEFVLTEAANRVETVRSQKVDLILANFTQT
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 LNNVNGEIAAMKKDGRLLKAAVEKTLFPVYGEKVKPRAALLAE

SEQ ID 613

GTGGCGGATTTTTTCAGCGCGCGAAAAATATTGCAAATTCAAAGGAAAAATCAACTATCTCATCGTTTTATTTTATTTTATTATTCTTGCGCGTGGGAAATCAAGTTCTGTCGGGTTTTCGCT

SEQ ID 614

VRIFFSRRKYCKFKGKINYLVLFILLFLRVRKSSSSGFACF

SEQ ID 615

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SEQ ID 616

MTIWKFPRIOKOAKPDELDFRTRKNNKINKTMR

SEQ ID 617

TTGACAGAGAAAATCCGTATCCGCATTTGAAGCGGGTCGGGATTTTTTTCAGCCGCCGAAAAATATGCAAAATTCAAAGGAAAAATCAACTATCTCATCGTTTTATTTATTTATTATTCTT
GCGCGTCGGGAAAATCAAGTTCGTCGGTTTTTCCTGTTTTTGAATTCGGGAAATTCACAAATCGTCATTCAGATAAAACGCTTCAGCTTATGTTTCCGATGACCGTTTTCGCGGGA

SEQ ID 618

LTRKSVSAFEGGCGFPSSAAENIANSKEKSTISSFYLFYYSCACGNOVRPVL PVFEFRETSKSSFOIKRFSLMFPMTVVFAG

SEQ ID 619

TTGAAACAAGCGTGCCGCAAGCCGGAATAAAGTTTCAAGCCGATCGCGGCAGACGGGACGAAATGACGTTTGACGAATGTTGGGCTTGTCAAACATGCCTAAAATTGAAGCAAGGA
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CGGCGCGGAAAAATGCGCGGATTTGGGCGCGGGTCAAAATTGCACACGGTTCGTGGTTTCGACACCGATATCGCTCGAAAGGCAATGGGACATCATCTGTCCAAACCCGCCCTATAT
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ACGGGTACGCTGGGGAGGTATGAAATTTGAAA

SEQ ID 620

LNKRAAKPEKMFPHRRQTGRKMTDEWLGSKLPKIEARMLLQYVSEYTRVQLLTRGGEEMPEDEIRQADRLAQRRLANGEVPAYILGVREFYGRRTFVNPNVLIIPRPEHILVEAVLARI
PENGKRVNDLTGSGGAVVTVALERPDFAVRASDSTPALETARKNAADLGARVEFAHGSWFDITMPSERQWDIIVSNPPYIENGDRHLSQGDILRFEPQIALTFPSDGLSCIRTLAQGAPDR
LAEGGPIILLHGFDGGAAYRGVLAENCFSGVEILLPDLAGLDRVTILGKYNKHLK

SEQ ID 621

ATGAATGTCAGCTCGTAGTTGCCGTAATCGTTATGCTGGTGTCTGCTGCTGCGCGGTGCACGTGGTATTGAGCCCTGACCGTTCGGCGCGCTTTGTCGGCGCGCGGTGGCGGGTATGCCGCTGC
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TGCCGCGCAGGGTTTTCGCCCGGTGATGAATGCGACCGGGCATATTCAGCCGCTGGTGGAAAGCAGTATGCGCATATTCGCGAACAGCAAGGTATGGCGGCTTGGCGATGCTGGTGGTG
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CATOCACTACAACATCCCGCTTCTGATGCCCGCTGGATTGCCGCGATGGTGTCTG

SEQ ID 622

SEQ ID 622

MNAVVVAVIVMLVLSLRVHVLSLTVGAPVGGAVAGMPLQNTADAAGQVSQAGIIPVFNKGLEGGAKIALSYAMLGAFAMAIHISGLPQOLAGAVVRKLNRRGMPDVSRSGECAVKKILL
STILVNGTISQNVIPRIHIAFIPMIVPPLLIVFNRLKIDRRLIACVITPGLVTTYMFLPYTGFAITFNEILLGNTHSAAPQOLVKNINVMAMAIPALGMLAGLLPAVHYRKRPLRYQSNA
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GLLVINGIGSSFSTLPIIAITYVPLCTGLGFSPLATAAIVGTAGALGDAGSPASDSTLGPTFGLNADGRHDHIRDSVIPFTFYNIPLLIAGWIAAVL

SEQ ID 623

SEQ ID 623

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TGGAACAAAACCTTAAAGACGTTTCAACCCGTCATTAAACATTTTGAAGAAAAAACCCACGCACTGATTTTCAACAACAGCAGCAAAAGACCCCTATCCGAAAGGAAGCGCA

SEQ ID 624

SEQ ID 624

LLSTRKKRNNTDNPSPPPNGHAQARVRKNNFTLSAVWLVLPLIALIAGGWLWVKETNRNGFVVTTLMDSAEGIEVNNTVIKVLSDIVGVRVTRIKLRDDQKGVVETAGLNADVSGLIRSDQFWFV
VKPRIQDSGVFTGLFTLLSGSYIAFPFGKSGEAKDVQVQVDIPPVTAIGQSGRLRLMLGKNDRILNVNSPVLVYENFMVQGESAHVPDSDQSGVHYTTFITQSPNDKLHSASRFLWLESGINTE
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ADEQSEKHWWKQPPQATALNKGLTATISNNLLTGGKMIELANDQFASPKLRPHETVYAGDTVIATRGKGGDLDLQVKLADLLDKFPNNLPLDKTVARLNGSLAELKSAKLSANAALSSIDKLGVN
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SEQ ID 625

SEQ ID 625
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CCTCCGCCCCGTTTCAGACGGCATATAT

SEQ ID 626

SEQ ID 828
VVGTLNRCRLKGFCFVTAWFVRAGRVPQPAGMRLMPYGHPSAPFSDGIY

SEQ ID 627

SEQ ID 627
TTGGAACGCCGTATGTGCGAACTGGAAATCCAAACCGCGCTTCAGGAGGACGTAATCTCCGGTCTGAACGCGATGGTGGCGGAATTGCGGCAGACGTTGGATTTCAGCAGGCTCAGTTGA
GGCTGCTGTATCAAAAAATGCAGGACAGGAATCCCGACGGCGAAGAGCCGTATTCCTGCGCGACGAGATTCCGCCGCATTAT

SEQ ID 628

SEQ ID 628
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SEQ ID 629

SEQ ID 629

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SEQ ID 630

SEQ ID 630
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QQESGQHSQCGNHRCHRHVDVFIHLKLRRGGMDVAQQDPVQKNRAEAVRQEHISRNQPESSDARNQAAVDPAVKHKQKRRNNHRDKGDDVGYDLTHNAHHKDDGKQOPFORALARTHVR
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SEQ ID 631

SEQ ID 631
ATGAACCGGGTCTTGTCGGAACGGCGATGAGCGGCTTCCCCGCTGCAAAACAGATAAAACCAACCGGTATTCAAACACAGCCAAAAAAGCCGTCGGAACCAAAGGGGACAGACGGCT
AAACACATTACGGGGAACAGCTTACTCAATGAGTCTCGAAACAGACATTGCTAAACCAACTGCAATT

SEQ ID 632

SEQ ID 632
MKPVLVRTAMSGFPRCKOIKPTGYSNTAKKSRPNPKGTDGQTHYGENVLLNESAKQTLKQLQL

SEQ ID 633

SEQ ID 633
TTTGACGAAATCGGCATCGAAGGCGAGCAGAAGCTTTCCGCGCGCATATTTTGGTCGTGGCTGCGGCGGATGGGCGCGCGCGCCCTGCCCTATCTCGCGGCTCGGGCGTGGCGACGC
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GTGGCGGCGTGTACCGCAGCAGGAGTGCCTCGTCGTTGTCTGTCGTTGCTGGTCGCGGTATGATGATGTTCCGGAATAAAACAGTTGCGGGCGATTGTAACGCCGCCGTCGGCGGCGGTTCACACTT
CAGACGCGCATTTCCGGGACATGAGTCGTTTAAAGTGTGAACGGTTTGCCACGGATCGGCCATTGAGGTACATTTCACGTATTTACGGCAA

VAAPFOOECVVVVVFGRGHDDVRKKTAVAGDCNAAVGRRSTSDGLSGHEWLK CERFGTDAAFEVHLQYLRO

Seq ID: 637
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SEQ ID: 638

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TETVRRLLKAGKADGKSVQRQLDNTSVTAVLTAHPTFVQRQTVLFNRRIRALLPQRECTNADALARLRREIDTVLLGLNQTSETRHRKLSVNDEINNGVSIPIPMSEFFALPKLYRKHED
FQTAYPDVRVPNILKIGWIGGRDGNPFVSGETLRFAPRRHADAVFRPYRSELDKLYRELPLSTRVVKVNDVDVALAALSPDEBIARTBEPTRYRALIYIMARAMKGAARSIGLGMCKPGF
LEPYASAQKFLDLDKLQRLSLDNGSRLLAEGRLADLIRSVSFGPHMPLDLRQHAGKHADVVAELFQHAGLEDYNSLNEEBQKQALLRELGHQRPLYSPPFITYSWHLTRELAIIFNEARK
IKDFEGEDAVTQSIISNCEBQPGDLLALLLKKESGLLAVENGKPHSRINTIVPLFETIEALEANCFVMEFLRLDWDYDALLESRGNIQMLGSLSDNKGDDGYVTSFDCHLQAEGLVLEFK
KYDVRRMLPHGRGGSVGRGGGSPYQAILAQPAGSVAGQIRITEQGEVITAKYADPGNAQRNLETVAATLEASILDLPKDDQKQRLDNGVSPKSYRLEITHPDIDYFLTQSPITQELAT
LNLGSRPASRKLARIQDLRALIPWFSWMQNRMLPAWYGFCSAVETLCEGSPETLALDLRGHAQNNPFFQAMLNMEQVMAKTIDITLAENYAGLSPESEKAVIFGMKIEEYRRSRKALD
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SEQ ID 539

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ATGCAGGGCGAGGCGCGGTACCCACGAACTCGCGCGATAACGGTAATTTCATTGGTGGTCTTTCAACATATCAGTCGGGTTCACCTTTAAAAAATCGGTGTTCTCTGCAAGTGGCGTC
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ACGGACTCGAATACGGACTCAACGCCCGTGCCTGCTTACGCGCGGACTGGCCGAANTACCCGCTTGCTCCGCAATGGGCGCGCAGCCAAAACCATGATGGGGCTTCCGGCAT
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GTCAGCACCATAGAAGAAGTCTTCAATACCGCTGCAAAACCAATCGATATGCGGATACCCAAACCTGCTGCACTCATCCGCAAGAAATGACCCCTCAGCAGGTGCTCGAAAGGC
TGATGGAACGCGCGCGTTTCGAA

SEQ ID 644

MQEARENKRLPGFSPFETLEVCADLAELKDSGLVLIVTSVAGLRSSABELLKQYAGHLPLVLAACKGFEQDTGLITPQVLKEVLPDNKKIIVLSGPSFAQELAKQLPCAVVLASENQEWI
EKLVPQLWFTVMRLVGSQDVIQVAVGGSVKNVMAIATGLSDGLEVLNARAALVTRGLAKITRLASAMGAPKTMMLAGIGDLILITCTGALSRRNRVGLGLAEGKELHQLVREIHRVSEB
VSTIEVFNPAQYQIDMPTTQTLQLIRKENTPQQVVERLMERSARFE

SEQ ID 645

ATGCCCTCTGAACCCCGACGCGCATACAGACAGGTAAAGTCATGAAACAAATAATCGAAAACTCGAAAGCAGCGTTTATACGTTGGTACAAAAATCGAAACCTCGTCAGCGAAAAAC
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AGACCTGCAAAACAAATCGACAGCCTGACGGAAGAAATGACGATACCGCGCCCTGCTCGAACAGAGCAGGGAGAAATCAGCGCACTGGCAGCGGCTCCCCAACCGCAGGAAACG
CAGCA

SEQ ID 646

MPSEPPDGIQTGKVMQNIKLESSVYTLVQKPFETLVSENRRLKETVAELERAHERQKLEHETAVDELSEALLVQVVKLEDLQNKIDSLTEENARTRALLEQSRKISALAARLPRQET
QQ

SEQ ID 647

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TCCCGCAGGCGCGCGCTCGCGGACGCGAAGAAATCGTCATTATGGCGCGCTCAACGTCGTCACGACCTATTGAAACCTCCCTGAACGCGCGCGATTGGCAATCGGCGATTGTC
CGCTAAATAACCGATATGGAACAGCGCTGCCAAAGGCACTATCCGCTTGGGGCAGGAA

SEQ ID 648

MNIQVYIEVMHARLTVMTPAEKDTLLQAVGMLNGKAEAREGGRVADSEKIVIMAALNVHDLRLKTSLNGDLAIGDFARKITDMDNACQKALSRLQGE

SEQ ID 649

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GAGGTTTCAATAGGTCGTGGACGACGTTGAGCGCGGCAATATGACGATTTTTCGCTGTCGCGCAGCGCGCGCGCTTCGCGGATGGCTTCGGCTTTGCGGTTGAGCATTCGACTGCC
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SEQ ID 650

LLTRRLPRVVSAGASGRSRPLLPAITLSELIGSKEYMPSRTPGKRGYSCPKRDSAFWQALSISVILRAKSPIAKSPFPREVFNRSWTTLSAAMTIFSLSATRPPSRMASALPLSIPTA
CNSVSFSSAGVLTVSACMTSM

SEQ ID 651

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CTGAAAGTGTACGCTGGTCCGAGCATGCCATGCTGCGCAACCAACCAAGTTTGGAACTGAAA

SEQ ID 652

MKTFSAKPHVEKREWFIDAQKVLGRVATEVASRLRGKRPETPHVDYDYLIVINADKLKVTGAKFEDKKYFRHSGFPGGIYERTFREMDDQFPGRALQAVKGNLPGPLGYANIKK
LKVYAGAEHAAQPKVLELK

SEQ ID 653

GTGTCTTATTATTTCAGTTCAAAACCTTGGGTGTGTCGCGCAGTGGCGATGCTCCGCCACCGCTACACTTTCAGTTTATTAATCATGCGCTAACCCAGCGGACCTTTGGCGAGCATA
CCTTTTACAGCTGCTCCAAAGCGCGCGCGGGAATGATCTTCGATTTCCGCGAAAGTGGCTCGTAGATGCGCGCTGGAACCCGGAATGGCGGAAGTATTTTATCTTCGAATTTGG
CACCAGTTACAGCAGTTTTCGCGATGATGACGATGATGTAATCGCGGTATCGACGTGGGGGTGATTCAGTTTGTGTTTGGCACGAGAGCGGTGGCGACTTCGGTTGCAACGCG
ACCCAAAGACTTTGCTTGGCATCGATGACGAACCATTCGCGCTTCACTCGTGGGGTTTCG

SEQ ID 654

VSLLFQNFGLLRSMGLRSTSVHFQPFNHGVTQRTFQHTFFYSLLQSAARELILHFAESALVDAWKTGMABEVFFIFEFGTGTTQFVRIDDDVIAGIDVGGVFRFVFATQTAGDFGCA
TQDFVLGLDDEPFAHLVGF

SEQ ID 655

ATGAACGCTAAATACTACTACGGCACAGCGCGCGCAAAAGTTCAGTGGCTCGTGTATTCCTGACTAAAGGTACGGGTCAAATCATCGTAAACGGCGCTCCGTTGACGAATCTTCGCAC
GCCAAACAGCCGATGTTGTTGTCGCCAACCTCTGTTCTGACTGAAAACCGCCAACTCTCTCGACATCAAGATAAATGTTGTCGGCGCGCGGAAACCGGCAGTCGCGCGCAATCCGCCA
CGGTATTACCGCTGCCGATGATTGATTTGACGCTGCTTTGAAACCTGCCTTGTCTCAAGCGGTTTCGTTACCCGCGATGCGCGGAAGTCGAACGTAAAAAACCGGCTCTGCGCAAGCA
CGCGTGCAAAACAAATTCACAAACGT

SEQ ID 656

MNGKYYGTGRKSSVARVFLTKGTQIIVNGRPVDEFFARETSRMVVRQPLVL/FENAESLDIKVNVVGGGFTGQSGAIRHGITRALIDFDAALKPALSQAGFVTRDAREVERKKPLGLKA
BRAKQFSK

SEQ ID 657

TTGATTTTGGAAATTCAAAAACCTGCTTATCGCAGGGTTTTTATTGTAACAGCGGTTTCCCATTTGGTAATCTAAAGATTACGGAFTGGGCAAAAATCAAAAACAGCACCGGTATCG
ACTACACGACGAAGTACCGTCAGGGATGGCTGTACTGAGAGGACATCGTATTCTACTTTG

SEQ ID 658

LILEIQTLIAGFFICNRRFPIGNLKITDMAKIKNSTGIDYDTELVRDGCYWRGHRISTL

SEQ ID 659

ATGCGCTTTTCCCCATCGCGCGCGCTGACGCTTGCCGCTGCGGTACTGTGCAAGACACAAATTTCTGTTGCCCCGACAGCGCTACATCCGCTGCAACCGAAGGGCGGAA
CCGCGCTGCAAGTCCGCTTGGCGAACCGCTCAAACCGCGCGGAGTGTATCAACACGACCCCTTACCGCATCAACACCGCAAAAACCATGTTTGGCGAGACCTTTGGACGATATGCT
CGAAGCGCGCTTGAGCAATGCAATCAACCGTTTGGACAGCACAACGACCTTTGTTCTGCTCAGCAGCGGCGAGTACCGCAAAATGGACGGTCTATATGACGCAATTCGAAGCGACTAC
ACGGGCAAAACCTCATCAGCGGTACGCGCTCTACCGGACGCTACGAACAGACCTTCAATATCGAAACCGAACAGCAGGTTGACGGCTACCGCGCATGACCGCGCACTCGAACAGG
GACTGAAACAGCGCGCAACAGATGCTCAG

SEQ ID 660

MRLFFIAAALTACAGTVQSTQYFVLPDSRYIRPATQGGTAVEVRLAEPLKRGGLVYQTDPIRINTAQNHVWADTLDMLAALSNAFNRIDSTRTPVPSRSGSTDKWTVYIDAFQGSY
TGKTLISGVAVLPDGTNRPHIETBQQGDGYAAMTAALQGLKQAAQQWVE

SEQ ID 661

ATCCGATTGCGACACGGTAACCGGTATGCCGCGCAAGCGCGCAAGCAGCGGTCGCCCTTCGTGTTCTGCGCGCAACCGCGCTTGTCCGCTTGGTCAATTCGGGTGTCCGCAATGCG
ACCGAAACAGGATTGACGGGCTGCCGCTGTATGCGCGCTCTGTAATGCAAGGTGCGCGCCGCTGCAACGCCCTGTGCAACCGCAAAACCGATGACCTGCGCGCGCGCACATGCGCTTGTG
CCTGCGAAACCGCGCTCAAGTGGCGGTACAGCGTTTCCACACCGTTGGCGTGGCGTATCATCACCGGTTGCCGTATCCGCCCTTCGCGCTTTAAAGGTAAATACCGCGTCCGCGGAAGC
CCTGACCGCGCTTCCCTGCGGTGCGGCATAATCGATGCCCGTGTGCAAGCGCCATGTGTCAGGATGGGTGCATACGGTAGCCGAAACCGCGGAAGAAATGCGGTATAGACCGCGCTCG
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GGTGGCAGCAAAATGCGCGCAATCGGCTTCCGCGCGCATATTTTCCGTGATTCGGGCAATCTGTCGCGCGCATACCGCAACCGCGCGAGCAGTCCGCGCGAGTCCGCGCGCTGCAC
CGCTCTGCAACCAATATGCGCTTGAACCGCGCTGCGCGCGCAAGCAGCGCGCGAGTTTGTTCACCGCTGCGCGCTGACCGCGCTCGTCCCTCTGTCGAAGCAATGTATGCC
CGCGACACCAAGATAATCGAAACCGCAAGCGCGCGCGCGCATTTCCGATGTTTTCGCAAGTGGGAAGCAGCCAT

SEQ ID 662

IRLRHGNRYAAQARKQVRLLFLRGKRLVRLRQFGRQCDNRIDGLPVDARLVQVRPGRTPCRTDKTDLAAAHIALCLAKRAQVRVQRFHTVGVYHHRVAVSALPAFKGNHVGGS
PDRSLRCGIIDARVQPPCVDGVHTVAERRRNARIDQLDVEAFLQHPAVTIVILAASAPLVRTVIERLMGCAALNFRQNIARRHLLFVEIQAVVQKQAGLIAFLQTVKAEAGKN
PA*GPADPDGFRPRQRTARRRFDHRTQCRQNLHIRIRSRFPFYAAFFQSDQLALAVFVKGKILHARTAVAADQNMRLVGTQMPQIGFAAIFPRDSGNLVRHRTTRQHVQRVARLH
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SEQ ID 663

ATGAGATTACGAAATATCCTTATACTCCATAAGAGAGTTAGAAGACTATTATAAACACCTATCAAAATATATTATTCTACAAGAGGAGGAAAGAGATTTATCGATGTTTTATTCT
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TTGATTTCATACAAATTAAGGTTAACAATAATATAGATGAAATAGTTTGTGATTTATTTATGGAATCAAAATTTGATTTATTCATGAGTTGGGTGCAATTAATAC
GATAAAATTTATAAGAGAGAAATCAGTATCTACCGATATAATATCAGACTGGGAAATAGATAAAGTTAATAAGTTAATCATATTAAGAGATTAGACTCTGAAAAATAATTTCTCTAA
ATTATGAT

SEQ ID 664

MRLLKYPYNSIRELEDYLINFYQKYIILQEGGKEIYRCFILSFYKEFNIGIGLAVSCISIPPKVIMLDKRNIFIGFDSVVFICISQNSKVNILNDIGVDFIYLLDNQKICIIHELGAIT
DKNLIRENSVSTDIISDWEIDKVNKLIILKELDSKTIISLNYD

SEQ ID 665

ATGGATTCCATTATCGAATTGCGCCACCTCAAAACCCCTGCTGGCACTTGAAGAAACCGGCGAGCTCTCCCTTGGCCCAACCGGTTTCTTACCAATCCGCGCTTTCCACCGAGATCC
GTATGCTCGAAACCACTACCGGACCGCGCTGTGCAACCGCAATCCACGCGCTTGAACCGGCGGAGGCTTACCCCGGTGGGCGAAAGGCTGCTGCGCTCGCCACGAACTGATCTCAAGTTGCTGT
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CCCCAAGTCGAATCGGATATCGTATCAGGATTCGAAGCGGATCCGCTGCGGCTGCTGCTGCAACCGCGCGGAGCTCGCCATTGTCGGAAGCGGAAACCAAGAGCATCAGCTTCC
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CGAGATGCTGGATTATCCCAAAATTCGTATTCGAAACCATCAACCGCGCGCGCGGACAGCGAGCTGACCATCGCCATTATCCAACTGGTTGCGCAGCAGCTGGCATTCGCGCC
CTTCCCTATTTGACAGCTATGCGCTTACCTTGAAGAGGCTATGCTGCTCCACCGCAATTAATGCGCGAGCTGCAAGCAAACTGTATGCCCGCATCCGCTGGAAGACACAGATAAA
GTTATCTGAACACTTTTGCAAAATCATACGTGAACCGGCTTCCGCGACTTGGCCGATTAAGTGAGTTGGAACCGGTC

SEQ ID 666

MDSIIELRLKTLLEAETGVSLSAARVFLTQSLSHQIRMLENHGYTPLFERKSTPLRFTPVGERLLRLAHELIPQVAVARDLARITBGEAGELRIAVECHTCFDWLMPPANGFEPKH
PQVELDIVSGFQADPVGLLQHRADLAIVSEAKQSSISFHLPAYEMVIGCAPDHLAARNVWTAEDFIFGETLITTPVPDEMILDKPKLIPKNINPPRRSELTAIIQLVASRRGLAA
LPYWTVMFLEKGVVHRQITADGLQSKLYALRFEOTDKSYLNNPQIIRBERGFADLPGLSELEPV

SEQ ID 667

TTGTTTGGAAATGACAGGAAATATGGTTTGGCCAGAGATTTTATAGCTGGTGGCAGAAACGTTGCAGACGGCATCGTTTAAAGATTACGCCCCCAATGGTTGCGAGTTGAAGGGA
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GCCGACCGTTACCGTTGGAAAGAAACGATTCGCCGACTGTTACGGCAGCAGATCAATATGGCAGGCTACCATCTGCCCTGGATGTGATCCCATACTGGGCAACAAATGCCAACTC
GCCGACAGATTGGGTTTGGCAGAGAAACCGTTGCGCGAACAACCTGCTCAACTCGGCGAGCTGAAACAGCCAGACACTCGGCGCATTTGGCGCGCATATTGAACAGTTTTC
AACGTAGCGCTGCGCATCGGCAATCCCGAACCGGAAATCGCAGGGTGCATGGTGTACCGCGGCTGCACAGGCTTTTTCAGAGCGCAATAGATGAAGCGGTGCATCTGTATCTGAC
GGGTGAATTTCCGAAGCCCAATACCACTCGCCAAATGAACCGGTACCGCTTTCATTTCCGCGAGGCGATCACCGACGGAACGTTACCGCGTACCGCGCTGCGAGATCGCGCGAG
GTTTTCGGGTTGGAAGTGTGCCATTTTGACGAAAAACACCGGCT

SEQ ID 668

LFGNDRKMLRRDLAWCDETLQTASFQDYAPNQLQVEGREYIGKIVTSVTSRAAIDFAVEQKADLLLVHGMFWKSELPTVTGWKKERIAALLRHEDINMAGYHLPLDVHPIILGNNAQL
ADRLGFATREKRFQGNLNSGSLQAKTLGALAAHETVLQKRPVAGNPERIRRVAVCTGGAQGFFQTAIDBGVDLYLTGEISEAQYHLANETGAFISAGHHATERYGVRLAESAAE
VFGLEVCHFDENPA

SEQ ID 669

ATGGCACACTTCCAAACCGAAACCTTGGCGCGGATCTGCCAGCGCGGTACGCGCTAACGTTCCGTCGCGTATGCCCTGCCGAAATGAAAGCGGTACCGCTTTCATTGGCGAGGTGG
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TCCGATGGCGACAGGCTTACGTTGCAAACTGTTCAATATCGCGCGCAATGCGCGGAGTCTTTCGCTGTTTCAGGCTGCGCGAGTTGACCGAGTTTGTTCGCGAACCGTTTTC
TGTGCAAAACCAATCTGTCGCGGAGTTGGGCTGTTGCCAGTATGGGATGCATCCAGGGCGAGATGGTAGCTGCCATATGATGTCTGTCGCG

SEQ ID 670

MAHQPENLCRRPQRAYAVTFRVRMPCRNESRPIGEVVLGFGNFTROIQIDAFITCRLKALCTAGTFCPSDFAFGLADGRLTLQNCFMNRQCAECLGLFQARVEQVLFAPFPF
CRKTSVGLGIVAQYGMHIGQMVAICHIDVVF

SEQ ID 671

TTGAGAAATATCAAAACCTTACCTATTATTAATAATGCTTTGAGTATCACTGCAAACTGGGTAAATGCAATGTTTAAATGCTGCGCATTCCTCAAAATATTAGGACGACTGAA

SEQ ID 672

LRNLIKLYLILNALSITANWVKLQCLMARHSQNIPTTE

SEQ ID 673

ATGGATAATCAAGAAATCAACAAAGCGCGCGCGCTTCTGACACTTGGGACTTGGCGCGCGCGGAGTGGCAGCATTGGGTGTGCAACCGCGCTTTGTGGCAGTTTTCCTTTCG
AAAAAGCAAGCGCTTCGCTGCGGTGAGGTGTCAGTAAATCGAAGCGGCTGAGCTGCTGACCGCGGAGTGGCAAGCGCAACCGATTGGGTGCTCAACCGTACAGATCAGCA
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GGTATCTGCACCCATTTCGGCTGCTCGCCCACTTCCTGCCGACATTGCCCCGCGGATTTCGGGCGCAGACTGGAAGGGCGGCTTCTTCTGCCCGTGCCACGGTTCGAAATTGCACTTGG
CCGCGCGGTATATAAAGGTGTTCTCGCCCCGACCAACTGGTTGTCCCGCCATATAAATACTTGAGCGACACAACATATCTTGGTGGGCGAAGAC

SEQ ID 674

MDNQBINNGRRRFLTLATCGAGGVAALGVATPFVASFFPSEKAKASGAAVEVDVSKI EAGQLLTAEWQKPTIWLNRDTQQLKDLKGLNGELTDPNSDAEQQPEYAKNETRSIKPNILVAI
GICHTLGCSPFFREDIAPADLGADWKGGFPCPCGSKFDLAGRVYKGVAPTNLVVPPYKYLSDPTILVGED

SEQ ID 675

SEQ ID 675
TTGGTTTGCCTAATATTATCGTTCCTATTCTTAGTCTTCGCCCACCAAGATAGTTGTGTGCTCAAGTATTATATGCGGGGACACCAAGTTGGTCGGGGCAGGAACCTTTATATACG
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AGATACCGATGCGGACAAAGATGTTTCGGCTTAATACGACGGGTCTCGTTTTPAGCATACTCGGCTGTCTGTTCCGCATCGGAATTTGGGATCGGTAAGTTTCGCGCTTCAGGCCCTTCAGGTG
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CGTTTCTTTCCGAGGGGAAAAAATCGGCCAACAAAGCGGTTGCCACACCCAAATGCTGCCACTCGCGCCCGCGCGCAGGTGCGAAGTGTGAGGAAACGCGCGCGCGCTGTGTGATTTCTTGAT
TATCCATTATTCACTGCTCCTAATATTTTGGGAATCGCGAGCAATTAAACATTGCAATTTTACCAAGTTTGCAGTGATCTCAAAGCATTTATTTAAAAATAAGG

SEQ ID 676

SEQ ID 676

LVCNYSLSFLVFAHQDSCVAQVFTWRDNQVGRGRNFTFYAAGQVEFRTVARAEALPVCAQIGGCNVGTEGGRAAQMGADTDGDKDVLNRTGLVPSILRLRLFRIGIGIKFPAQVAFQV
PKLLICTVEHPNRFALPILGGQQLTRFOPTDIHLDSGGGLGFFPREKTGHKKRCHTQCHSARAAGKCKQETAAAVVDPLIHTYSVVLFPWECRAIKHCNFTQFAVLKALFKIR

SEQ ID 677

[illegible]

SEQ ID 678

MANQTSKAKALLGMDARFPLSKMWNHLAQYAPKNFNFWYFGSLALLVLVLIQIVSGIPLTHNYKPDGNDINAHLPAFPAFVAVETLHEDVGGGTATPHMTPGPTTPTVZLNN
IYGSYKKPRELWVWIFGSLIFLALMAEAFMGYLLPWGQMSFWGAQVILNPLSALPIVIGPOLSTWIRGDFNVSDVTLNRRFFALHVIAPVLVLGLVVAHIALHEVGSNNPDGVEIKKNKDN
GIPRDIPIPHPYTIVKDLIGVWVFLIVPCAFLFAPEGGGGYLEAPNPDAAANALKTPTPHIAPWYFTTFFYAILRALPSFLGTQVWGVIGMGAAVLIALLPWLDRGEKSVRYRGPIKTA
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SEQ ID 679

SEQ ID 679

ATGTATGCGCCGCGACACCAGAATAATCGAAACGGCAAGCGCGCAGCGCGTATTTCGATGTTTTGCGGAAAGTGGGAAGACAGCCATTATGTTCTCTTTTACGGCGGTTTGCGCCGAAT
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CAACAAAATCTGCAATACGGCTGACCGACCGCCCAAGACTGACGCGCTTTCGGCATTTTACGACGTTATTGTTGGTGCGGAAGACTGGCACAACGCCCGCGCGCAAGCCTGAATATGCGG
TCTGCAACCGCTCGCGCTGCTGCCACGCCCGCTGCGCAAAAAATGGGGCTGCATCAGGCAAAATGTCTGACGCGCGGAATATTTTGGATGTGGTACGGATGAAGCGGAACGGCTCTGCCCGCATC
TGTGCGCGTTTTACGCGGCACATTCGTGGCGTTTCTGTTCCCGTCTGCCCGAAATATGAGCTGGTTTCCCTTCCCGCGCGTACCGCTGGGGCGCGAAGCCGTTTTTGACACTTGGGCGGACT
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TCCGAGCTTATGCGGAAACGGCGGCACACCTGCCCGATGACGACCAACCTCTGTTATGACGATTTCGCGCTGACCGCGCTGACAGGGGACAGGGAGCGGTATGCGGCAATATTGCASCA
GTGGGAAGAACGCTGGTTGCGACCGCTTTACGAAGCGCTGCCGACCGGCAAAATCAAACGGCTGGACATGCCACGCGGACAACAGCGCGGTACGCTGACCTTCAACCCACAGACAGG
CGGAAGTTTTGCGCGTGCACGAAAAACCTTTGACGGAACTGGG

SEQ ID 680

SEQ ID 680
 NYADTRIIETASARSAYTRCPAESGKTAILFLPDGVCAESSIIISARSSFVRHQTKMLTALPLSLNLDEDEIRIPLCLPAFNKILQYGSFHRQSCASAFYARYLWCGRLAQRPAQSLAMP
 SETVALATPVWQKMGHLQANVLTAEYLDVGTDEAERLCRDLSPAYGDIPIWRFPVPLPELWLVSLPRAYRWGAKPVLDLGGILGADDQPDGEDALEWLRVQTEIQMWLNAHPVNHNRKKRGL
 PELNGLNLWDSLHGSAGGTLFADTVWSRFHFNRRALPDSFRAYAETAHLPDTHHILPMDLRLTALTGDRERYAAILQWEERWFAPLYEAVRTGKIKRLDLATDQGHGGTLATFKPTDR
 RKFWRCTKTFDGIN

SEQ ID 681

SEQ ID 681

GTGTTGGAAATCAATCAGGCAGGATTAAAGTTGGACGCTGATGCTGAAGAAGCGGCAGCGCTTTTCAGACGGCATTGTAAGGTTTCGACATCGATACGGTCCGCGCATTGGCGAAGCCGATA
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CACGCGAAGCTGTCGGTTTACCGTAAACCTGAAATACCAACCCGAAATGGCTCGATGCCGTC

SEQ ID 682

SEQ ID 682
VLEINQAGLSWTMLKKRQAFQAFEGFDIDTVAAFGADIERLLTDAGIVNRNLKIDAAINARQIQALQOEHGSFKNWLDAHPRSKDENVKLFKKHFKPVGGEIVGEFLMSTGYLGA
HAESCPVYRKTKLYHPKWLDAV

SEQ ID 683

SEQ ID 683

ATGCGCGTGAAGCCATCTGTTTAAAGAAAACCATGCTCAATAAAGACCAATTTCGCGGACCAACCATTTACCGCAACCATCATCGAAGACGACCTCAAAGCGGCAACACGAAGCCGTC
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CAACCCCGAAACCAAGCAGCATACGTCTAACGCCATCAAGAAGATGTGAGTGGCTCGGTTTCCATTGGGCGGGCGAGCCCGCTTCGCTTCGCAGTATTTGACCGCGCTTATGAC
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CGTCTGTACGACCGCTCTTTACGTCGAGCGTCCCGGTGCGGTGCGCGGAGACGCGCAATACCTGCCGTTTACCGATTCTCTCAATCCGAATCCGTTAAGGAAATCACTGCTTACG
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SEQ ID 684

MPSEAIKLTMLNKDQFADNHPRTIIEDDLKSGHEAVQTRFPPEPNGLYHIGHAKSICLNPLGLAYIDGLCNLRFDDTNPKEKENDYVNAIKEDVEWLGFWAGRPFASDYPDRLYD
YAVGLIKDGKAYVDLTPPEMREYRGLTPEAGKNSPYRDRSIEENLDLPTRMKNGEFPDGSKTLRLKIDMAAGNINMRDPVTYRIRRAHHNTGDKCTYPMYDYTHCISDALEGITHSIC
TLEFEARHPLYDWNIPALHATRPRQYEFSLLELLYTTISKRKLNLVVEKHVSGWDDPRMPTISGMRRRGYTPBGVRLFAKRAGISKENIVMSVLEGAIREELNSAPRILMAVILNP
LKVTLTNFQAGTKQSRRAAPHNHEMGDREVPVSQTYIIEADFAENPKGPKRLIPGGEVRLRHGVYIKCGEVVKEAGNVVLEKCSIDHDTLGNPBGKRVKGVIVHWVSAEHAARIV
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SEQ ID 685

TGCTGCAAAACCCCAAGCTGCGCGTCATCGCCGTCATTAACGACAGCGGTTGCGCGCATCTGCGCGTCATTGCGCACGACATGCGCGAAATACCGACCTTTCGCGAGCGGAAC
GCGCGCAATPGATGGAAATGGTGTATCAAAAGTCGAAGCGCTATGCGCCCAAGTGTTCGCGCGGCAAAAATCAACCTCGCCAGCTTGGGCAATGCTGCGCGCAATGCGCATATTAT
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SEQ ID 686

LLQTPKLRVIAVHNDSPAPFCRVIVHGHIAETDLSAAERGLMENVYKVEAMRQVFRPAKINLASLGNVPHLHWHILARFENDATFPAPIWANPVKRGHTLPQNWTEQLKLL

SEQ ID 687

ATGACTGATAATCGGGGGTTACACTGGTTGAATTAATATCAGTGGTCTTGATATGTCTGTACTTGTCTTAATTGTTATCCGAGCTATCGCAATTATGTTGAGAAAGCAAGATAAAATG
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SEQ ID 688

MTDNRGPTLVELISVVLILSVLALIVPSYRNYVEKAKINAVRAALLENAHFMKPYLQNGRFKQTSKHPSLPIKBAEGFCIRLNGIARGALDSKFLKAVAIDKDKNPFIIKMNENLV
PICKRSASSCDGLDYFKGNDKCKLLK

SEQ ID 689

ATGAGGCGAGTCGAATGAAACAAGCTATGAAGAAATGGTTTGTGCTGCTGTCGCGAGTACCATGAGTGGCGCATTTGCTTCGCGCGGTATGCACACTATGAGAAAGTCGATATTG
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SEQ ID 690

MRAVEMKQAMKNWFAALLSAVPMASAFASGGHAHYEKVIDIDLRDQVSLQGAQIFITNYCLSHSASGHRFNRKIDIGLTDEEIKNLMFTTNDVGDVMSAMNPKDAKWFGAAPPDLTLI
ARSKGADYLYAYMRGYKDPTRPSGWNNTVFDKVGMPHLWEQGVQAVELDAKQPVVMDHEGEMKPKLYWESTGLHSRLPNKGVIQKEYDAYVRDLVNYLVNMGEPALQKRKIGYV
VMIFLPAVMLPLAYFLKKEYWKNVH

SEQ ID 691

TTGAATATTAGGATGATGATGAGGCTGATGACTGTTTGTGCTGCTTTGCGCGGCTTGGTGTGCGCGGTGTTGTTTACATGCTGCTGATGAAGGCGAGTTTCAGGCGAGTTTGGCGGT
TTGAACGCGCAATTCGCGGAAAGCGCGCAAGATG

SEQ ID 692

LNIRMDGADDCFAAFGQVGVGRVVYVMADEGQVSGRVCERFIRAIGGKGGM

SEQ ID 693

TTGGCGGAAAAGCGCGCAAGATGTGATTTTATTAACAGGCACACGCAAGAAATGCATCAGAATTTGCGCGCTTTGGATGGGAAATACGAGCATTTGCAGGACGAAAATATGCTTTGAGCA
ACCGTTTTTCCCGAGCGGAAAAGCAGATGCCCATTTTCAGGAAAAGAGCGGAATCGGTTGCGTTGAAGCAGTCTATATCGATTTCAGGAAAAGCGCGAGGTTTGGCGGTGAAAA
CGAAGCTTTGGCAACCGAGCTCGGGCAGGAACGGAAGCGGTTTTCGCGCAATATGCGCTGGAACGCGCAATCCGCCAAGAGTTCGAAACCGATTGGAGAAAGCGCGCAACATGTCGCC
GACGTGCAAAACGACTTTTCGATGTCGCGAACCGTTTTCGCGCAGCGGAAAACAGATGCTTATTTGAGGAAAAGAGCGGGAAGCGGAGCGGTTGAGGACGTCGATACCGAGTTGC
AGGAAAAGCGCGAGGTTTGGCGGTTGAAAACGAACTTTGGCAACGCAATTCGAAACAGGACGCTTGTCTTGAAGAAAAGCTGCTTGTGTCGGCGAGGCGCGCAAAAGCTTTGAGCGA
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GCGCGGATGCGGATGAGCGGCGACGCAACTGCGCGGCTATATCGCGAGCATACGCGCGCATATGAAAGGCTTGTGCTGAAGGATTACACCGATTGGAAGGTGGAACATTTGGATT
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GACTTTGCGGAGCGGTGGCGAATATTTCGCGCAACGAGCAGCAAAACCAACGCGCTGCGGATTCGCGCAACGAGCGGCAAGCTGTACGCAAGATTGTCGCTGCTGCTGACGAGCTGCA
AGCGTCGCGCAAGGATTCGATCAGGCGCAAAACAGCTTTTCAGACGGCATTCAGCAACTTCCGAGGAGCGCGGGAATCTGCTGCGACGCGCGGAGAACTGCGTCTGTTGGCGGTGAAG
CAGGCAACAGCTTCAACGGGATTGCTGAGCGTGCACAGCAACAGCGCATTTGCTTTGGGCAAACTTCGGAACAGGAAGCGGCTGACGAAGCGGA

SEQ ID 694

LAEKARCDPIEQAHAELASELAALDGKYEHLQDENYALSNRPSAAEKQIAHLQKEAESVRLKQSYIDLQKAQGLAVENERLATQLQERKAPAEQYALERQIRQVETDLESRTVR
DVQNDLSVGNRFAAEKQIAYLQKEBAERLRQSHLELQKAQGLAVENERLATQIEQERLASEEKLKSLGARKSLSDQPNLANFTILEEKSRRFTQNRQLHQLVNLINERIHGPG
ELVROTVDKESRERLTLENELKRLQGLNAQLHSAKALTNALGTQNKVQGMEMILETVLENSGLQKGREYVQAAASVRKEEDGGTTRLOPDLVNLDPNKKQIVIDSKVSLTAYVRYTQ
AADADEAARELAAYIASIRAHMKGLSLKDYTDLEGVNTLDFVFMFIPEPAYLLALQNDAGLFQECFKRINLVGPSTLLATLFTVANIWRNEQQNLAIADEGGKLYDKFVGFVQLE
SVGKIDQANSQTAFAKQLABGRNLVGRAEKRLRLGVKAGKQLQRLDVERANEQTAFAIKGPSEQEADEAR

SEQ ID 695

ATGCGCTCGAAACGATCCGCTTCTCTATTCGCTTCGTCAGCGCTTCTGTTCCGAAGGTTTGGCCAAAGCAAAATGCCGCTGCTGTTGGTGGCAGCTCGACCAAAATCCCGTTGAAGC
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TGCACGCGCTTCGAGAGCTGCTGACGAAGCGGCAAACTTGTGTCAGCTTTCGCGCAACGCGCGCGGCTTTGCGTTGCTGCTGCTGCTGCGGCAAAATATTCGCCACCGT
CCGCAAGCTGCCAGCAGCTACTGGGCGGACGAGTAATCCGTTTGTGAAACACTCTTGGAAACAGCGCGCTATTCTGCAACGCGCAGGATAGGCGGCTTGCAGAGGATAAAC

ATAAAGACGAAATCCAATGTGTTACACCTTCCAAATCGGTGAATCTTACAGGACAAAGCTTTTCATATGCGCGGTATGCTGGCGATATACGCCGAGTTTCGGGTGCGGCTCATCG
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TTCTCTTTTTCGAGCGAGTGCCTGAAACCATATATCCGCGCTTTCGAAAGCGGAAATTTTCCAAAACGTTTCCAGAAATCATCTCGCCCAATTCGCTGAACTTGTTCGCGTG
CGGTCACGCGCTTGTGTCAGGCGCTTTCCTCGCTGTGTCAGCTGCGCATTTCAACCTTGGAGCGGTTTCAATTCGTTTCCAAAGTCAGCGCTCGCGGATTTTATCATTAAGTTTGGC
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GCCTTTCTCGCACTCGGTATGCGCTGCTCAACCGCTCGCTTCGCTCTTTTCTCGCAATAGGCAATCTGTTTTCGCTCGGCAAAACGGTTCGCGACATCGGAAAGCTCGT
TTTGCACGTCGCGGACAGTTTGGCGGCTTTCTTCCAAATCGGTTCGACTCTTTGCGGATTTGGCGTTCACGCGCATATTGCTCGGCAACCGCTTCGCTTCGCGGAGCTGCGTTTC
CAACGTTCTGTTTCAACCGCAACCGCTGCGCTTTCTGCTGCAATCGATATACGACTGCTTCAACGCAACCGATTTCGCTCTTTTCTGCAATGGGCAATCTGCTTTTCGCTGCG
GAAAAACGGTTGCTCAAGCATAATTTCTGCTGCAATGCTGCTATTTCCATCCAAAGCGGCAATTC

SEQ ID 696

MPSETHPPPLPGFVSRLFRFAQSKRLFVGTLDQIPLKFLACLHAQQTQFLGASDQIPASLGLKLECRKAVLRILIDAFADAFERLYEADKLVQVLAAPVRNRQVRLVLLVAPNIRRR
PQSRQORTGADQHNPFVETLLEQARVILQROQVGRDRDKHDEIQCVHTFQIGVILQRAQFMRAYAGDIRQFACRLIRIRLRVAHISRQNLGINDNLLVVGQVQNDVNGLEAARA
FLSDGCRNLNHFPPFLKAGIFQNRPNHLAPIALNLVLRAGQVQGLCLAVQLRIQPLEFPQFVPSQPLARFFIISLPDLASTVDAPVQVRLMELLAVLLGKTAAPFPQNRVGI
LKLIAQAPARLAQGGQFLFRSKAFPLDLRCQTFVFNQFLRLFLQLEMLRPLRLPFLQIGNLFPFGGKTVDIGKVLHVADSLAAPPQIGPDSLADLAFQRIILLGRLLPFLPELRC
QTFVFNQFLRLFLQIDIRLLQPNRPLPFLQMGNLFGCGKTVAQSIIFVLQMLVFPISQGF

SEQ ID 697

ATGACCTTACGTTACGAAATTTCCCGCTTACCCCTTCCGCCAAAACGTCACCTTGATTGGGACGACGAAAGCGGCAAGCGCTCTGACCGATTCGCGCGGACGCTGCGCTTCTGC
TGCAAGCGTTGGCAAAACCGCAAACTCAGCTCAGGCAATCTGCTGACGACGCTGCTGCTGATCAGTCACGCGCGGCGGCTGCTGAGATGCTGGAACCGCATAAAGTCCCGCTCGCGCC
GCACCGCAAGATGAATCTGCTCAATCGCTGCGCAAAACCGCGCAATACGCGATTCGCCCTGCTGCGCGGCTTTCGCGCAACCGTTGCTCGAAGAGGCGAAACGCTCAGCGTC
GACGCTATGCTTCCAGTCTGCTGATATTCGCGGCGACACGCGGACAGCTGCTTCTATTGTCGCAAGCGGAGCTGCTGATTGCGCGGCGAGCTGCTGTTTACGAAACCATAGGCA
GGACCGATTTCGCGCGGCAACCGCGGACTTAATCAACATATCCGCAACAAATATTGCTTCCCGCAACCGTGCAGTTGTCGCGGACAGGCGATGACTTCCATCGGACA
CGAAAAACGGCACAACTCCGTTTTTC

SEQ ID 698

MTLRYELLPTVPPFRQNTLWDESGEAVLTVGGDVFPFLQALANRLTLTAIWLTHGLDHAGGVVEMLETHKVPVLGPHREDFLLQSLPQTAAQYGFVPVSPAPAPNRMLEEGETLTV
GRYAFQVLIHPGHTFGHVVFYCARAELLIAQDVLYETIGRTDFPRGNHADLNNIRNKLFAFPETVQVVGHERMTSIGHEKRNHPPF

SEQ ID 699

GTGTTCTAAAACGGTTTTTCAGACGGCATCGGTTTGCCTTTGTTTTATGCGGTTTTCGCCCTGTTTTGATATTGGGGAATCAGGTGAT

SEQ ID 700

VFLKRFRRHRVCRFLFYGLPFPVLIIGESGD

SEQ ID 701

TTGGCGTGGGTTTCGGCGGATTTTTCGCGCGAGCGGTAAGAAGCAACGCGCTGCGCGGAGGAGGAGTTCTTCTGTTCAATGGTTTTCAGACGGCATCGAGCATTTCCGGTGGTAT
TTCAGGCTTTTACGTTAAACCGGACAGCTTTTCGCGCTGCGCGCTTTGAGGTAGCGGCTTCTCATAGAAATTCGCGGACGATTTTCGCGCGGACGATTTGAATGTTTTTAAAGAGTT
TGACCATTCGCTTTCGCTGCGGATGCTGCGCTGCGGACGATTTTGAAGCAACCGGTTCTTGTGCAACGCTTGGATTTCGCGGATGAAATGCGCGCATCGATTTTCAGACG
GTTGCGGACATACCGCATCGGTAAGCAGCGCTTCAATATCGGCTTCGCCAAATCGCGGACCGTATCGATGTCGAAACCTTCAATCCGCTGAAACCGCTGCGCGCTTTCAGCATC
AGCGTCCAACT

SEQ ID 702

LAWVRADFLPQAVRSNAPARRKVLIFIGSDGIEPFRVVPQFTVNRATFGVRAFEVAGTHQKPADDFADEFEMPFKEFDPFVAFSRMVRVEPVLERTVFLQLRLDLCIENGIDFQF
VADNTRIGKQFPNIGFAKCGDRIDVETFKRLKRLPLLQHQRP

SEQ ID 703

TTGCGGATCGGCTGACAGCTATGTCAAAGCGCGCAAGTGGGTACAATAAACACATCATCAACCGCTTCAGACGGCATACGGAACCGCCCAATGCGGCTGTAAGCCATCTGTT

SEQ ID 704

LPMPSEYVVKRKSGTINTSSNRFRHTEPPQCRKPSV

SEQ ID 705

GTGATTAGAAGATAATCGCGGCATCATACGATTTTACGCGGTTTTCATCCCTGCATCGGCGGCGCGGCGGATTTGATGCTGGCGCAGGAATACAAAGGCGAGACATTCGCGGCT
GGCGGATGAGCGAGAACTCAGCGGCTGCGCGCTATTGGGACGGAAGCACTGATAGCGCTCAGGCTTACGCGTTTACGCGGCGGCTTACCGCGCAGTTTCCGCTTATCC
TTTGGACGCGAATTTGATAGCGGCGCGGCTCAGTTCGAGCAGATTTCGCTACGCTGCGCTTCTGTTCTTTCAGACTGGCGCGGCTCCGCTGACGTTTTCGATGTACCAAGCGCGAG
GGCAACTCTACCAACGTTTGGCAGTCGCAACGCACTGGCTGAAAACGCAATCCGAACGCGGCTTACCATCATCCGCAATCAAGTTCGCGGACGCGGCGCAGCGATGAGCTTTTAA
AACAAATCGAAGTTCAGGCGCGGCGGAGGCTGATGCTGCGGCGCGGCGGCTTACAGCGCGGCGGAGGAGCAATTAATGAAGCTGAAAGCGCAATACGACGAGGATTCAGCGT
AACGCGGCACTATGAGGCGAAAGGCGGAACCGCGGCGGCTGGCGCGGCTGCGCTGCAAAAACGACACGCGCAATTCGCGATCGGCGGCTTTCAGGACAAAGACCGCGACATCCG
CCCAAAATCGGCACTGATTACCTACCGTTACCGTGGCTTACCGGAAAGGCAACCGGAAATTTGCCACATTTGTCGCGCTGCGTACCGACCGC

SEQ ID 706

VIKKIIGGIIPITAVFIPASAGAADLMLAQEYKQDIAGWAMSEKLDGVRAYWDGKHLISRQGYATPPKGFPAQFPYPLDGLYSGRQFQEQISATVRSVSSDWRGIRLHVFDVPAQ
GNLYQRLAVATQMLKTHFNAPITIIPIQIKVRDRRHMDFLKQIEVQGGEGVMLRQPESTRYSGGRSSQLLKLKSYDDECTVTRHYBGRNAGRLGAVGCKNRHGEFRIGSGFKDKDRWF
PKIGTLITYRYRGFTKGTTPKATFVRVETDR

SEQ ID 707

TTGGTTTATAATTTTCTTTTACCGACCGATTCGACATATGACCGATTAGAAACCAACCGCTTGAACACAGCGATGCTTGAACCGCGGATCTTTTGTTCGACCAAGGCAATGCC
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TTTTCCTTAGATTGTTGATTATGTTACGTTTCCGTTACGCGGCAACGCTGAGGCGCGGCTTCACTGGAAGCGTATGCCGATCGGAAACAATCCGGGCGAGGACGCTGCTGCTG
TTGACGATATTTTGGACGAGGCGATACGATGCTCGCCATTCAAGCCAACTTTTGGAAATGGGTGCGGCAAGCTGCGCTGCGCGGCTGTTGCCCAATAAATTAATCGACAAGAAAAA
CGGTCAAAGCGGATATGTCGAGCTGATGTCGCAACCGTTATGTTTTCGTTACGCGATGATGCGGCGGCTGCTGCGCAATTTGGCGGAGATTACGATTTGGCGGAAAA

SEQ ID 708

LVNFPPTDRFRHMTLETKRLETQAMLENADLLPDQGCRAALQKVADEITRDLGDKYPLLLPVMGAVVFTGQLPLRPLDFDYVHVSRYGDLBGAFFNWKMPDAEQIRGRHVV
LDDILDEGHTMSAIQAKLENGAASCRAAVFANKLIDKEPKVADYVGLDVPNRYVFGYMDAAGCWRNLGEIYALGGK

SEQ ID 709

ATGATAGGCTTTTAAATCATCACACGAAACCATAGGCGAAGCTTACCGCAAGCTGGCGCATCATTTTTCGCGGCGGCTGCTGAAACCGTCCGCATCTCGGCGTGCAGCCGAGCG
AAGACCAAGACGACATTATCAACAACCGCATTTCCGCGCTGCAAGAGTTTCTGAAACACCGGTGATTGATTATGACCGACATCTTCGCGCGCAACCGCTGCAATGCGCGCGCGGCT

SEQ ID 722

VAGRHPTIGCAMELNLGLCKPFGKTVADNICLTVGRGKILAVLGRSGCKSTLLNMTAGIVRDPGGEIRLNGENTCMPPEKRRISLMPQDYALFPHMSALENTAFGLKMQKMPKAEAR
LALSALAEVGLNEAHRPEKLSGGKQRLALARALVVRPSLLLLDESFSLSLTHLRDLRLRRMTAEIRKGGIPAVLVTHSPERACTAADEIAVMHBGKLLQCGTPPETLIQTGAGVQVRL
MGLPMTDDDRHIPQNAVCLDNHGTBCLLLSLVRLPDSLRLSAVHPHEGELTLNLTVGQHTDGI SGNGTVRLRVDEGRIVRFR

SEQ ID 723

ATGGTAGCTCGTGGGCTCATACCCGAAGTCGTAGGTTGCAATCTGCTCCGCAACCAATATCAAACCCCTCGGTTCAATGCCGAGGGGGTTTGTGTTTCTCTGTTCTGCGGCT
CGGTTTTTTCGCGGATTTCTCTCTGCCGAATATCGGAACGGCAGCGCGCTGTTTTCGCGGTGCAAAATTCAGCGGGTTTGGCTTACAATCTTCGCGATTTGTTCTAAGAAAGCGGCT
TATGCCGACCGTCCGTTTACCGAATCCGTGAGCAAAACAGACCTTGATGCCCTGTTGAGCGGGGCAAAAGCAAGTTACGGTCCGGAAGTTGCTGGAACCGCTGATCTGAACCGCTCTT
CCTTTGGGCAATCTGTGCGGGGAATGGGCTGAGCGCATCAAAAAGACTGGGAGGAGGCTGCTCCGAGTCTTCAGACGGCATTTTCTGAATCGGACGGCTGGCGCGATATGGGCGGAC
GCTTCGAGCACTCGCGCGCATGGAACAAGCGGGGCTGCTTCACGGATGGCGCAAGAGTGTTCGACCTGACCGACGGCGGGCAACCCCTTTGTTACGCTCGAAGCGCGCGCTT
CCGTCGTTTCGGAATCTACGCGCGCGCTCCATCTCAACGGTTTGGTCGAATCGAAGCGGAGATGGCATTTTGGATAGGCGAGGCGCATGCCACAAAGCAGTCGATCCCGGCAAGCTC
GACAAATATTCGCGCGCGGCTGTTTCCGCGCGGGAATGCCGCTGTAAGCGGCTGTCGCGGAAGCAGCGAAGACCGGTTTGGATAAAACGCTGTTCCGCTCATCCGCGCATATCGC
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AAGATGGACATTTGGCGGCTATTTGATGCCATGTGTGCAAAAACATGATGACGACGCGCAACTGTTTACGCTGGAGCGGTTTACCGTTACGCTGATGATGCCGCCATCCGCTG
TCGAGTGGCTGGACGGCATACGTTA

SEQ ID 724

NVARRAHNPVKGNSNPAPATKYQTPRFNAEGVLFFLPAAVFCRIFLPAALISERQAACVLRLLQIAVWLQSSALSRKPAMPTVRFTESVSKQDLALFERAKASYGAESCWKTYLNLRL
PLGNLSPENAEIRIKDWEAGSSESSDIFLNADGWPMGRLQHLARTWNKAGLHGWNECFDLTDGGGNPLFLIERAARPPGLLSRAVHLNGLVBSNGRWHFWIGRRSPHKAIDPGKL
DNIAAGGVSOGGEMPEAVCRESSSEAGLDKTLFPLIRPVSRHSLRPVSRGVHNEILYVFDVLPETFLFENQDGEVAGFERKMDIGLLDAMLKSNMMDAQLVTLDAFYRYGLIDAAPHL
SEMLDGIHL

SEQ ID 725

TTGCGTTTTAGACGGCATTTGAAACCAATGCCCTCTGAAAGACAGAATCCGTGAAACTCCACGCGAGGTATTATCCGATCGGGTG

SEQ ID 726

LRFTAFENQCLKDRIRENSPRRYTPDRV

SEQ ID 727

TTGGTTAACAATCGAAACAGGGGTGCTGCCTGATGTTTCAGCGGGTGAGAAATACCCCTTTACACCGGATCGGGATAATACCTGCGTGGGAGTTTTCAGCGGATTCGTCTTCAGACGGCAT
TGGTTTTCAAAATGCGCTGAAACCGCAAAAGCTCCGTGTTCTTTATTC

SEQ ID 728

LVNIEGTGLPVDQAKEYPLHPIGLIPAWGVFTDSVFQALVFKRLKTNAPVSLF

SEQ ID 729

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GCAGCGCGGACGACATCCGCGTGCCTTTGCGGAAATCCGTGAGGACGACACTACACGCGCAAGGTACGGAAGCAACCCGCTTATCCGGTGTACGACACAGCGCGCATACGGCGA
TCCGCGCGGACATCGACCTGAAACAAGGCTGCGGACATCCGACGCGCTGGCTGGAGCAAGCGCGGATACCGAAATCTGCCCAAGCTCTCCAGCGAATACGGCATCGAAGTGGC
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AACGCAACTTTGGGCAATTTCCCGCTGACCTCCAGCTGACCGAAGAGTCGAAAAATGGTGTGCTGCTGCTGGGCGCGGACAGCATATGAGCTTATCCACAGGCGCGGACATCC
ACGAAACGCGCAATGAGATATCCGCAACGCGCGCTCCCATCGGCACAGTGGCATTTACCAAACTTTGGAAAAACCGCGCGCATCGCGCAAGATTTGACTTGGGATTTGTTCCGCGA
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CGAACCGCGGAGAGCTTCCACGACGAAACCTGCGCGCGGAGCGCGGAAATTCGCCATTTTGTCTCAATGTCGCGCGCGCAAAATTTGCTCGATGAAATACCGCAGGAAGTGGCGGAC
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SEQ ID 730

HTPPKTKAKISGNEARELSLSEIDIGIRFKYQNSERVYLQSRDDIRVPLREIRQDDTYTAQGTANPPIPVYDTSAGYDPAAHIDLKQLPHIRTAWLDERGDTFLPKLSSEYGIERA
HDPKTAHLRFNQITRRRAKAGRNVTQLHYARQGIITPEMFAAIRERMLDELFRPFEYAKLKHQHTQSGFANIPTRPDIITPEFVRQETIAGRAIIPANINHEPELEPMIIGRNFVKI
NGNLGNSAVTSSITEEVEKNVSLRWGADTMDLSTGAHIRETREWILRNAPVPIGTVPITQTEKTGGIAEDLTMDLFRDITLBEAQEGVDYFTIHAGVLLRYVPMANRLTGIVSRGS
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GIGAANIWGYTAMLCYVTFKEHLGLPKEDVRTGIIYKLAHAADLAKGWPAQLRDNALSKARFEFRWRDQFRLSLDPERAESFHDETLPAEGAKIAHFCSMCGKFKCSMKITQEVRD
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SEQ ID 731

TTGCTTCTTACCGCTGCGGCGAAGAAATCGCGCGAAGCCAGCGCAAAATTTCCGCAAGCAAGCGGCTGCTTGCCTTGGGCGATTCGCTCACTTCGCGTACGAGCAAAACCCCGCGAAT
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GCAATAATAATCGAAATCCGACCAATCCACGCCAAGCGCAAGGCTATCGGAAATTCGCGGAAATTTGATCAATTTTGGAGAAACATGGGTTTGA

SEQ ID 732

LLLPACGRKSARTHAKIPGSTVLALGDSLTPFGYANPGESYPAQLQKLWGNIVNGVSGDTSQAQLSRLPALLARKPKLVIVIGGNDPLRRVPEEQTRANIAKIISTVQKENTIPAVLV
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SEQ ID 733

GAACTGTTTGTAAACTCGAACAACGCCCTGTTTTCTCGTATTCGTTAAACACATCGTTGCTCCACGTTTCGCGGTGCGACAGCTCAGCGCGCGGCTGATGCTTTGAAATGCAATGCC
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TGCCGCCGGAACACCTGCGGTATATCGTTGAATTTCTTATTCGCCGGAATAACCTGCCGACACGTCGCCGCCGCGTCTGTACACCGCTTTTTCAGCGACCATTTTTCCTCCG
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AATTCGGGATTTTTCAGCAGGTTTCGCGCTCAACCTGCAAACTTTCTTTTTCGCGACCTGCCCGGTACCTTCTCCCTGTGATCGGTTTGACCTCCGCTTCATGAAGCTGAAC
CGGACGCGCTTCTCAATCCGCTTCGACGCTGTTCTTTCGCGGTATGCGCGCTTGCCAATAAGGACGACGATCCATCTGTTTCTGTCAGGCATAATGCTTCCACAAAAATAAA
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SEQ ID 734

ERFVKLDRPVFLVFKHIVAPFAVRQRRDAFEMQCPVKAQGCVRFFIPAPFFPKTAEKAGFFIMPFRHAEQRRQAAAAFLLPPGKAQAVTVEIVATVGGVALAVKIQTARPIL
ARIPVKHQRIGNLQNGIVGTAPARILQTPPLRRRQLPSRGLPTVELKACAVGVRIISVAVGAAPVEHCQPDITFPVKTDAAGNTCRHIVEFLI PRINPAGHVAARRRVPVFPFPLR
AEFVIDCRVHLFRSPILAVLLFRGLVDIVFAGNAETAVYLPRIFAQCLALDLHLRRQIFCFQAVELVCRRLVLPVFKQCRRTHTDGGRVGLGNGFPVVMGNRLHLPALCLBQ
PLCIKQHLILPRL*VNRQNHADTGNIV*DHCGIHETROQFGIFQGFVNLQNSFFPHLPRYLLPVDRLRFMKPELGTASQIRFARCFPGVCRACQ*ROQHPVSVSRHKLPLTKIK
IKNHYQ

SEQ ID 735

TTCGCTTCAAGGCCCTGCATGACCTCATTCGCCACCCGTTTAAACACGGTTTTATCTGACAGCGCGCAATCCGCCGCCCATTTCCGGAACAAGCGGTCCGACTCCGCCGCCGCGG
GAATGACGGCGGAAGAATCTATTTTCCGA

SEQ ID 738

LRFKALHVPCHPFFKHGFFYLGAQSAPFFAEQAVRTPARAGMTAERFYFSR

SEQ ID 737

ATCGAGGCGCTTGAAGCGCAATCGATATATTTTCCACCGGAACGGACGCCCGCGCGCTTGCACAACTTAAAGACAAGCGCGCGGTGATCCGGCGCGCGTGGGAAATCACT
TACCGCTTGATTTATTAATAAT

SEQ ID 738

MQGLEAQSIYYFHRNGRPRPPCKPLKDKPGLIRAAVGNHPLDLFKI

SEQ ID 739

GTGGCATCCGCTTCAACATCAAGGCAATATGTTTCAGAAAGTTGAAGTCACAAACGGCGTCTTACCGCCCAATGGCTTCAACCGCGGTAAACAAGAAATCAAGGCAAAAACTCT
CCCTGTGGCGCAGCGCTCAAGACGGTTCGGTAAATGGTTCGCGGACAGCCGGTAAAGCGGACGAGCGCGCGCCCAAGACGACACCGTCAACCGGACGCCACCGGCAACGCGCA
AATCGACACCAAGCACCTGCCGTCAACCTGCGCGGATAAATCACTGCCCTTTCGACGAAACACCAACCGCGCGATTTCAACACTTCCAAAAATCAGCGGTTCGCGGTATTACCTGAAT
CAGCGCAATGGCGGAAACCAACTTCTGCCGCGGTGGCATCTCCGACAAATCAAGGCAAAATATGTTTCAGAAAGTTGAAGTCGCAAAAGCGCTGTTACCGCCCAATGGCTTCAA
CCGCGTAAACAAAGAAATCCAAGGCAAAAACTCTCCCTGTGGGCAAGCGTCAAGACGGTTCGGTAAATGGTTCGCGGACAGCGGTACGCGCAACGACGCAAAAGCGGACGAGCT
CAAGCGGACGCCCAACGCGATCAAAACGACGCTGCCGTCAACCTGCCGCGATGAATCATCTGCCACC

SEQ ID 740

VASASTIKGYVQKVEVTNGVVTQAQMASTGVNKEIKGKLSLWARRQDGSVKWFCGQPVKRDAAAKDDTFTADATGNDGKIDTKHLPTSCRDKSTAVCTKHAPISNTSKKSAVAGYYLN
HGBEPENWTSAGVSSDKIKGYVQKVEVAKGVVTAQMASTGVNKEIQGKLSLWAKRQDGSVKWFCGQPVTRNDKADDVKADANALETKHLPTSCRDESSAT

SEQ ID 741

TTGGCGAAGGTCAAAATCAGCGCTCACGAGTATTACCTGAATCAGCGCATATGGCGGAAAGCAACACTTCTCGCGCGGTGGCAAAACCCACGACATCAAGGCAAAATATGTTGAAA
CGGTTACGCTCACAACCGCGCTGTTACCGCCAAATGCTTTCAAGCGCGTAAACAAAGAAATCCAAGGCAAAAGACTCTCCCTGTGGGCAAGCGTGAAGCGGTTCGGTAAATGGT
CTGCGGACAGCGGTAAAGCGCAGGACCAACGCCGACGCGCGCGCAAGACACCAACAGCGCATCAACACCAAGCACTGCGCTCAACCTGCCGCGACCGCTTCTGCTAGC

SEQ ID 742

LABQKSAVTEYYLNHGIWPKDNTSAGVANPTDIKGYVESVTVNGVVTAKMLSSGVNKEIQGKLSLWAKREAGSVKWFQGPVKRTEANADAAGKDTTNGINTKHLPTSCRDPFSAS

SEQ ID 743

TTCGCTTCAAGGCCCTGCATGACCTCATTCGCCACCCGTTTAAACACGGTTTTATCTGACAGCGCGCAATCCGCCGCCCATTTGCCGAACAAGCGGTCCGACTCCGCCGCCGCGG
GAATGACGGCGGAGCGGTTCTGTTGCTCCCGATAAATTC

SEQ ID 744

LRFKALHVPCHPFFKHGFFYLGAQSAPFFAEQAVRTPARAGMTAERFILLPINS

SEQ ID 745

ATGACGCGCTTGAAGCGCAATCGATATATTTTCCACCGGAACGGACGCCCGCGCGCTTGCACAACTTAAAGACAAGCGCGCGGTGATCCGGCGCGCGTGGGAAATCACT
TACCGCTTGATTTATTAATAAT

SEQ ID 746

MQGLEAQSIYYFHRNGRPRPPCKPLKDKPGLIRAAVGNHPLDLFKI

SEQ ID 747

GTGCCGACAGCCCGGATTCGCCCTGCGCGGAATGACGAAGCCATCTTTTGGCGGAAGGTCAAAATCAGCGGTACCGGTATTACCTGAATAACGCAATGCCCGCGGACAAAG
GCGCTGCCGCGGTGGCATCCCCGCCACCGCATCAAGGCAAAATATGTTAAGGAAGTTAAAGTCGAAACGCGCTGCTACCGCCCAATGGCTTCAACCGCGGTAAACAAATGAATCAA
AGGCAAAACTCTCCCTGTGGGCAAGCGTCAAGACGGTTCGGTAAATGGTTCGCGGACAGCGGTAAAGCGGACGCGCGGCCAAACCGCGCGGACGAGTCAAGCGCGGCGG
AACACGCGCATCAACACCAAGCACTGCCGTCAACCTGCCGCGATAAATGATGCCAAA

SEQ ID 748

VPTDPSRLRNGDEAILLABQKSAVTEYYLNNGKWPADNGAAGVASPATDIKGYVKEVKVNGVVTQAQMASTGVNKEIKGKLSLWAKRQDGSVKWFCGQPVKRDAGAKTGADNVKADG
NNGINTKHLPTSCRDKHDAK

SEQ ID 749

GTGCGCGCTGTGTGTCAAAACATTTCCCGCGCATCAAAACAACCATTTGACCGACAATGGCGCTCTTTGTGCGCGTCCGCTCTTTTGGCGTATCCGATGCGTGGGACATATGGCT
TTCCACCGGCTTCAATGCCAAACCGCTTCGAGCGCGTCTGCTGCCAGCGTCTGTTTTCCGCGTCAATTTCCATGCCGAAAGATTT

SEQ ID 750

VCRLCVKTFGASKQPFDRQCGFFAVRPFVSDACGRMAFFTGFNAKPPFERRPACQRLFFAVHFAERF

SEQ ID 751

TTCGTTTATATCTCTCTTTCAGCGCGCTGCTGTTTCGCGCATCGGCGATGGTGTGCTGGAGAAAGGTTTGGCGATGGCTTCCGCTTCGCTGGTATTCCTCTCGGCTTGG
GTAATGACCGAGGCTTACCGGGCGGTATGGGCGACATCATGCTGCTGAACGATTTGGCAGGAGAGCTGTTTGCACTGGCATTTATCCGCTGCTGATGAAGCGTTTTCCGGATCGCGCG
TGGGGTTCGGCGCGGACAGTATGGATTTCAATTCGCGGTAATTCAGGTCGCGCGGTTTGAAGTCGTCGCGTAGCGGTACGCTTCGCGGTGCTGCTCAATATCGCGCGCGCTT
TCTGATGGTGTGTTTTCCACGCTGGCTGAACGCGGTAAATCGGCATCCGATGCAAGGACGAGAAACGATGAACCGGAAATCCAAGGATGAGAGATTTAAGCTTGTGCG

CGGCATCAGT^{TT}TATGTCGGTGGACGAGCT^{TG}CCGCCGCA^{TT}TGGACG^{TT}TACCCGCGAGACGATACG^{TT}TGCGACAT^{CC}CGCGAG^{TT}TGGAGGAGGGTGGCAGC^{CT}GAAACGCCAT^{CA}CCGGCGGG
CAT^{CT}TCGGGCGGAAAC^{TT}GC^{CG}GGAGGG^{CT}TGCCCGCGACCGCCAAACCCGGT^{GT}CAAAACGAAAAAAGCCCA^{TT}TGCCCGGG^{CT}GAT^{TC}CGGAACACAT^{CC}CCGACGG^{TT}TCGTCGG^{TT}
CGTCAG^{TAT}TCGGTACGACAT^{GG}GAAGCCGCGGCATCAGAGC^{CT}TGGTGAAGCGGGCGAGCAGC^{CT}CGGGAT^{TATT}TACCAACAAT^{TCC}ACGTCGCT^{CG}CTCG^{TT}TGCGCAGCAT^{CG}GATTAC
ACGG^{TCAT}CATCACA^{TCC}GGCG^{TCG}TCGCGCC^{TT}TGGACGGCGGTAT^{TAC}GGCG^{TGG}CGCAGC^{CT}CGCAT^{TT}TATCAACCA^{GTT}CAAA^{GT}CGGAT^{TAT}GCGGT^{TAT}GAGCAGCAGCAGCGCG^{GTG}
AAAGCAGCGC^{CT}TCGCT^{TT}TGGAT^{TAC}GAT^{TAC}GAAGGAAGTCAGCG^{TCAT}CGCAGGCGATGAT^{TG}CCAAACGCGCGCG^{CT}CCG^{TTT}CTCGGCGTGGAT^{CA}CAGCAA^{ATT}TCGCGAGCAAGCG^{CT}
GGTCAGGCTCGCGGCAT^{TAC}CGGCT

SEQ ID 752

SEQ ID: 152

LDVYVISFRRRAVCRIGRWCVVDERFGDGRRLRLVPLGPGNDRGLRGGGQHHAERFPTRAVCTGTYSAADEAFSGCGGGGRRRDQYGFHIAHNSGCCRGFSRAGSQQLRGGGQYRRPV
SUGGVGHAGLNAVKSASRCKEAEENDETENPKAWRDFKCPPPASVYVGRACRRIGRYPADDTLHHRPVGGGQWPEPFSRRRIPGRKLAGGSARRPPNPFVSKRRKRCPADCGTHPRRFVAV
RQYRYDHGSRGIRAGEAAQQPADYTYQYPRRLRRFGTYGLGHGHHIRRRPPFGRYTYRRGDKRLYQFVQSRLCRDEHARRGKRRPAPGLRLQSGQRHAGDDCQRARPPFSRRGSGQIPQQRRA
GQARRHYGV

SEQ ID 753

SEQ ID 753
ATGCCCGACGGTCTTTATAGCGGATTAAACAAAATCAGGACAAGCGCGGAAGTCATTGCGGTATTCGCATCATAGGCCGGAATAATCCGGCCTCCGTCATTCCCAGCAAGCGGGAATC

SEQ ID 754

MPDGLYGLTKIRRRSHCGIRIIGRKNPASVTPAKAGI

SEQ ID 755

SEQ ID: 755
TGTGACGAACACCCACGCGCGCGATTTCAACACACTTCAAAAAAATCAGCCGTTGCCGGGTATTACCCGAATCAGCGCAAAATGGCCGGAAGACAACACTTCTGCGCGCGGTGGCAATCCCGCCCT
CCGACATCAAAGGCAAAATATGTTCAAAGCGTTACGGTTCGCAAAACGCGTCTGTACCGCCGGAATGAAATCAGACGGCGGTAAACAAAGAAATCAAAGGCAAAAACTCTCTCCCTGTGGGGCAG
CGGTGAAAACGGTTCGGTAAATGGTCTCTCGGCACACGCGGTAAAGCGCGACGCCAACACGCACAACAGCAGCCGTCACGACGACACACCACCGGCAACGGCAACGAAAAATCTGAAAC
AAGCACCTGCGGTCAACCTGCCCGATGAATCATCTGCCGTTTGCATAGAAACACCACTACGCGCTTTTATATAAAATACCCAAACCGTCATTCCACGAAAGAGGATATCCGACAGCA
AGTCTAAAGAAACCGTCTTATCCCGATAAGTTCCGCAC

SEQ ID 756

SEQ ID 756

LHETPRADFKHFQKISRCRVLPESRQAGRHCFRRRGIPSPDIKGYVQSVTVANGVVTAEMKSDGVNKEIKGKLSLWGRRENGSVKWFQGPVKRDNANNAANDAVTDDTTGAGNEKLETF
KHLPSCTREDESSAVCIETPPPTAFYKNITQVPIPTKAGIONAKSKETVLPDKFFH

SEQ ID 757

SEQ ID 757

GTGGCATCCGCCCTCCGACATCAAAGGCAAAATATGTTGAAAGCGTTACGGTCGAAAAGAGCGCTGTTACCGCCAAAATGCTTTCAAGCGCGGTAAACAAAGAAATCCAAGGCCAAAAACTCT
CCCTCTGGGGCAAGCGTGAAGCGCGGTTCTGGTAAATATGGTTCTCGGGCAGCGCGTTAAGCGCAACGACGCCGCCAACGACGACGTTACCGCAGCAGCGCGGCACCGGACAACGGCGGCAAGG
CAAAATTCGACACCAAGCACTTGCCTGCAACTGCGCGGTAATAATCAACTGCGGTTTGCACGAAACACCACGGCGCGATTTTCAAACACTTCCAAAATAATCAGCGCTTGCCTGGGTATTATCCCG
AATCAGCGCAAAATGGCCGGAAGACAACACTTCTGCGCGGCTGGCATCCCCCTCCGACATCAAAGGCAAAATATGTTCAAAGCGTTACGGTTCGCAACGCGCGTCTTACCGCCGAAA

SEQ ID 758

SEQ ID 758
VASASDIKGYVESVTVKGVVTAKMLSSGVNKEIQGKLSLWAKREAGSVKWPFGQPVKRNDAAANDVDVDDAGTDNGGKGKIDTKHLPSTCRDKSTAVCTKHEAPIISNTSKKSAVAGTYP
NHGKQPEDNTSAGVASPPPTSKANNFKALRSQTASLPFK

SEQ ID 759

SEQ ID 759

ATGTCGCCGGCAAACGAATTTCGCCGAGATGAAGCCGGGTGCGGTTTGTATCAATTGCGGGCGCGGGGGCGGTGGATGAAAAACGCGTCTGCTTCGCCACTCAAATACGGGCAGATCGGCG
GGCGGGGTGTCGATGTTTTCACGAGGAACCGCCAGGGGGCGGCAATCCCTTGCTGAATGCACGATTACCCAACTGATTTGTATCCGCGCATACCGGTGGCGAGCCGCGAGGCTTTTGA
TCGGTTGTTTGAATATATGTTGGCGAACATTCACGCTTTGTGAAAGGCGAGGCGCAAAACCGCGTGGTT

SEQ ID 760

SEQ ID 760
MSGEVETLROMYPCAVI.TNCGEGGPUDENAI.LAAIKYGOIGGAGVDVL.TREPFRGNNPLINARLPNLIVTPHTAWASREALDRLFEILLANIHFVKGEAQRVV

SEQ ID 761

SEQ ID 761

TTGGCAAAATGCGCGTCTGAAGCCCGATTTTTCAGGCTTCAGACGCGATTTCGCCGTTTGATTTCGGCGTATAAATCCGCCCTTTACCAATGTTTTCGAAAGCACAATATGACACGCAAAATCT
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CTGCGCCGACGACACCCACGGCACGCCGTTATGCTTGC CGCGCAAAACAAAGCATTCGCGCCCGAAGACATGATTGCCAAGTGCGCAAGAGCAOCTTGCCGCACTTTACCGGCTTTTTC
ATCGGCTACGACAATATTATACAGCACCCATTCCACTGAAACAAACAGTTTTC CCAAGACATTACCGCGCGCTGAAAGCCCAACGGGCAAAATCGAAAGCCGCGCTCATCGAGCAGCTTTTCG
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GCACACGGCTTTTGCACCGTGGACGGACAAAAATGTCCAAATCGCGCGGCACCTTCATCACCGCCAAATCTTATCTGGAACAAAGGCTGAAACCCCGAGTGGATGCGCTACATCGTCGCG
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CAAAACGCTTTGAAAGCTGTCGCGAAGACGCTTTAGGCAACGATTCGTGCGCAAAATTCGCGCGCAAGCGACACCATTCGCGGCAATACGAAAAACCGGAATACGCGCCGCGGCTTCGCG
GACATCATGGCATTTGGCAGACATTGTCAACGAATACGTCGATGCCAAACAGCCGTGGAGCTCGCCAAACAAGAGGTCAAGACGAACGCTTCAGCAAGATGACGAGAACTCATCAACG
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TCGGTTTGTAAAAACGCATCATCTCTTCGCGCATTCGCGCGCTTATCCAAATCTCGCCGAATGGAACGCTGCGATGTCATCGCAGTCGCCAACTTGCGCCCAACGCAAAATGGCAAAAT
CGCGGTATCCGAAGTATGATCTCTTCGCGCCACCGGCAGCGCAAACTGAAGCTGCTTGACGTGGATGCGGCGCTCAGCGCGCGCACAAAGTCGGT

SEQ ID 762

SEQ ID NO: 762

LAKMPSPEARFRLQTAFPRILGIIIRLYPLPAKHNMTRKILVTSALPYANGSIHLGHMVZHIQTDVWVRPQKLRGHECYCCADOTHTGTPVMLAAQKQGIAPEDIMAKVRKEHLADFQTF
IGYDNYSTHSTENKQFSQDIYRALKANGKIESRVIEQLFDPKEQMF.LPDRFVKGECPKCHAQDQYGNCEVCGTTSPTTELINPYSAVSGAKPELRESEHFFPKLGBCADFLKAWTSQNN
PHDGKPHLOPEALNKMKEWLGEGETTSLDWDISRDAPYPGFEIPDAPGKYFYVWLADAPGVYMASFKMLCDRIGIDIDFETYPKADSQTMYHYFIGKDILYPHALFWPAMLHFSGHRAPTGVY
AEGFLTVDGQKMSRGTFTTAKSYLBEQGINPEWMRYTAAKLNKGIETDNLNQDFISRVSNDLVGKYVNTAARASGFIAKRFBGRPKDQVSGSALLAKAESDITAEQYNREYARALR
DIMALADITVNEYVDANKPWEAKQBGQEDRHELVCEKLNINAPTMITATYLAAPVLQPTAANAARFLNLDAITWKTRETFGEHAIKNTVEHLMQKQVDDILIRANKQSITQASAPVEBKY
EYFQAGQGTGPNKIDREUAKVCEKAVESGSKLLKPLDQGFGRKILISGTAASYNPAPELINGEMDITAVANFAPMKAKPGVSEGMLISAAFDGKLLJLDVDAQAQPGDRVG

SEQ ID 763

SEQ ID 763
ATGTGGCGGTATCGTCGGCGGCATCCGGCCCATCACAACGTGTCGATTTTCTGACCGACGGCCTCAAACGCCCTCGAATACCGGGGTTATGACTCATCAGGCATTGCTGTGTATTCAGACG
GCAAAATCAAACGCGTGGCGCGCTCGGACGCGTGCAGCTTATGGAGGACGGCGCACCGCAAAAGGCATCAGCGCGGCATCGGCATCGGGCATACGCGCTGGGCGACACAGCGGGCGGT
TACCGAGCCCAACGCCACCCGCACATCAGCGCGGTATGATTGCGGTCGTCCACAACGGCATCATCGAAAACTTTGAAACGGAACGCAACGCTTGAAGGTTTGGGATACCGGTTTGA

TGCGAAACGGGATACCGAAGTCATCGCACAGCATCAACCAAGAAATACGCGCAAAACGGCGGAGCGTGTTTGAAGCCGTGCGAAGAGCGGTCAAAACGTTTCCACGGCGCATACGCCATCGCGGTATTATGCCCAAGACAAGCCTGATGAATTAGTTGTGGCGCGTATGGGCTGCCCGCTTTTGGTGCCTTTGGCGCAGCATGAACACTTTATGCTTCGGACGATATCCGCCGTCATCGCCCTTACGCGCGCGTGGGTACCTCGAAGACGGCGACATCGCGCTGCTGGCTTCAGACGGCATCAACGGCTGACGATATAAAACGGGCTGCTGCCGGAACGCAAGTCACAGGTATCCGAAGCTCAGCGCGCTCTTTTGAACCGGGTCCGCAAGCCACTTTATGCAAAAAGAAATCCACGAGCAGCGCGCGCGGATTCGGGACACGGCGGAAGTTTTCCTCGACGGCGGATTCATCCCCGAAACTTTCGGCAAAAATGCCAAAACGCGTGTTTGAAAGCATCCGACGGCTCAAAATCCTTGCTCGCGGCACGTCTTATTCACCGCGCGCTGACCGGCCAAATATTGGTTGGAATTCATCGCCAAATCCCGCGACGCTCGAAATACGGAATACGGAATACGCGCGGTGATTGCCAGCCGCACTGGTCTATTACCAATTCOCATTCGGCGGAAACGCTGGACAGATGGAGGCTTTGAAATACGCGCAATCTTTGGGACACGGCACAGCCTCTCCGTGCAACGTGATGGAATCCGCCCTGCCCGCGCAAGACAGCCTTGTGCTTTATACCCGTGCCGGTCCGGAATCCGCGTGCCTCGACTAAAGCATTTACACGCAACTGGTCTGTCTGTCGTTTGGCGGTAAACGCTGGCGGAAAGTGGCGGGGTGGTATCCGGCGAAGATGAAGCACTTACACCGAAGAACTCCGCGAGCTTCCCGGCAGCGTGCAGCACGCTTTGAACCTCGAACCGCAAAATGCGCGCTGGGCGCAACAGTTTGCACGAAGAAACACAGCGCGCTGTTTTGGGCGCGGCATCCATTACCCGATGTGCCCTTGAAGGTGCTTGAAGCTAAAGGAAATCACTACATCCACGCCGAAGCCTATCTCGCCGGGCACTGAACACAGCGCGCTGCTTGGTGAGCAAGAAACATGCCGCTCGCTGTCATCGCGCCAACACGACAGCCTTGGGACAAAGTCAAGGCAATATGACGAGAAATGCGCGCGCGCGCAACTTTTGGCATTCGACAGCAATTTAATGTGCACCGAAGGCGTACACGTATCGCGCATCTGCCCATCTGCGGCACTGCTGCTGCTACCCGCTCCCGCTGTCAGCTCTCTGCTACCAACACCGCCCTCGCGCGGCACGATGTGCACAAAGCCGCGCAACTGTGCAAAATCCGTAAACCTCGAA

SEQ ID 764

SEQ IV 674
MCCIGVCAIRAHNNVVDFLTGLKRLVEYRGVSSGJIAVSDGKIKRVRRVGRVQLMEDAAREKGISGGIGIGHTRWATHGGVTEPNAPHISGGHIAVVHNGIIEFSESERKRLEGLGYRFE
SQTDTVEIASHNHEHYAQNGGRLFEAVQEAVKRFHGAYAIAVIAQDKPDELVVARHCCPLLVALGDDETFIASDVSAVIAFTRRVATLEGDGDIALLASDGKIKRLTKNGLPAERKVKVSEL
SPASLEPGPHSHFQKRIHQPRATADAEVFLDGGFIPENFGKNAKSVFSESIRSVKLIACGTSYTAALTAKYHLESIAKIPADVEIASERYRSVIAADPDQLVITISQSGEFLDTHEAL
YAKSLGHRHSLSVCNVMSALPRESSLVLYTRAGAEIGVASTKAPTQLVFLGLAVTLAKVRGVSGSGEAEARTTEELRQLPGSVQHMLNPEQLIAAWAQFKAQTSALFGLGRIHYPIAL
EGALKIKETIYTHAEAYPAGELKHGFLALVDENMPVVVIAFNPDSLLDKVKANMCEVVGARGGELPVFADLOSNFNATEGVHVIRAPRPHVGELSPVVHVPVQLLAYHTALARGTDVDKPREL
AKSVTE

SEQ ID 765

SEQ ID 765

TTGAAAAAAGATGCGGACGGCTTCGCTACCGCACCTTCGGTTTCGGATTATAAACCCGCTCCCGCGCCGAAAAACAGCAAAATGCGGCTCTGAAGGCTTGGGCTTGCTCAAAAAAGGAG
GGATTTCCTCCCGCTGACCGCGGATGGCGCGTTCAGACGGCATTGCTGCCGCCGGTTTATAGTTTTTGCAATCAATAT

SEQ ID 766

SEG ID 768
LKKKMRASVPHLPFRIINRLPRRKTAKRLKAWACSKKGGISPPDRDGESDGIACRRFTVFANQY

SEQ ID 767

SEQ ID 767

TTGTATCAGTTTTTTTATGCGCGCTGTTCCAAACCTGCCGCCGATGCGCGCAGAAATGCCGTCTGAAGCCAGAAATCGGGTTTCAGACGGCGGCAAAAAACCGGCGGTTTTCCGCGGTTTTCA
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GCACCGCAATTCGCGGCTCTCTTGTGCGCGCTCCGTCCTTTTGGCGTATCCGATGCGTGCGGACATATGGCCTTTCCAACCGCGTTCAATGCCAAACCGCCCTTCGAGCGCGCTGCTGCTGCC
AGCGTCTGTTTTTCGCGGTCATTTCCATGCCGGAAGATTTTGACCTGTGCAAAACATTAAGAGCGGCAAAAGGC

SEQ ID 768

SEQ ID 768
LYOFFMFLPQTLPPDAATMPSEARIGFQTAAKNRRFSAGFTIMPRSPGRQSGDRFAGERTGPCRCAACVSKHPPAHQNNHLTDNAASLSPSVLLPYPMRADINWFPQASMPNRPSSAVLPA
SVCFSPSISMFKDFDLCKTLKAARG

SEQ ID 769

SEQ ID 769

ATGAGCAGCGTGAATGACGTTGTTTTCGGTATTTGGTACCGATGTTTTCGGGATTTTTATCCGATTTCCCAAGCCTTACCTGCCCGCTTCGGACAAGGTGCTGTGGTTTTGGTGATATGCCG
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ACCGGGGGGGATCCGGCTGTGCGGTTTGGTTTATATGTGTCATCTCTTACGGCGGGCTGCTGTTTGGCGCATCGGCAGATGTGTGTCGGTGGGACGAAAGTTTGGCGATAGGCTTCGCGCTT
CGGTTGGTATTCCTCTCGGGTTTGGTAAATGACCGAGGCTTACGGGGCGGTATGGGCGACGATCATGCTGCAACGATTTGGCGACGAGAGCTTTGTGCATCGGCATTTATTTCCGCGCTG
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TGTGTGCTCAATATCGCGCGCCCGCTTCTGATGGTGGTGTTCACACGCTGGGC

SEQ ID 770

SEQ ID 770

MSSLMTLFSVLVPMFAGFFIRVPKPYLPASDKVLSVLVYAVILLIGVLSRVEDLGSRLGDMALTIVLNLFCVCTVCANLLALAVLGLKLSPPWRIGGKGKGVSVGVSGSVRQLGCVLLGFWVSGK
LMCDIWMPSSEACHYCLMLLVFLIGVLKSSGVSLRQVLLNRRGIRLSVWFLLSSLSGGLLPAASADGVSWTKGLAMASGPGWYLSGLVMTAYGAVWGSIMLLNDLARELFALAPFPL
MKRFPDAAVGVGGATSMDFLTPVIOGAGGLEVPVAVSPGVVNNIAAPFIMVVFSTLG

SEQ ID 771

SEQ ID 771

ATGGAAATGAACAAATGCTTTTGGCGTGGCGTGGCGGCGGTGTGGCGGGCTGCGGCAAGGATGCCGGCGTTTACGAGGTTATTGGCGCGAAAAGTCGGACAAAAAGAGGCGGTGA
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AATCCGATCAAACTTCCGACGACGGGAAGAGCGTGTATGTGCAAGCAGCGCGGTATGTGAAAAACCGATGCGCGAGTGAAGGACAAAATCATCGCCACCAAAAAAGTGGCGGACAAACG
GCACAGGCATACCTCGACGCGCGAAAATGCGTTCGCCGTCAAAACAAACGTATCAGCAGCGTCAGCGCGGATCAGCAATGTGAAACCGCGGTTTGCAAGCCGAGTTTGACGAATTGAAAAAG
AAATCAAAATGCAACCGGACAAACCGACATTTGTTGTTT

SEQ ID 772

MEMORIALAVGVAVLACGGKDACGGYEGYNREKSDKKEGVIAVKKKNYFLNKINVPTGKEESLILLSEKDGALSTNTGTGETPKLSDDGKELYVERRRYVKTDAAHKDKIIAHQKKGQT
ADAYI.DARNALPSNOTYOOORAAIEOLKRRFEAFDELEKEIKCNGKPTLLP

SEQ ID 773

SEQ ID 773
TTGCGATACCGCAGGCACAAGCCGGCCGGTCGGACAAAACGCCCTTCTTATTGACCGGAATGGATTTCGCCCGCAACGGAAATCCCCCTTCGAAACGGACAGAATCGGACGGGTATTCAAA
CCCATCCGGAACAAAAAAGCCGGACATTCCGCCCGCCGGTACCGGTTATGGAAACACACGGTCCGATTTCGGACGGCGCATCTCCCGGTTGTCTACGCTAAAAACAACATGTCTCGTTTG
CCGTTGCATT

SEQ ID 774

SEQ ID 774
LRYRRHKPKAGTKRLSYLFWISARTEIPLANGQNRGTGIQTHPNKKRRTPFPARTGMETTRPTRTAASSRLSYAKTMSVCRCI

SEQ ID 775

SEQ ID 775

GTGTAAATATCCCTCTCCCGGGCTACCGCAACGCCGCCGGAACCATCTTTTATTTACTGACGACAAACATTGTCCATTATGAAAAAACACCTGCTCCGCTCCGCCCTGTACGGCATCG
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TGCCGGCGGGCGGGCCGCTCTATACCGTTGTGCGCCACCTGTCCATGCCCCACTGGCGGGCGCAGGATTTTGCCAAAGAGCTCGCAATCTCTCCGCTCTGGCTGCGCAATTGTGAAAAACCGC
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SEQ ID 776

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AIKGRFEGSRFLPYHTNQINGGALDGKAPILGYAEDFVELPFMHIQSGRLKTPSGKYIRIGYADKNEHPYVSIQRYMADKGYLKLQGTSMQGIKAYMRQNPQRLAEVLGQNPSTYIFRE
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SEQ ID 777

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GCCCTCGCTGCGGTAAAGCCGCGCTTACGCCCAAG

SEQ ID 778

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SEQ ID 779

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SEQ ID 780

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SEQ ID 781

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SEQ ID 782

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SEQ ID 783

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SEQ ID 784

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SEQ ID 785

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SEQ ID 786

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SGVKETAAKLMTDVEALQKEIDALAFPPGKVVGGASELIEAAGSKIISGEEDRYSHDTLSDFPQANADGSKKIVDLFRPLIEAKNKALLEKTDITNFKQVNETLAKYRTKDGFEYDKLSEAD
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SEQ ID 787

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TACCGGTTTGT

SEQ ID 788

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SEQ ID 789

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SEQ ID 790

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SEQ ID 791

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SEQ ID 792

LSQESAFSHAGQDEEIAAABGADVFPQRFAVEEVLHEDTGVKICLIADHQPDKLSA

SEQ ID 793

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SEQ ID 794

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SEQ ID 795

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SEQ ID 796

MEYCEFEASDPYATYRRANLHAGLPLFVVLVLLNVVPLPAHFLANLVPMPFVLGGGFLSLPLVALLVPTCCILARCPLSLRLCHPCPNHPSKNSA

SEQ ID 797

AAACAACCAATTGACGCAATCGCGCTTCTTTGTGCGCGTCCGCTCTTTTCCGCTATCGATGCGTCCGCGACATATGGCTTTCCAAACCGGCTTCAATGCCAAACCGGCTTCGAGGCGC
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SEQ ID 798

KQPFDRQCGFFVAVRPFVSDACGHMAPPTGFNAKPPFERRPACQRLFFAVHFHAERF*PVQ

SEQ ID 799

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SEQ ID 800

VPSEAGFRFPQTASQNKHPIRTANRVTPLPAMRLRIHL

SEQ ID 801

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SEQ ID 802

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SEQ ID 803

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SEQ ID 804

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SEQ ID 805

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SEQ ID 806

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SEQ ID 807

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SEQ ID 808

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SEQ ID 809

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SEQ ID 810

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SEQ ID 811

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SEQ ID 812

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SEQ ID 813

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SEQ ID 814

CPALRGGRVIRIGLGGARGRAGVPPVCQNISRRKTT*PTMRLLCRRPFCRIRCVRTYGLSNRLQCTALRAPSCLPASVFRPFPCKRILTCAKH*KRQKARD*HRYAKQNGFLPECR
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SEQ ID 815

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SEQ ID 816

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SEQ ID 817

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SEQ ID 818

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QAVFFGFVAVCYKTLVLEPLRTACNACECGKHSARAGFTAYGLTFFRQVSGDVQRVHPFFPPFQAFKN

SEQ ID 819

ATGCAAAACCGTCCACAGGAAACATCAAAATGAAACCGCTACTTCTTTTCCCTTTGCGCAAGTTCGGCTGCGCTGCTTGGCGTGGGCGCTTGTTCGCCCAAAATGCTGATGCGCGA
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ACGGAACCCGAGCTACGAAGAGCTGCTTACCGCATACGCGTATGCGGAGCGTCAAGTGAACCTAGCATGCGCGCAAACTCAGCTGAGCAGATCTGCAATATATTTCCCGG
TCGTTGATCCGACCGCTCAACAAACAGGTTACGACCGCGCACATACCGCAGCGCGGTGACTACCGACCGCGCGGAAAGCGCTATCGCGCGCGCTTCAACCGCGAGCA

GCACAAAATACCAACTGCCCTCGTTGTTGAAACGAACCGCTGAAAACTTCTACGACGCGAGGAATACCATCAGGACTACCTGATTAAAAACCCCAACGGCTACTGCCACATCGACATC
CGCAAGCCGACGAACCGCTGCCGGGCAAAACCAAGCCGACCCGCAAGGCAAAAGGCTTCGACGCGGCAACGTATAAAAAACCGAGTGACGCCGACTCAAACGACCCCTGACCGAAGAC
AATACCAAGTGACCCAAACACGCGGACCGGAATACGCTTCAGCCACGAATACGACCATTTGTTCAAAACCCGGCATTTATGTGGAACGTTGTACGCGGGCAACCCCTGTTACGCTCCGCGGA
CAAATATGATTCCGGCTGCGGCTGCCGAGCTTCACGCGCCGATGTGATGCAAAATCCGTTACCGAAACACGATGATTTCAGCTTCAATATGCGCCGCACCGAAGTCAGAAGCCGCGCGCC
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SEQ ID 820

MQTVHTGNIKMKHRTFFSLCAGPGCLLALGACSPKIVDAGTATVPHTLSTLKTADNRNPASYLYLKKDKPTLTKFMAW#CPLCLSELGQAEKWAQDAKFPSSANLITVASPGFLHEKKDGEFOK
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 TENPSYEDVSYRHTGAETVKVITYDAADKLSLDDILQYFVRVDPTSLNKQNGDGTGYQYRSGVYYTDAEKA VIAAALKREQQYQYLPVWVENEPLKNFYDAEETHQDYILKKNPGYCHIDI
 RKADEPLPGKTKAAPQKGFDATAKTYKPSDAELKRTLTBEQQYQVATKSAFYAFSEHYDHLFKPGIYVDVWSGEPLSSADQYDGGCWGSPSFTFRPIDAKSVTEHDDFSFNMRRTVEVRSRAA
 DSHLGHVDPDGRDKGLRLRYNGASALGKFTPLIPELMDAATLGAALQKGVKVK

SEQ ID 821

ATGCGCAAACTTACGGCCGGGATTTTCAGACAACCTTGCGCGCAAAATACGCTACAATACGCCCTATTTCAGTTTCTAAAAATTAAAAGGAAAATTCATGTTCAGCTTCTTCGGTCGCAAGAAAAACAGGAAACCGCGGCTCTGGAGGAGGCCCAAGTTCAGGAAACCGCAGGAAAAAGTAGAATC

SEQ ID 822

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SEQ ID 823

ATGCCGCTGTAAGCAGGGGAAGCGCGTGA AAAAAGCGGTGGAACGCGTTGAATCCGCAAAAGAAGCTGTGCCGAAACCGTCGGCGAGGCGTGTGGGCAAGTTC AAGAAGCCGTTGGCAGCAA
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SEQ ID 824

MPSEAGAEAAKAVERVESAKEVAEATVGEAVGVQVQEA VATTEHKLGMWAARLKQGLAKSRDKMAKSLAGVFGGQIGEDLYEELETVLITGDMCEATFYLMKDVGRVSLKGLKDGNEL
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SEQ ID 825

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SEQ ID 826

MPSENGRPNRHSHGSGNLGRGVWATVLSDKFPCGOVRISACAGMTNFEIAVLSDGFRDCGIVGNDGSGISPRPFRACKRRALKNAV

SEQ ID 827

ATGCCGTCGTGAACCTTCAGACGGCACTTTTAAATCGCCGCGCGTTTACAGCGCGGGGCGGGGCGGGGAAATACCGGAACCGTCATTCCCGACAATACCGCAATCTCGAAACCCGTCGAC
AACACCGCAATCTCGAAATTCGTCATTCCCGCGCAGGCGGAAATTCGGACCTGTTCGCAACGAAACTTATCGGA

SEQ ID 828

MPSEPSDGI FNRPPFTGAGRARGNTETVI PDNTAI SKPVROHRNLEIRHSRAGGNPDLSARKLIG

SEQ ID 829

GTG CAGCG CGATT TTAGCCTAC GCGCCGAACGCATTAC CCGGAGTATTC CGGAACCAACCGCTCC AGGCAAAAACAAAATAAG CACGGTAA GCGATTATTT CAGAAAACATCGTACGCATT
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CAAGATATCAAGATTAAGAGAGACCTGAAGACGGAATAACAGAAACCGGACGCTTCCACGCGCTTCTCTCTCGCGCTTATCAGCGGTTTACGATTTCAAACTCAAGACAAAATTCAAACCC
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SEQ ID 830

WQADLAYAERITHTDYPEPTAGPKNKISTVSDYFRNIMTHSIHPRVSVGYDFGGWRIAADYARYRKWNDNKYSVDIKELENKNQNRDLKTENQENGSHFAVSSIGLSAVDYFKLNDKFKP
YIGARVAYGHVRHSIDSTKKITGLTAYPSDADAAVTVYPDGHPOKNTYOKSNSRRILGFGAMAGVGIDVAPGLTLDAGYRYHNMGRLENTFRFKTHASIGMRYRF

SEQ ID 831

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SEQ ID 832

LPSLAACAAEEKRREEKRRREEKRVFCGLDSFSAPYSV

SEQ ID 833

TTGGCCTTCAAGGCCCTGTCATGTGCCTCATTTGCCACCGGTTTTAAACACGGTTTTTATCTGCAGGCGCGCAATCCGCCCCCTCATTTGTGTAATCCGCCATATTGTATTGAACACACCGCCCG
GAACCCGATATAATTCGCCCTTCAACATCTGAAAAATTTTTTTTAAACCGGT

SEQ ID R34

LRFKALHVPCHCHPEKRGVYL TGAOSAPSFVNPPYCIETPPGSTRYNPPENTSENTFLTG

SEQ ID 835

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ACCGCGCTCAAGCCGCTTATGCGATGATAAGGTGCGAAGAAGAGGCTCTCCGACAGGGGCGACCGCTCGCTGGAAACCGCTGTCCAAATGCCCTTCCACGTCGAACTGGCGCGCTGGTGG

GCAACGATGTCGTTCGACATTATGAACACGCTGTGCGCGCGTCTTCCCTGATTGTGCGCGTGGGGCGGTGCATGCGGAGAAAAACACGCCATCAATACGCATACGCATTCCGAACA
CCGCGAANTCCTCGAGCTCTGCTGCGCGGAGCGCCAAACCGCGTGGTCAAAATCTGCGCGCGCATTTGGCGCACTGTATGAGCGTTTGGAAAAGACTTTGGAAGAT

SEQ ID 836

SEQ ID 836
MNFENDDIHAPTSSLLIEERHDSLFRVVALILDGITDQVLLPGKKLTSELCRQMVCSENFVRGASLLAHDKIVDLQPNRGAFVHVPLDKEMQDVFNARIEMETMTLNLGLAGLPDLR
TRLKPVIYAMTRCEEASGRDGVGNRLSNAFHVELARLVGNHVLFDIMNTLCARSSLIIVAGVHREKKHAIWTHYSEHRETLDLLAGRRNRVVKILRRHLGNCMERLEKYLEQ

SEQ ID 837

SEQ ID 837
ATGCAGGGCCTTGAAGCGCAATCGATATATTATTTCCACCGGAACGGACGCCGCCGCCCTTGCAAAACCTTTAAAGACAAGCCGCCCGGGTTGATCCGGGCGGCCGTGGGAATCACT
TACCGTTTGAPTTATTAAAAATT

SEQ ID 838

MOGLEAQSIYYFHRNGRPRPPCKPLKDKPPGLIRAAVGNHLPFDLFKI

SEQ ID 839

SEQ ID 839

ATGGCCGGAAGACAACACTTCTGCCGGCGTGGCATCCCCCCTCCGACATCAAAGGCAAAATATGTTCAAAGCGTTACGGTCGCAAAACGGCGTCGTACCGCCGAAATGAATCAGACGGCG
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CGACGCCGCCAACGCCATCGAAACCAAGCACCTGCCGCTCAACCTCCGCGATGAACCAACTGCCAAA

SEQ ID 840

SEQ ID 840
MAGRQHFCRRGIPPSDIKGYVQSVTVANGVVTAEMKSDGVNKEIKKKLSLWGRRQDGSVKWFCGQPVTRNDKADDDVKADAANALETKHLPLSTCRDEPTAK

SEQ ID 841

SEQ ID 841
ATGAATACCCCTCAAAAAGGCTTTACCCCTTATCGAGCTGATGATTGTGATCGCTATCGTCGGCATTTTGGCGGCAGTCGCCCTTCCCGCCTACCAAGACTACACCGCCCGCGCAAGTTT
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GGCAAATATGTTCAAAGCGTTACGGTCGCAAAACGGCGTCGTTACCGCCGAAA

SEQ ID 842

SEQ ID 842
MNTLQKGFTTLIKLMTVIATVGLAAVALPAYQDYTTARAQVSEAILLAGQKSAVTGYTLNHGINPEDNTSAGVASPPPTSKANMFKALESQTASLPK

SEQ ID 843

SEQ ID 843
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SEQ ID 844

MRLSLYNCFYFVPSFRWVFAEVGGGSVENCQF

SEQ ID 845

SEQ ID 845
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AATGCTTTCCAAGAAAAACGGAGCTTTTAAAAAATAGAAAAATTCGCCACCCAACCCACCTATTTC

SEQ ID 846

SEQ ID 846
VGM TGF NDAAGNEKIETKHL PSTCRDASSAGCIETPRADFKCFPRKRSFLKNRKFTPTQPTLF

SEQ ID 847

SEQ ID 847
TTGTCCTTTTAAGGGTTTGCAAGCGGGCGGGCTCGTCCGTTCCGAAGCCATCCCTTTTGGCCGAAGGTCAAAAATCAGCCGTTACCGGGTATTTGCCGAATCACGGCATATGCCGGAAAAAC
TTCGTCATTCCCCGCAAAGCGGGAATCTAGGTCGTGTCGGCACGGAAACTTATCGGG

SEQ ID 848

SEQ ID 848
LSFKGLQGGGRPFRRSHPFGRRSKISRYVLPESKHMAGKLEHSRESGNLGLSARKLIG

SEQ ID 849

SEQ ID 849
TTGGCCGAAGGTCAAAATCAGCCGTACCGGGTATTGCCCGAATCAGGCATATGGCCGAAACTTCGTCAATCCCGCGAAAGCGGGAATC

SEQ ID 850

LAEGOKSAVTGYCPNHGIWPFNFI PARAGI

SEQ ID 851

SEQ ID 851

GTGCCGACAGACCCGGATTCCCGCCTCGCGCGGAAFGACGAAGCCATCCTTTTGGCCGAAGGCCAAAAATCAGCCGTGCGGGTATTGCCGAATCAGCGCAATGGCCCGCAACAAAG
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CAAAAGACTCTCCCTGTGGCGCAGGCGTCAAGACGGTTCGGTAAATGTTCTCGGACACGCCGTTACGCGCAACGACGCGCGCGACACGAAGCAAGTGTGCCAAAGACGACGCCCGCGC
AAGCCCATCGAAACCAAGCACTGCCGTCAACCTGCCGCGATGAACCAACTGCCACC

SEQ ID 852

SEQ ID 852
VPTDPSRLRGND EAILLAGCGKSAVAGYCPNHGKWPANNGDAGVASSAEIKGKYKSVTVANGVVTAEKASSGVNKEIKGKRLSLNARRQDGSVKWFCGQPVTRNDADNDQVAKDDAAG
NAIEKHLPSCTCRDEPTAT

SEQ ID 853

SEQ ID 853

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CGGTTTGGGTTATTACCCGACCCGCGTGCCGAACGTGATTTTTCGCGACAGTATTGATGTTGAAAACCCCGGGCTGGTACACCGCTTACACGCGGTATCAGCGCGAGATTGCCCAAGGTCGTGTGGAA
CGGTTGTGTAACCTTCCAGCAGGTGTGGATTCGATTTACGCGGTGTTCCTTGTGGCAGCGCGCTTCTTTGTGGACGAAGCGACCGCGCGCGCGAAGCGATGGCGATGGCGCACCGCGTGGGCA
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SEQ ID 854

MKISELPNPNFAARHLSFGDEAALLAAVGEKSMDEFVGNLTPQSIRMPSELDPALTEADALAKLKGIAKSNVINKSYIGLYPTTRVNVILENVLENPGWYTTATTPYQAEIAQGRLE
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EPTSESKAELDRFLAALXIRREVQKVIDGEWPKDNLPLVNAPHTAADITGEWHPYSREEAVPLPLFVREHKFWPFVNRVDDVYGDRLNLCSCPHENYED

SEQ ID 855

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CAACAGGCATATATATGACGGCGAGGATGCCGTATTTAGTGTATTTACCCGTAATATTGATTTCGCATACAGGCTTCAGATGATTTTGTATCGGTTTACCGCTGGAGAAATATGGA
AACACCGTTTGC CGGCTGTCTGAAAATGAAAATCGCGAGTATCGCCACATTTGTAGGACGAGTATCCGAACCGGGCTGATAACTGAAAGCACCAGCAATCAAAAGACAC

SEQ ID 856

GTQYIRSEYLFYF*RIINLRRHLLKFKIKHIFRNSKILLYLFPMPPFFIFFPSLGSFV*IL*LLFNCLL*ISSVIIICNIFLNRHIIDGKDAIVVFRNIDFVIQGR*FLIGFTAGRIE
HTVCRLV*K*KIGSIANICRTSIRTGLITESTEAIRKH

SEQ ID 857

AACGGTTGCGCGAATATATTGTGTAACCGTGCAATTGCATATCGTAATAAAGCTAAATAAATAACAATATAAATCAGCATGTTGCAACTTTGTTTTTATTTTGTGTTGACGGGCA
CATATCAT

SEQ ID 858

NGCANIFV*PCICIS*INVKNNNINQHVAFLFFILC*RAYTH

SEQ ID 859

TTGACGCAAAATATCTTATCTTTGTCGCTGCAGATGGGCGAGGTTGGCGGTCATTTTCTCTTATCTCTGAAAGTGTTTAAAAACGG

SEQ ID 860

LQNLFILCRADGAGLGHFSLPLKVFKR

SEQ ID 861

GTGCTTCATCACCTTAGGAATCGTTCCCTTTGAGCGGGGCGGGCAACGCCGTACCGGTTTTTGTTAATCCGCCATATCGTCAAGATGCGGTTTGTGTTGCAACCCCTTAAAGGA
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SEQ ID 862

VLRHRESFPLSRGGATPYRFLIRHIVARCGLLPATLKGRTNKKMFVLPCLMFSAPSLAAVNINAASQLEALPGIGPAKAKIAEYRAQNGAFKSVDDLIKVGIGPAVLAKLDQA
SVGAPAPKPAKPVLPVKK

SEQ ID 863

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SEQ ID 864

VETDTLANITIEKHSLLFRFYRIIPKLPPLIRKRFMLQRTLAISIGVPGVGLHSGERVALTLHPAPENSIGISPRFTDLGEMGEQIKLNPYLINDTRLSSFTIVTDKGLRVOTIEHIMSALSA
YGINALIELNAPEIPIMDGSSLPFIYLLQDAGVVDQKAQKRFLKILKPVKEAGKWRFTPYDGFKVLTLIEFDHPVFNRSPPFTFIDFAGKSYIGELIARARTPGFMHEVEMMRAHNLG
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SEQ ID 865

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SEQ ID 866

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SEQ ID 867

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GAATC

SEQ ID 868

LRPKALHVPCHPFFKHPFLITGAQPAPSPFAEQAVRTPARAGI

SEQ ID 869

ATGACGGGCTTGAAGCGCAATCGATATATTTTCCACCGGAACGGGACGACCGCGCGCTTGCAAAACCTTAAAGACAAGCCGCGCGGTTGATCCGGGCGCGGTTGGGAAATCACT
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SEQ ID 870

NQGLEAQSIYTFHNRGRPRPPCKPLKDKPPLIRAAVGNHLPDLFKI

SEQ ID 871

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SEQ ID 872

VASASTIKGYVQKVEVAKGVVTAQMASTGVNKEIQDKKLSLMAKRQDGSVKWFCGQPVTRTGDNDTVDADANNAIDTKHLPSTCRDKHDAK

SEQ ID 873

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SEQ ID 874

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SEQ ID 875

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SEQ ID 876

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SEQ ID 877

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SEQ ID 878

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SEQ ID 879

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SEQ ID 880

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SEQ ID 881

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SEQ ID 882

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SEQ ID 883

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SEQ ID 884

VIQAIPEGNDSSRQVDRCLVSLVPAVSSLATSSVPALALASVRLTGPCQNHTEPFSRLAHRESFLPWLSLFTFVFAISAVTTPFATVTLTYLPLNSEADATPALSFLSCHSP

SEQ ID 885

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CAAAATCGACACCAAGCACCTGCGGTCAACCTGCGCGGATGAATCATCTGTTGCGGGTATTGCC

SEQ ID 886

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SEQ ID 887

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SEQ ID 888

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LPGIT

SEQ ID 889

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SEQ ID 890

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SEQ ID 891

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TCCGTCTATCCATT

SEQ ID 892

VGNLCRFADENRSRTVPFGRHLNGALNGRFPQIMPDIYLEDVDFGKHRRIVRPFRRNRRTAVSHFLTLFFGNHYHIDARTARHPQQQHPQAGPALGRAPCRRLHNDVAPFRRADKTH
SVYFP

SEQ ID 893

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SEQ ID 894

SA*FYHVSQAVCLYNTAFRKGVDVFLVQ

SEQ ID 895

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SEQ ID 896

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SEQ ID 897

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SEQ ID 898

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SEQ ID 899

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CAAGCAGCTGCGGTCAACCTGCGCGGATGAATCATCTGCCAC

SEQ ID 900

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SEQ ID 901

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SEQ ID 902

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SEQ ID 903

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SEQ ID 904

LNKILHGLRGLPAGILKHPKKSAGVAGYCPNHGKWPENNTSAGVASPPLRHRQIC

SEQ ID 905

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SEQ ID 906

LGGVLIFFRANLIGRANVFYSIIPAPMOTRASG

SEQ ID 907

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SEQ ID 908

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SEQ ID 909

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SEQ ID 910

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ESSLPGLA

SEQ ID 911

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SEQ ID 912

SLHLEADVVGNGIPLFPFKLLHFLPGIQFADQSGQTAVDDGGDFVFAVFFLHCRCLKIQTPAPQICCKAVADV*IEFDGFENFASVLR*GFIRFVYPPDFITPPKRFACITPLFGRVNANMF
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SEQ ID 913

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SEQ ID 914

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SEQ ID 915

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SEQ ID 916

SEQID 510
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SEQ ID 917

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SEQ ID 918

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SEQ ID 919

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SEQ ID 920

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SEQ ID 921

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SEQ ID 922

SEQ ID 922

VSGQFVSVLGERFFAFSGQNGRQGSADGDIDCLQIAQAVADQPSFRLSGVEAFEDVFNHARFGLAAVAAVGAGMRAEPDAVDFFACLITDEAVHFGMHFGFVNLGKILFAADAGLVGGDNGAA
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SEQ ID 923

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SEQ ID 924

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EKRHPLDENVRQMFVYVLEAMKEHGFYRTDIDNVPLDALDPAIKATYSALNDYIGRLADLDKAVESDRYLRHERGKPPVFGTFGDHQVPFEGVSVRKKNDYAPDYVTFVAVRSNLAGGFV
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SEQ ID 925

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SEQ ID 926

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SEQ ID 927

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SEQ ID 928

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SEQ ID 929

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SEQ ID 930

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SEQ ID 931

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SEQ ID 932

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FACRPAP

SEQ ID 933

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SEQ ID 934

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SEQ ID 935

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SEQ ID 936

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SEQ ID 937

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SEQ ID 938

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SEQ ID 939

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CCGTC

SEQ ID 940

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SEQ ID 941

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SEQ ID 942

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SEQ ID 943

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SEQ ID 944

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SEQ ID 945

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SEQ ID 93:

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SEQ ID 935

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SEQ ID 956

MNEQLQDLQKVMGVAVNALEDIKARDISVLETPQKTSLSFARNIIASGDSTRQVKALANNVAVDLKEAGFEILSTEGDSGEWTLVDAGDLVVHVMLPAVRDFYDIDITWGGGKPSFHAGNQ
KPNHAAD

SEQ ID 957

AGCTGGAAAAATGCCGTCTGAAGCGGCTTCAGACGGCATCTGCCTTGCGGTTATCCCTTGAGGTAATGCACGAATGTATATGCAACGCCCTTGTCTGTACACGGCGTTCCGTCGCTCTG
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SEQ ID 958

SWKNV*SGFRRLPCGYPLR*CTNVTATPLLLTRRSVRSASLQCVRSISGKNASPTDKSTSVIRKSVANGIACPYICAPPIMTASSAPAHNANATSKLATVSPAAQ*SACRIATMFLR
PGRGLTGRDHSVFRPIMTGLPKV*ALKNAKSSGHCQGIAPAPMHRFSAHAALIMVLSIFSPQ

SEQ ID 959

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SEQ ID 960

MAYSADLRNKAHNSGLTKIRTRRAAGSTNGTEPIRALPHLHRESFPLSRGGATPYRFLILIRYITDIAKTFAKPKQRLTQGETRFTCGFALKNKQAA

SEQ ID 961

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SEQ ID 962

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SEQ ID 963

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SEQ ID 964

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LPVHCFFPNGMFSGIIASPY

SEQ ID 965

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SEQ ID 966

LNITVLAVGTKMFRVDEVAEYAKRFRDAAAYAFKEIKPEKRGAGVNAVQGMAAEKRILEAIPQGAFLVVLDERGKAPTSVELAEHLKSWRONGEHVCFVIGGADGMDRLKQQAAMM
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SEQ ID 967

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CGTGACGGATACGTTCCGCA

SEQ ID 968

MARMVFCVILNKLEAGMKFPPLPNELGKRIFENVSQEAWAAWTRHQTMLINENRLSLADPRAREYLAQQMBQYFPDGDADAVQGYVPO

SEQ ID 969

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SEQ ID 970

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SEQ ID 971

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SEQ ID 972

VYSVTFSSRLHSRLCFYVFAVLYAQNMPSENKCFQTAWFAMCFAYISRRLRTAGC

SEQ ID 973

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SEQ ID 974

MLPHTPRRAVYAGSFPPTLGLHLMIRQAQSMFDELIVAIGINPKRNTYVAERQDMLCAITNFPNVRLEVQNRFLVHYAREVDAGFIVRGIRSTDYEYERSHRHNSDLAPEISTV
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SEQ ID 975

TTGTATATTATCAACGGTTTGAATAATATGCACTTTATCATTTGGCGATATCTCAATAAACCGTTATGCCACAAGGTACATAGCACTCAGACGTCTCTAATTTCTCAATCGTGGCT
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SEQ ID 976

LYIINGLKIMHFIIGDILNKPLSPQGYIAFRASNFSNRGFH

SEQ ID 977

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SEQ ID 978

LFLIDYKINGLAIQYPIISFPIILLFIHPIGQTFDKDEKPIILFTPI

SEQ ID 979

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SEQ ID 980

VFDSONPGMIVCRIVAVRYRHNPLRYNRAAIQLGRNEMRTAGNAATCFQSAFVRMKPGERGQDGRMDVHQPAFVMAELRGQNPHTKQNHQIGLICVDFPHHGRIBKS

SEQ ID 981

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SEQ ID 982

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SEQ ID 983

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SEQ ID 984

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KTFNLLDGPAYYADALAVGYQAEAGKGAIALGKQAKATKQNGMALGVSEAGDPTAVAGNESKAGGGVGLGNQSKAEADFAVAVGNKAEATKENSIVIGRYARANGNHSVSLGSR
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SEQ ID 985

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SEQ ID 986

MKI THCKLKKEVQKEPLRSFVPEVTARSAADILGIHPDAAALFYRKIRTVANHRLALAADGVFEGPAGPGSGYFGRRKGRRGGAAGKAVVFGIPKRKRAYTVAALNAEPETLPAVK
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SEQ ID 987

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SEQ ID 1000

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SEQ ID 1001

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SEQ ID 1002

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SEQ ID 1003

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SEQ ID 1004

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SEQ ID 1005

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SEQ ID 1006

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SEQ ID 1007

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SEQ ID 1008

VQRVNAVKNRNLGCLQNGDIGAKPPVGQTGTALERINDNLYQLIRTDV

SEQ ID 1009

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SEQ ID 1010

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SEQ ID 1011

ATGAACGCGCGTTCGCGCTCAGCGCTCTCGCTCACACTTGGCGCGGCTTGGCCACGCGCGAGAAATATGCAATGTCGATTTGATACCGTTACCGTAAAGGGGACGCGC
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CGGCTACGCGAGCAATGTAAGGCGCCCAACCATACCGAATCGGCACTCGGGCATGAATTCAACTTCGACAGCGCGCTTTCGCGCAACAACTGTTGAAATACGGCATCACTACCG
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SEQ ID 1012

MNAPFFRLSLISLITLAAGFHAHAENNANVALDITVTVKGDROGSKIRTNITVTLQOKDESTATDMRELLKEEPSIDFGGGNGSQSLFLTRGMGQNSVDIKVDNAYSDSQILYHQGRFIVDPAL
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 LQTHKGRGIISADGQKAKRANRITIEFNGYNDQTPAANGSYFPAQTLKDALANQNRHDSVAVREAVNAGYIKNKHTEGLASTYGTGKLTAKVGVSRSKRPFIVTHTPKLLSNAPFEQAQTGR
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SEQ ID 1013

TTGTTAATCCACTATACATTTCCGACAAAACCTGTCAACAAAAACAACGCTTCGCAATAAAAACGATAATCAGCTTTACACAACCCCCCCCCCCCCCGCTAATA

SEQ ID 1014

LLIHYTFPTKPVNKKQRFANKNDNQLYTTPPPPLY

SEQ ID 1015

ATGACATCTCGCTCTTACACGACGCGCTCGTCTCAACGCTTGAAGCTGAAGAAAAAACCGCCTCTGGCATCGTCTCTCGCGGGCGGGCGCGGAAACCCGATATGGCGGAAGTCA
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GCTGTGTGTAATCGCGGAAGAAGATATTTTCGGCATCGTGTGAAAAA

SEQ ID 1016

NTIRPLHDRVVVKRLEAEKKTASGIVLPGAAAEKPDNGEVLAVGAGKIGKDGARRPLDVKAGDKLIIFGKYSQOTVKADGEELLVMREEDIFGIVEK

SEQ ID 1017

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SEQ ID 1018

MPSEGGLPFOTASCPYLFFNDAENIFFAHYQQLFAVGFYGLAAVFAENDFVAGFDIQTARAVFADFARTHGDDFAHIGFFGGRARQDDARGGFFFSQAFDDDAVV

SEQ ID 1019

SEQ ID NO: 1019
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SEQ ID 1020

MAAKDVQFGNEVRQKVMNGVNILANAVRVTILGPKGRNVVVDRAFGGPHITKDGVTVAKEIELKDKFENMGAMVKEVASKTNDVAGDGTITATVLAQSVIAEGRHKYVTAGHNPDTLKRIGD
KAVAALVEELKNIAKPCDTSKREIAQVGSISANSDEQVGAIJAEAMEKVKGEVITVEDGKSLSELEJUVBQGFQDGYLSPTTINDEKQIAGLONPVVILLPKKISINIRDLFLVLEQVAK
ASRPLILITAEDEVGEALATLVVNNIRIGILKTVAVKAPGGQRRKAMLODIAITLGGVVISSEVGLSLEKATLDDLQAKRIEIKGENTTVIDGFGDAAQIEARVAETROQIETATSDYDKB
KLQERVAKLAGGVAIVIKVGAATEHEMEKKDRVEDALGHATRAIEVEEGVAGGGLVLRALAELENLHTGNAQDAGVQITVLRAVESPLRQIVANAGGESPSVVNMILBEGKNVGYDYNAGSGE
YGMHICVGLNDPAKVTVSALQHAESAETAGLMLITDCHMAIEPEEKPAVPDMGNGMGMMGM

SEQ ID 1021

TTGTGTGCTGAAGGTTTTCAGACGGCAATGCTTACATCATGCGCCCATACCGCCCATATCCCGCCATATCCCGCCATATCGGSCACAGCCG6TTTTTCTTCAGGGATTTCGGCAATCATGCAGTCGGTCTGTC
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SEQ ID 1022

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SEQ ID 1023

TTGTTAATCCGCTATATTTCGCCCATCCAAAAACGAAGCGGAGGAAATTTATCGGAAAAACAGCAACCTTCCGCGTCATCCCGGAAAGCGGAATCTAGGTTCTGTCGGTTTC
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GGTGTGTTCTATAGGATGGTTTTGTATTGGA

SEQ ID 1024

LLIRYLSRHPKNEERQKFGKATATPPSPFRKRESRPFRLPFLIDSCRVOGLDRLRGNDRFLGFCFCSVFAHMTGKLAVVSYGVVFPV

SEQ ID 1025

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SEQ ID 1026

LATKNFLSKYKNHSIRNNRQLPRHSRKNRKTET

SEQ ID 1027

TTGGATAAAAAATTTTTGTTTTCAAGCTTCCACGCTTGCCATCGCGTTAAATTTTTTACGATAAGCACATAGATTGTAAACAATCGGCCACAAGCCGTTGTTTTTTCAGAGACA
TTATCCCTGTGACAGCGTGTCTATATATGTTGCTTATAACGGCTTGTTTT

SEQ ID 1028

LDKKFFVFKPSPLAIGVKIPYDHRIDCKQSATSRFVSEDLIPVRCPYICLPITACF

SEQ ID 1029

TTGATAAAACAAATACCGCCATTTCATTGGGCAAAACCGCACGGAACATCCGTTTTCCCGTTTCCAGACAATCCGGTACAGGACACCCCGCTGCGGATTCCGCTGCACATCCGCAAA
ATTCATACGCAAGGAAATGTTGAAAAACAAAAGAAC

SEQ ID 1030

LIKTIPTHSRGTARNIRFPVSTTIRYTPRCRFRHLHIRQNFIRKENVENKKN

SEQ ID 1031

TTGAAAATACCGGATTATCTCCAAGAAACTCCCTTGTGCGCCATACGCGCTGCGGCGCAAGATAACCTTTGCCAATTTGCAGAAATTTACGTTAACCTTACGTTTTCCGCAACCA

SEQ ID 1032

LKIPDYQENSPCAAIRRLPAQDNLCQFAEPTLTLRFPHP

SEQ ID 1033

TTGAACCCCGCACTTGGACATCTGTCTTCGGGGCGGTAGAATCAAACTTATTGGAAGTTCAATCCCTTCCAAAACAGGGCAACACAGATGACGCTTTATGTGTCTCTCTGTG
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SEQ ID 1034

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SEQ ID 1035

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SEQ ID 1036

VLGNISSARKVTVSANATEKDSVFGDAVHIVLAT

SEQ ID 1037

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SEQ ID 1038

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SEQ ID 1039

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SEQ ID 1040

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SEQ ID 1041

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GAGGAGAAAA

SEQ ID 1042

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YYAVIIGWASYYTYSVNAAGWADPQFPFKDFLQAGPEALGLDFVGKVGAGLAVGVVFTAAIMALGVQKGVARASSFPNPLLVVFLDMVGLISLPLGAAGKGLDALFTPDWSKLADSKY
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AAIQDLKINIGRVNATLLVCIPIGIVSTLLFGTATGLPVLDMDFVNTYGTIVAGFVYVAIIIGRLPLRRHLNALSIRVGLWTACVFTVVMGLVNYLQDTAGLLEKHYGDIYDGF
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SEQ ID 1043

ATGAGTACTTCGCGCATTTGTGATGATGGTTCGCCCATCGCGGTGATTGGGGCGGCTGCTGCTTTCCCTGTAAAGCTGCCGGAAGAG

SEQ ID 1044

MSTSAIVMVAIAVIMGGLLLSLRLPEE

SEQ ID 1045

ATGAAGCACGCTCCGATTTATCTCTCTTACCGCTTCGTCGCGCGCCCTACTTTCCGCGGGCTGCACCGCCCTTCCCTCTGACCGCGCGCGCTTCGCACTCCGCGAAAGCGCGCCA
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SEQ ID 1046

MKHAPIILLITASSAALLSAGCTALPSDRPPLRLTLPKSAPIQANPYSRPPSGTPDGAFTSTRASNGRVLKSTIVKGVFDRFVDIYHFNKLSHSTPVENGVAQGTTEQGIILTRILYRDGH
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SEQ ID 1047

ATGACCTGTTTTCGCAACAGTCCCTTACCCCGGCTTCGCGAAGAAFTTCGGCAGCGCGCTTTATGTGTACAGCCAATCCGCGCTGACCGGAGCATTTGAAACTATCAAAACCGCTTTG
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CTGCTCA

SEQ ID 1048

MTLPCQVFPYPRLAEEFGTPLYVYSQALTGAFENYQTAFAALNPLVCYAVKANGNLSIIKHFAISLGGFDIVSGGELARVLAAGDAAKTIFSGVKGSEAEIEFALNAGVKCFNMESIPE
IDRIQIKIARLKGTPVSLVRNPVDKATHPYISTGLKANKFGIAYADALEAYRHAAQPNLKIIGIDCHIGSQLTDLSPLEACERILLVDALAABEIVLEHLDLGGVGIVYKDEBVP
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SEQ ID 1049

ATGAATACGCGGTATTTTTCGCGCGCAACCCGCTCTCTGCTTTCGCGCTGCGGTTACAAAGGCGGCTCTACCTGCCCAAGAGGCGATACGCGCGGTTTCGCGGTATCCAAACCG
GTTTGCAGCTTCAAGGCAACCGCAATCCGCGCCACCAACCAAAAA

SEQ ID 1050

MKYGVFFAATALLSACGYKGLYLKPEGDTARFVGIQTGLQLQKGPQSAPPTQK

SEQ ID 1051

TTGTCGCAAAACAGGGTCATATTTTCGTTTTCATTTTGGGTTGGTGGGCGGATTCGCGTTGCTTGAAGCTGCAAAACCGGTTTGGATACGCGGAAACGCGCGGTATCGCTTCTTT
GGGCGGTAGAGCGCGCTTTGTAACCGCAGGCGGAAAGCAGGAGGCGGTTCCGCGCGCAAAAAATACGCGTATTTTCATCGGTAACCTTCTTCATAGCGCGAATGTGGCAAGATTG
GCATCTTAACAAAAACACGCAAAAGCTA

SEQ ID 1052

LPAKQGHLPVFLVGRJAVCLEANRFGSRNPAPYRLWAGRGRLNRRNRKAGRLPPQKIRISSVNFHLKRECGKIRHLKQTRKKL

SEQ ID 1053

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SEQ ID 1054

MTTESEPIRASALEFHEIEDQIDENGWDFCRFAGNVLTIEAGDGTQIIVNRHPTNQELWIAAKSGGYHFAEQNKWLAIRDSRDPYDVLNZAASAASGEAVETAEAL

SEQ ID 1055

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SEQ ID 1056

VAFDGTASAVGGKAFARVVGELPQAVADDFQNARGQDRSGVPKTVGQVQNGHAFGNSQQLAVAGKQDGCVRRHGGFFRFPNFVRNKTGLGLVLPKHVQVFLKPSERVGPHQYPAAVSDSARNQ
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SEQ ID 1057

TTTCAAAGAAAAAGAAACAGATTGTATAAAACAATACCCGCCATTCTATCGGGCAAAACCGCACGGGAACATCCGCTTTTCCCGTTTCCACGCAATCCGGTACAGGCACCCCGCTGCCGAT
TCCGCCTGCACATCCGGCAAAATTTCATACGCAAGGAAAATGTTGAAAACAAAAAGAACTAATTGCTTGAAAAAAGATTAAATTGGAATCGGGGTATTTCAC

SEQ ID 1058

PQRKRRLIKTIPAINSGKTARNIRFPVSTTIRYRTPRCRFRLHIRQNFIRKENVENKKN*LLKRFNAGISH

SEQ ID 1059

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SEQ ID 1060

MYRHLEYYPCDPTLSLVETFKNDPRPEKVNLSIGITYFDDEGRNPFVLESVSRAETARAAAPSPSYLPMEGLDWYRSVAQHLLPGKNPALAQRGIVTVQTLGGSGALKVGADFLHGHFPEA
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SEQ ID 1061

ATGATTTGGGGATATGTTTTCGGATACATCTTCGACATTGTAGATGTGCAAGGCATCCAAAATCCCCCTCTTCGGAAGCGGCATAGAAGTAGCCCGTGTGCCATCATCTTCAAAGACAACA
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SEQ ID 1062

MI~~GD~~MFVGYIFDIVDVQGIQNPLLRSGIEVARVAIIFKDNTIRDMFGK

SEQ ID 1063

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SEQ ID 1064

MAQLPLRYTAEIGNFTVGTGPKVLESFSKHIPIYGVVFEDDGNFTGYFYAASQEGILDALHTYINVEDVSDKHIPNHLIL#DGACTIONALCINDYTHAVYDFVEQAGYCRNGPPEAGGENVKVE
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SEQ ID 1065

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GAGTTGAACGAATACCAATCGCGCACTTATCTGATGCACCTGCTCGCGAAGCGCAACAAATCGCGCAAAACGTTGTCGCGCGCAAAGTGGCGGTTAACCGAAACGGCGAATTGGCTTTGG
ATGAAGACCTGCTGCACAGCTT

SEQ ID 1066

MPLLDSPKVDHTRMHPAPVRVAKTHTTPKGDITTVFLRFCIPNKEILPEKGIMTLEHLFAGFMRDHLNGAGVEIIDISPHGCRGTGFYHSLIGTPSEQQVADANLASHQDVIANVKDQSKIP
ELNEYOCGYTLMHSLAEAOQIAONVLARKVAVNRNGDLALDESLIAA

SEQ ID 1067

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AAGCGGGTTTTTATGTCCAACAGACCTACACTCTCTCGTTGACGGCTCTTCCATCTCTACCGCGGTATCACGGATGGGGCAAAACC

SEQ ID 1068

MLSEGGFQTAFAFVITRGCTGAGFKPASSFPISVTPYRFQAGFLCPTDLESSSLTALPISTARITRGKT

SEQ ID 1069

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SEQ ID 1070
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TLQNSRLAKLKSTYTDKLEPMSIPDRNRVHTTYAQAVAITGLRLASNPNLQNIPIRTAEGRVRRRAFTAPPGSGVIVSADYSYQIKLRIMHLSGDKTLIAAPQSGDEVHRRTAEQVLPQAFPE
NVSPQRRYAKTINFLGIYMGQYGLAKSLIDNLSAKNFIIDRYPARPGVAYEYQRTKEQQAAGGVVETLPGRRLLYLPIDRKLNANARAGAERAINAPQGSTASOLIKRAMINVRNMLS
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SEQ ID 1071
TTGAGATGGCAGGCCTTTTGTGGATACAAGTATCCGACCTACGGCTTGCTATTGATTCCAATCATTCGAATCGGGTATTTTACTTCCTTAAATTT

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SEQ ID 1073
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SEQ ID 1075

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MI LHYFCYADISRDDKTGAKKPDWKIRIRLFCDLVFDLCANCRPERPRPVWQVGSNPTAI

SEQ ID 1077

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SEQ ID 1079
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TGGAGGGCAAGGCA

SEQ ID 1080
LPCRLKLFRRHHFVKCSNNMPKVTPYTHVDQIPLPTCLRLIARIAIRDGGRILVWSDSFGRLQELDKMLWQYEABSFIPHEIWETEEAMPSDTSVLLACDGNLPRIEGMAVLNLSDFWNT
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SEQ ID 1081
ATGCAAAATCATGACAAAACCGGCGGAGGTTACACAAACGGATGAAATCAACCGATATTCAAACACAGCCATTTTTAGCGCATTTTCAGCGTATCTTTATGCGGAAAAATTCG

MONHDKTGARLHKRMKSTDIQTQPFLAHFORIFMRKIS

SEQ ID 10383

GTGTTTCCCGGCAAAATCAAGTTGAGTTTGGGAAGAAATATTTTCTGGCAAGAAAGTATTGGTTGCTCAAATTCACAACCTCAGCCGTTTTGAGAATNGTCAGACGACCTTGTTGCAGACGGCAAAATATCAATGACAAAAATGATAGCCTCCGCGTCACTGGAAGACATCCAAACCATCTTGAACCTGAAACGTGCCATCAATATATGTGATTTCGCATATTTCAAACGGCGGAACCGGTCAATATTTCACTCCTTAAAGAAATCAACACATTTGTGCCCAAGGACGATCTTTGGTACCCGPGGATTTCGATACCGTTCGGTTCGGGCTAACCGCTATTGGACGGTTCCCGTCATCGCCGGAAATTCACCGGTGAAGGAAATTTGAAGTGGCCCGCGTGTGTGCAAAATATCGGACTGCAAAACGGGTTTCGACGACGGAAACAGCCGTTTCGTTTTCATGCTCTATTGTATCGGACGACAGGTTTTCGGACGGCAAGCATACCGGATATTCCTCAAAATTTGTATATCGGGCATAGACTATTTCCGGCGCGGACGAAGATATA

SEQ ID 1084

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VPUKRTFVARVLONIGIOGSGSTETAVRFLYCMRCQOVFDGDKKRTATLFLANGLMAGCGGILEISEQMMPRFNEKLSAFYRTGDDTDISKFVYQNCISGIDYFGADEI

SEQ ID 1085

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SEQ ID 1088
LPRILAVLELLSAASPCPDNLTHYRFPRLAEHLKINLTVIRRSRHKVAEKGV

SEQ ID 1087

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CGGCAAAATCGATGACGAAAGCCCGGATGATTGATTTTCTGTGGTATCGCGTAACGGCGTGGCGCATTTGGCGGGCGATCAATATATTGTGAGCGTGCACATAACCGCGGCTATACCAAT

[illegible]

SEQ ID 1088

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 TRSDWTGLASFCTEKFTITDKVIAISLSTKDIRGSGVADHAHLNLTGLATLNGSLNSAGGDTHYTVRNATQNGNLSLVGNAQAATFNQATLNGNTSASDNASFNLNNNAVQVNGSLFLSDNAK
 NVFSEHALNGVSLADKAAVPHFENSRPTKIRKNGKDTALHLDKSEWTLPSGTGLNGLNLDNATITLISAYRHDAAGAQTSAGAADAPRRRSRRSLVPTTSAESRNFNPLVNGSLKQGGTF
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SEQ ID 1089

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SEQ ID 1090

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SEQ ID 1091

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SEQ ID 1092

LGGRGFRFRAARGMWLYVRPGVFCRFCEMVQGRAGRKRGFLSTRSNWVAHKGILLATKSYTHLLYPRSPFSVGTPTPPSAVKTDRRRNAGQGFVPGVGISPTTSRQCCLKAEPSPDR
HLL

SEQ ID 1093

GTGTCCGCCGTACGGTAGCCGATATTCOCGAGTCTAACGGCAAAGGCGAATACAAAGTCTTTACCGCTTATGTTAAAGGCAAAGCCACTGCCGGCAATTTGAAAGAAAAA

SEQ ID 1094

VS AVTVADI PRSNGKGEYKVF TAYVK GKATAGNLK EK

SEQ ID 1095

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SEQ ID 1096

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SEQ ID 1097

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SEQ ID 1098

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SEQ ID 1099

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SEQ ID 1100

MTNFRFLVFCPCNDILLSFRNLSEKTETAPPSFRRRESSPVGTETRIKRF

SEQ ID 1101

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SEQ ID 1102

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SEQ ID 1103

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SEQ ID 1104

MCQRLKPDLDGFRHFLRSHRRPLSLGLYQAQSRNSPFPQLSVIPREVG

SEQ ID 1105

ATGCCCATTCCTTCAACCCGATTTGGCTGCCCGCGCATTCGCCAAGCGTTTCCCGCTTTCGCGGACGCCCGCGCGCAGTCCGCCCAACGCTGAAGCAATCACCGTTACCGCA
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GAAGTTC

SEQ ID 1106

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SEQ ID 1107

TGTTAAAGGCAAGCCACTGCGCGCAATTTGAAAGAAAAATAACGCACACCGCTCCATCGGTTTTCGTTCAACGAACGCCACGATATCGGTTTAAAGCAGATACGCCGAGCAAAACG
ATCGACAGCAAAAGAGGGAATGCACAC

SEQ ID 1108

C*QSHCRQPERKITHTVHRPFRNHRMRPKARYARSKNDADDERGNAH

SEQ ID 1109

ATGAATGACTACACGCGAGCAGCTTCAAGGTAAGAAAGACTACCTTAAACCCCTTTTGCAGGTTTGGATGTTCTGAGTGGGAAGTGTACGAATCTCCGACAAACACTACCGCATGCGG
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SEQ ID 1110

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SEQ ID 1111

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SEQ ID 1112

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SEQ ID 1113

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SEQ ID 1114

VSIPTATPLPAGVEFLSSDNGNIENINTAGAGSASDAPSRSRSLDAPQNTSGISIRQREVEKDYFYKSKETSFIKTPGGAQVALSSYADPITVSYSSPDFKLIPDRHAGQRLADGSRI
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SEQ ID 1115

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SEQ ID 1116

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SEQ ID 1117

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SEQ ID 1118

VPAPVCRVSTFVYSLTKTGTALPRLAVLSVLSAASSPCPDFC

SEQ ID 1119

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SEQ ID 1120

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SEQ ID 1121

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SEQ ID 1122

SEQID F122
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SEQ ID 1123

SEED ID: 1123

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SEQ ID 1124

SEQ ID 1124

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SEQ ID 1125

SEQ ID 1125

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SEQ ID 1126

SEQ ID 1126
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SEQ ID 1127

SEQ ID 1127

GTGCTAAATCCACGTTTATTCTCCTGATGTAGACGGTTGTGCGTAGTTTTCAGACGGCTTTTCGCTCAA AAAAGACCGTCTGAAGACGGCTGGCACGATTTGTACCCCAATTTTGAAGCAC

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SEQ ID 1128

VLNSTFILLIETVVGSFOTAFRSKDRDKTAGTIVPHFLKHRLKPCADNPPAPNRLPPP

SEQ ID 1129

SEQ ID 1129

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SEQ ID 1130

SEQ ID 1130

LPRIAMPYFALFDDAVSRRAKLYQNHVESRFFRPEELDALDGLQGWKGLHSVLFDATYFGLPLMGMESERGGNIALHWFADCA DTDABSWLARHSDGLPAGISTQSSVSETDYLDRI
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DGISLSHAVLNRLTDKQRVLI1SPTTLPQNYLRRFKTKTHRAIFDQAMQTAETQGWDSLFFNSDGLLGGERSNVFVKHKGQMLTPSLDLDITLNGIMRQAVSDEPKYLRTNQVLETHITQ
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SEQ ID 1131

ATGGCAATTCGGGCAAAATGTTTGTATACGCCCTTTTACACGGACAAAATGTAATTTTATGTAGAGAAAGCGGTGGCGAAAGTGTAAATTTG

SEQ ID 1132

MAIRGKCFDYTPLLHQNVLCRESGGSVKL

SEQ ID 1133

ATGGCAGACCGCAGTTCACACCGTTTGAACACGTAGAATTAGCGGAAAGCAAGACCGATTCCAGTATTTGAAAAAGCTGTTTGTGAACACGAAGGCAAGGTTCTGCCGAAGATTCCG
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CACACCCACACCGCGGACGCGCTTGGGTCAATCCGTTGCGACGACAAAACGCGCGCTTTGAACGTATCCGCTACTTCTGCAACCAAGTTGAGTACCCGGGTAAAGAGCTGAAAG
CCATCGGCAAGATGGACGATAAATCGTTCTTGTCCCGATACCGGTTACAAAGAGAAAACCATCGATATCGGTCAATGAC

SEQ ID 1134

NADRLQPPFENVELGKQDQFQVFEKAVLEHKGSAEDSGTVPLPENYPCRKRLRAAYEAKAKLQIELLKVQSWVKDSQQRIVSLFEGRDAAGKGTIKRPMELNPRGARVVALEKP
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SEQ ID 1135

TTGCGTAAATTCGCCAAGGCATACGCGGACGCGCGACGAGCTGACCGACCATCGTTGCCGAAGCGGCAAAACCAAGACTTGGCGCGCTGTGGAAGTGATGTTCACTGCCGACTATC
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SEQ ID 1136

LRKIAQGIRGADELDTIVAEKGKTKDLARVEVMPTADYLDYQAEWARRYEGEIIQSDRPRENILSPKRPLGLVIGILPRNPFFFLIARKMGPDLVTGNTIVVKPSSVPTINCHIFAEII
DAVGLFAGVFNVDGPGABIGNALSAHPQVDMVSLTGSVZAGQVMEASANTIKVSLLEGGKAPATVLRDADLDLAVKSLILSRVGTGQICNCAERYVHSSLDAPLEKHTAAMKGV
YGNPAEABAGAPFMGTLEBRAVKAIAEKVERAVRQGAQLVCGGKRTGGRYFFETLLTDTNDSMDIMKETPGLVLPVSADFTLDQVIALANDCEFLTSSVYTTNLNEAFYVTRRLQF
GEFYINRENFRAMQGFHAGWEKSGIGGADGKHGLEEYLQTVIYLETDI

SEQ ID 1137

ATGAAACAATTCGGCATGTATCATCAACGGACGCTTTGAAACAGATTTCAACGGCGAATGCGCGCAGCTATTGAACCCGCTCCACCGAAGAAACCATCGCCGCGGAAACCAAGCGCGCAGGG
CGACGCTTGACCGCGCGCGCGCGCGCAACCGGCTTGGGAGCGCTTGCCTCGCGTCAACCGCGCGCTATTTCGG

SEQ ID 1138

MKQLAMYINRGFENDFNGEWRDVLNPSTEETIAREPKGRADVDRGARGATGLGASACGRTRRVFA

SEQ ID 1139

TTGGTTTATTCCTCAAAATAAATTACCGTACAAGTTCTTTACACGCGGATTTTGGGTTCAAGTCAAATACCGCTTACCGGTTTCTTTTT

SEQ ID 1140

LVYSQINRYTSFFTRGFWSSQIRLTGFLF

SEQ ID 1141

TTGTTTCATTTCCGGCGCTCCAGTTTGTAGTCCGATGATGTTTGGTTTATTCCTCAAAATAAATTACCGTACAAGTTCTTTACACGCGGATTTTGGGTTTCAAGTCAAATACCGCTTACC
GGTTTCTTTTTAGTTTCCGACGGCGTCTGCCGCAAAATATGCTGAAATGCC

SEQ ID 1142

LFHFGSSFWGCSPLFPNKLFPKLYLTRILGFKSNTAYRFSPLVSAGVLPKYCLNA

SEQ ID 1143

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GGGCGCAAAACGTTGGCGCAACCGGCTATTGTTGCGCG

SEQ ID 1144

VEGSYRFDTLNNGISIHGGVTARCFSSRLAEPYVSFVLLLEGRDLPFGINRRFRIDADGGKIVLIVAGBEVLFSRYLYRGKTKVMTIKGMEQWLPFRPEYARFAPLLYREPVRINDLP
PNLRGLAASCLQTVPKHGLGETLRREADVRLRLSLDLDVSDGLEPAAGQTABADAMPSEDFSRITLNAAPDGAHQVNRITAAALNISERTLQRRMRDHFGITASEWLHKKMQHAYLLQLN
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SEQ ID 1145

ATGAGCGGGTGGCTGTCTATCTCCGCAACAAAACAGAAATAGCAATTCCTCCCAAGATGCCAACCTAAACTCCAAAGCGCGGTTCGTACGACGCGGTGTAATGTGGGCAAAACACTGA
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SEQ ID 1146

MSGVAVYLRNKNRIASQDANLNSKGRFVSSGLNVCKQLTGLSGVEFDPYRHRRAIRKSAEFVSNITTKTKTDEKPFNE

SEQ ID 1147

TTGATAAATCATAAATCGCGTCAGGGGGCGGTAAGCGGTTCCGCGCAGCGGATTTGTCGCGCAAGGTTTCAGACGCTGCTTCAAAAAATGGGTACAATCGTCCAGCGCTCTTCAG
ACGGTCTTTTGAGCGAAAGCGGCTTGAAAACTACCGACAACCGTCTCAATCAGGAGAA

SEQ ID 1148

LINHKIAVRGAVSQAQDCPRKVS DGASKNGVQSQPSSDGLLSERPSENYRQPSQSGE

SEQ ID 1149

ATGAGCCCATCCCCCTTTATCGAAATGAAGACGTCGCCCTTCGCGTATGGCGACCGCCGATTCGAACGACATCAATTCAGCATTCGCGAAGCAATTTTCCGCCGCGTATGGCGGTT
CGGGCAGCGCAAAACACGCTGATGAGGCTGATTACAGGACAGATTTCGTCGCGAGTCGCGGCGAGTTTGTATTGAAGGACGGGATTTGGCGGGTTTTCGCGCTGACGAACTCTACGAACA
CGGCCGCGTATGGCGTATTGTTCCACACGCGCGCGTGTATTACCGATTTCGCGTATTCGACAAATATCGCTTTTCGATGCGCGAACTGACGCAACTTCCGGAAGCGGTTATTCGCGAT
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SEQ ID 1150

MSPSFPIEMKDVAFYAGDRPILNDINFSIPQGNFAAVMGGSGSGKTTLMRLITGQIRPQSGQVLIBGRDLAGFSADELYEHRRMGVLFQHGALFTLSVFDNIAPFMRRLTQLPEAVIRD
LVLLKLNVAVLRGVEMLMPSSELSGMSRRVALARTIALDFRMLYDEPFTGLDPLISLGVLAHLISRVNKALRSTSMVTHDIEKSLIVDQVIFLAHGEIMPSPQEMRELDSPWVRQFV
GGLADGPFVARYPAQTSIQDQLLG

SEQ ID 1151

GTGTATTTTAAGGCTTATCGGGAAGACGGGCAATTTTCAGACGGCATACGGACGCGCAAGTGTGTGAAATGCCCTTGTGCGCGCGGATGTTGTCTGTGGCGAAAAATGTTATCTTTCA
AA

SEQ ID 1152

VYFKAYREDGQFSDGIRTSVVKMPLSAADCLLWRKMLSPK

SEQ ID 1153

ATGAATTTTATCCGTTCCGTCGCGGCGAAAAACCTCGGCCCTTATCAATCCTTCGCGAGTATCACGCTGTTCTGCTGAACATTTTGGCGAAATCCGCGACGCGCTTTCGCCGTCGCGCC
TGAGCGTGGCGCAAGTGTATTTTCCCGCGCTGCTGTCGCTGATGTTGTCGCTTTCGCGGCTGTCGCTGATGTTTGGGTTTTCGAGGCTATACGAGTGTGCGAAATCAAATC
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ACGATTTTCGCGCTGATTTTATATGACCGCGTGGATGTTTACAGT

SEQ ID 1154

HNFIKSVGAKTLGLIQSFGSITLFLNLILAKSCTAFARPRISVRQVYFAGVLSVLIVAVSGLFVGMVLGQYTLQSKPKSADILGTHVAASLLRELGPVLAAILPASSAGGAMTSEIGLM
KTTGQLEAMNVMVNPVARVVAFRWAGVFSMPLLASIFNVAGIFGAYLVGVSNLGLDSGIFWPQMNNITIHVDINGLIKSAAPGVAATLLAVHQFHCIPITSEGLIRASTRTVVSAL
TILAVDFILFAMMPTD

SEQ ID 1155

GTGGATGTTTACAGATTGACAGACTGCTCTGAAGACGAAACGCGGAACATCGGATATTCAGGAACCTTAATGAAAAAGAACATATTGGAATTTTGGGTCGGACTGTTGCTCTGATCGCG
CGCGCGCGGTTCGCTTTCGCTTTCGCGCTGGCGCGCGCGCGCGCTTCGCGGTTTCGAGCAAACTTACCGGCTTATGCGCGATTTTCGCGGACATCGCGGTTTGAAGTCAATGCCCC
CGTCAATTCGCGCGCTTATGCTGCGCGCTCGCGCTATCGCGCTTGACCCGAAATCTTATCAGCGAGGCTGCGCTTGTATTGACGCGCAAGTATCAGTTCAGACTGACGTTTC
GCGCAATTCCTGACTTCGCGGACTTTTGGCGCAACAGTACATCGCGCTGCAGCAGCGCGCGATACGGAACCTTCGTCGCGCGGACACCATCTCCGTAAACAGTTCGCAATGCTTCG
AAAACCTGATCGGTAAATTCATGACAGCTTCGCGGAGAAAAACGCTGAGGCGCGCAATTCGGAAGCCGCAAA

SEQ ID 1156

VDVYRLTDLKTKRGTSDIQSTLMKKNILEFWVGLFVLIGAAVAFLAFRVAGGAAGFGSDKTYAVYADPFGDIGGLKVNAPVKRAGVIVGRVGAIGLDPKSYQARVRLDLGKYQFSSDVS
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SEQ ID 1157

ATGAAAAATCTCTTCATCAGCGCATTTGGGATCGGATTTTGGAGCATCGGCATGGCATTTGCGCTCCCGCGGACGCGAGTGGGACAAATCCGCCAAAACGCCACAGGTTTTCAGCA
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CGCGCAAAAACAGCGTTGGCGAAAGAAATTCAAACCTGCTGATTCGCGACCTATTTCCGCGACGATGCTGAAATTCAAAACCGCGACCGTCAACGTCAGAGACAATCCATCGTCAATAG
GGCGGCAAGGAAATCTGCTCGTCCGTGCGGAAGTGGCATCCCGGTCGAAGCCGCTCAATATGAGCTTTACCACTACCAAGCGCGGCAAAATACCGTACCTACAGCTGCCATCGCAAG
GCACGAGCTTGGTTACCGTGTACCGCAACCAATTCGCGGAAATCATCAAGCCAAAGGCAATCGACGGCTGATTGCCGAGTTGAAAGCAAAAACCGCGCGCAAA

SEQ ID 1158

MKSSPISALGIGLISGMFAFSPADAVGQIRQNTQVLTILKSGDAASARPKAEAYAVPYDFDFMTALAVGNPWTASDAQKQALAKEFQTLIRTYSGTMLKFNATVNVKDNPIVHK
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SEQ ID 1159

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CTTCGCGACGGACGAGATTTCCTTGGCGCCCTTATTGACGATGGGATGTCCTTTGACGTTGACGCTGCGCTTTTGAATTTTCAGCATCTGCGCGGAATAGGTGCGGATCAGCAGGTTTG
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SEQ ID 1160

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KFGQRLFLRVGRGTFRVAIDRCQGTLEIEIENRIGFGFMACRSVAAPEDGQNLGVLADLSHCVGRGGKCHADAQNTDAQCADEGGFHHVDFPENGVCVLCFGFFRIALSVPLGEAGH
EFTDQVFQNHCRITGYGDSVAGSKVFRIAALLQPDVLFQAKRSQSLRGVNTAELILAVQIKAHPRLIGFRVKNPSADAPDQYACGFDGGLDLQYADVAEIGTVSFRVTAERARAARHS
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SEQ ID 1161

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CGAACTGTACGAAATCAAAGACTGGCTGAAATCA

SEQ ID 1162

MHTELKNGTLHIGGDITVKTLTGDAFGRFROOCLKETLAVDFGGVKRADSA~~CMS~~LLLEVLRGCKGSVRLTGIPESVRALS~~ELYE~~IKDWLKS

SEQ ID 1163

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TCGGACAAG

SEQ ID 1164

SECTID 116:
MAGNTPGQIPTVTTVTFGESHGAGLGCTIDGCPPELSEADIQFDLRRKPGTSHVTRREADOVEILSGVFEGKTTGTPTIALLIINTDQSRQSDYGNLATAFRPGHADYTYWHKYGTDRDYR
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VIEGAGFDSVTQRGSEHGDELTPQGFLSNHSGGILGGISTGQDICVNIAIKPTSSIIATPRRSIDIHGNPVELATGRHDCVGLRTAPITAEAMLALVILIDHALRHRAQNADVAADTPDISR
SDK

SEQ ID 1165

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CGGCAAAATCCATTTTGGCTCGGACTCTGCTCCTATGACACATCATCATGTTCTGTCATCGCAATCGTACTTTCTGGCGGTGCGCAGTATGCCACGCCAGCCCTTCTGGCAGGCGGTGGGCAA
AGTCTGCATTTGAAAGCGGAGAAA

SEQ ID 1166

MIYQRNLKELSFYAVGIFVLLAVLVSQAINLLGRAADGRVAIDAVLAVGVFWIGTPLLVLVAFISTLTVLTRY#RDEMSVWLSCGLALKQWIRPVMQFAVPVFAILLIAMBQLVFI
 PWAKRNSREYAEILKQKQLSLVEAGEFNNILKKNRGRVYFVETPDTESGIMKNFLREQDKNGGDNIIFAKEGN#PSLNDKRTLELRHGYYRSGTPGRADYNOVSFQKLNLIISTP#KLID
 PVSHRRTISTAQILGSSNPQHAEI#WRISLTVSVLLICLLAVPLSYFNP#RSGHTYNIILIAIGLFLIYQNGITL#FEAVEDGKTHFWLGLLPMHIIMFVIAIVLLRVRSMPSQFFWQAVGK
 S#TLKGGK

SEQ ID 1167

TTGTTTCACACAAACCGAAAATGCCGTCTTAAACCAATTTTCAGACGGCATTGTGTCCTTAAAAACAGTTTTTTTCAAGCGCGACCATACCAAACACCCACAGGTGCGCTTCCACCCCTTG
TACCAACCTTTGCTCCATCAA

SEQ ID 1168

LEHTNRKCR LKTNFOTAFVP*NTFFOARFYOTPTGCLPPFVQPLLHQ

SEQ ID 1169

SEQ ID 1169
ATGAAAAAACCGCGCTACGCATCTCTCTGCTGATCGGGTTCGCTCTCCGCCCTGCATTTGAGAAACCCGCCGCCGACCTTTATGAAGGCTACAACCGCGCGCTTCCAAATTCAAAG
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SEQ ID 1170

SECRET 170
MKTAYAILLLIGFASAPAFETRPADPYEGYNRAVSKFNDQADRYIFAPAARGYRKVPTPKPVRAGVSNNFFNNLRDVSFGSNILRLDIKRASELDVWVGINTTFLGLGLIDIAGAGGVPD
NKNTLGDTPFASGWNKNSNYFVLVPLGPSTVRDALGTGITSVYPKNIVFHTPAGRWGTTAAAAVSTREGLLDPTSLDEAAIDKYSYTRDLYMKVRARQTGATPABGTEDNIDIDIDELVE
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SEQ ID 1171

SEQ ID 1171

ATGCCCTGTCAAATCCGTGTCGGACGGCATTCCCTTCGTCGGAACGGACAGTCGACACTACAGATTGGCCGTATAATCCCTTTTTCGCGATACCCGCGGACAGCAAGGAAAAACCA
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CAATTCTCTACCTTGTCCGCCGCTGCAGAAACCGCCGACGAGATATGGGACGAAATCGAAGCCGTTTCGAAGACATTTTCGCCGCCGAATTCGCCGACTGGTGCAGAACGCAACCGAGTGG
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SEQ ID 1172

MSGID 1172
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SEQ ID 1173

SEQ ID 1173
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CTGGAAGGCTTGTCCGAA

SEQ ID 1174

MKLTVRNHLGDYGHVNNARYLEFLZEARWAFPEKRGMLHLAGLILIVARIDIRYSRPAVEGDVLQPSRLKTPGMRRIVLQTTITLPGKTAAREADITLMPVHAATQRTVSLPATLARA
LEALSE

SEQ ID 1175

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AA

SEQ ID 1176

MKKILTAAVALIGILLATVLIIPDSKTAPAFSLPDLHGKTVSNADLQGVFLINFWPSPCGCVSEMPKVTKTANDYKNKDFQVLAVAQPIDPIESVRQYVKDYGLPFTVITYDADKAVGQA
PGTQVYPTSVLIGKKGELIKTVYGEPPDFGLYQREIDTALAQ

SEQ ID 1177

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AATGCCCTGTCCGAGCGCTTTGTCCGCATATAATGACGGTAAACGGCAGTCCGTAGTCTTTGACGTATTGGCGGACGCTTCTATCGGATCGATGGCTGGGCAACGGCGAGGACTTGA
AATCTTTATTTTGTAGTCGTTTGCCGTTTGGTGACTTTGGGCATTTGCTCACACAACCCGGACAGGAGGAAACCAAAATTAATCAGGGTGACTTTGCCCTTCAGGTCGGCTGTGA
AACGGTTTTCCTGCAGGTTCGGCGAGGAGAGCGCGGCGCGGTTTACTGTCCGGGATGAGGACGCTGGCAAGGAGGATGCCGATCAGTCCGACGGCGCGCGCGGTGAGTATTTTTTC
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SEQ ID 1178

LRQRGIDFLVEFARIGPADISFEDFAFPADKDSRINLCABCLSDGFVRIINDGKRQSVVFDVLADAFYRIDGLNGEDLEIFVIVVCRFGDFGHPAHTTTRGGKPKINQDGFALQVGVG
NGFSVQVGGGEGRGFTVGDDEGGKEDAQCDGGGEYFPHSKASSARARVAGRLTVRCVAAWTGIIRVMSASAAVLPFGSVIVVSTMRMPGVFRRHENCNTSPSTAGRILYRMSMRATI
SMRPANSCISPRFSKNAQRASSRNR

SEQ ID 1179

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CCAACGTAATCGGACGGATTTCGGTGTAGCCCTCAAAGCGTTTGTGTTTTCACGGTCAAACTTGTGGTTGGTCAATAGAGCAGGCAATCCGGCCCATCATCATTTTTCGCCGACCCAG
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GCCAAAAAACCCGCGACCCGCTCTGCCGACGATGCCGATGCCGCGCATATA

SEQ ID 1180

MPSEAKTETMFLFQIIRPDITFRHSTFRQILFHRRRIACRQVRGRNVFCNHRACADRAASDGYARHHPAPRPDIVLQRNRTDFRVALKAFVFTVKLVVGRIBQAFRPHHIFADHQ
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SEQ ID 1181

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CGTGGTGAAAAAGAAATCTGCCGGAAGGT

SEQ ID 1182

MESKFFILLRFAGSVLPPSYMRGIGVRRVRGLARRVSPHIGRGVNIERGAYVFPDVLGDSGIGANCEICRGLVVGKVMMGPECLLYSTNHKFDRENKRFEGYTEIRPTILEDV
WPGRRVIVMAGVTVRGSVVGAGAVVTKDIPPYSLAAGNPAVVKNLPEG

SEQ ID 1183

AAACCAATTTTCAGACGGCATTTGTCCCTTAAACACGTTTTCAGCGCGACCATACAAACACCCACAGGTGCGCTCCACCTTCGTACAACTTTGCTCCATCAAACT

SEQ ID 1184

KPIFRRLSLKTRFPKRDETHKPQVAFHPSYNLCISIKH

SEQ ID 1185

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SEQ ID 1186

LIPSNLPQKNFLHFLIEYPLDETTENSEAELV

SEQ ID 1187

TTGAAAGGAAATCAAAATGAAACAAGGTATTCACCCGAATACCCGGAAGTTAACGTTACCTGCTCTTCCGGCAACAAATTCGTAACCAATTCGCAATGGAAGAAAGAAACTTTAACATCG
AGGTTTGTCTCCCTGTGCCACCCGTTCTATACCGCACCCAAAAATCTGTCGATACACCGCGCGGTGGACAAATTCACCAAAATTCGCGAACCTGTTCAACGCG

SEQ ID 1188

LKGNQMKQGIHPNYREVNVTCSCGNKFVTKSAMKEKFNIEVCSLCHPFTYTQKIVDTGRVDKFNKFGNLPKR

SEQ ID 1189

TTGTTTCATTTGATTTCCCTTCAAAAAGCGGGCATAGGGGATGTACCTATCCCTCAGACAGCTCGGCATTTCTGCTATTTCTGTGTTTCTGTCAGAGGATATTCGATAAAAAG

SEQ ID 1190

LFHLISFQSGHRCCTYASDKLILAIFFCCFKRIFDKM

SEQ ID 1191

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SEQ ID 1192

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SEQ ID 1193

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GCTATGCCACTGTGTCGGGCCAGGAAAAAATATTA

SEQ ID 1194

NGCFMIIQNVVPSIILYSGTAVDLLTYPNVIFCQKSRKDIINITYLGQFLGSVSLILLSLLPFVLDYTPSKETLGLGLIPIPIGLKVLILLGSDGSGIAKEGLRKDNKDLIFLVAMITFA
SCGADNIGVFVPYPTTLNLANLIVALLTFIVMITYLLVPSAOKLAOVPSVGETLEKYSRWFAVVVYLGIGITYLIEANSPDMLITVSCQEKIL

SEQ ID 1195

[illegible]

SEQ ID 1196

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LAGSPTPLVAHFLGQTFDGI PPVYLWVAAAFKHLLSPWAADFYDAARFAGVFPVAVIGLTSCGPAAGNFLGRHGRSVLVIHTIGCIGLIPVAHFLPNAFAAAAGLVLHGYLSARRRVTLAA
SFLILGTGWTLSLAAAYPAAFALMLPLPVLMPFRPWQSRRLMLTAVASLAFALPLMTVYPLLAKTQPALFAQWLNHYVFGTGGVRHIQTAFSLFYFLKNLMLFALPALPLAVHTVCKTR
LFSFTDGLIGVWMLAVLVLLAFNPRQRPQDNVLWLLPPLALFGAAQLDSLRRGAAAFVNWFGIMAFGLFAVFLWTGFFAMNYGWPAKLAERAAFYSPYYFVDIDIPMAVAVLTFLMLMA
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SEQ ID 1197

GTGCGGAAATCGCGTATAATTCGCGGATTAAACCTTATATAGTGGAATTAAATTTAAATCAGGACAAGCGCAGCAAGCCGACAGTACAAATAGTACGGCAAGGCGAGGCAACGCCGT
ACCGGTTTAAATTTTAAATCCACTA

SEQ ID 1198

VPEIAYNCAIKPLYSGNLNODKATKPOTVOIVRQGEATPYRFKFNPL

SEQ ID 1199

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CGGAAGGACCATGGCAACGGCCCTGACGATGTTTCCCTCTGTTCAGCAAAAAGCAATATCTCTCGCGGAGAAATTTTCTATGATTGATGTGTCCTCGCCGCCGCCGCTGTGTGGCGGGCTCG
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SEQ ID 1200

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SEQ ID 1201

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SEQ ID 1202

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SEQ ID 1203

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CAACGATTGGATCAGCTTTTCGCCCGCTTCGGCGGACAAGCGCAGCACAATATGGATACCTGTGCGGACAAGTCTCAGCCTTTTCGCAACGGGAGACCGGAGAAGGTATGGGGTTTGAATTG
GAGGAGTACCGCCCGCAGCAGCGCTCTGAAACACCTCTGCGAAACCGCGCCCGCGGCCAAAAAAGGTTTGAATTTGGTCAA

SEQ ID 1204

LQNPPFCRHHFIQAHHTFEPINPTSTKPYILRALCEWCSDNSLTPHLLVVMKHTRVPMQYVVRDNEINLTGATATQMLRIDNDWISFSARFGQAHDTIPVGHVLSLFARETGECSGFEL
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SEQ ID 1205

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AGACTTGAACGCGCGCTTTTGGCGCGGATATCGCAATGGCTTCGCGGGGCTATGCCCGGCGAGCGCTCCAGCTTCTGGTGGGAAACCGGATTGAATGTTAAACGCCGGAAGGAGAA
GGCGCAGGAGAACAGCATACAGAACATACAAACATTTTTTTCATGGTTTTTCTTTAAGGGTTCGCAACAACAAACCGCATCTTGCAGCATATGGCGGAT

SEQ ID 1206

EQ ID 1206
 LHRPFPYRSAGLSPAISLNPKEQKSAGGSRCPFLYRFPYFLTAGSTGLAGPFGAGAPTEAWSFSFASTAGMPFTLKSSTDLNAPPFCARYSAMAFAGMPGSASSFNWEFLNVRNRKGE
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SEQ ID 1207

EQ ID 1207
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SEQ ID 1208

SEQ ID 1208
MTQETALGAALKASAVQTMKKKQTEMIADHIYGYDVKFRKFKPLALGIDQDLAALPOYDSALIAEVLNHHCRPRYLKALARGGKRFDLNRRFKGEVTPPEQALIAQNHPFVQALQQQSA
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SEQ ID 1209

SEQ ID 1209

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SEQ ID 1210

SEQ ID 1210
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SEQ ID 1211

SEQ ID 1211
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SEQ ID 1212

SEQ ID 1212
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SEQ ID 1213

SEQ ID 1213
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SEQ ID 1214

SEQ ID 1214
METHRKTC SAVCFAPQ TASKPAVSIRHPSEDIMSLKTRLTEDMKTAMRAKDQVSLGTIRLINA AVKQFEVDERT EADDAKITAILTKMWKQKDGAKIYTEAGRQDLADKENAEIDVLFHY
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SEQ ID 1215

SEQ ID 1215
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SEQ ID 1216

SEQ ID 1216

SEQ ID 1217

SEQ ID 1217
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AGGG

SEQ ID 1218

SEQ ID 1218

SEQ ID 1219

SEQ ID 1219

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SEQ ID 1220

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VPDAGKNSVLMAEDGAIKRALVLFNRSRTAGDAKMRQQAQAEWRPATRGFDEKLLTAAQTAFDHGFYDMAVNSAERTURKLMYTLRYISPFKDTVIRHAQNVNDPANVYGLIRQESRF
VIGAQSRVGAQGLQVMPATAREIAKIGMDAAQLYTADGNIRMGTYWMAADTKRRLQNNKILATAGYNAGPGRARRWQADTFLBGAVYASTIPFSETRDYKVKVMTNAAAYASLPGAPHIP
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SEQ ID 1221

TTGAAAAGACAAAATGCCCTCTGAACAGCGCTTGCOCGAATATATGCGGAACTGCACCGCTTGGAAATGTTCCGACATAATTTATATTTTCAATCATTTGCCGTTGGGTCCGA
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SEQ ID 1222

LEKTKRLNRLPFLYAEFAPFLECFRENLYPSIICRIGANRCLPFPALSEHVARFLY

SEQ ID 1223

ATGPTAACCCGCGAAAGGAGAGAGCGCAGGAGAACAGCATACAGAACATACAAACATTTTTCATGGTTTTCTTTAAGGGTGCACAAACAAACCGCATCTTGCAGCATATGCG
GGATTACAAAAACCGGTACGGCGTTCGCCGCCCGCGCTCAAGGGAACGATTCCCTAAGG

SEQ ID 1224

MLTAEREKAQENSIQWNTNIFPMVPLRVANNKPHLATIWRINKNRYGVAPPRLKENDSLR

SEQ ID 1225

ATGCCGTCGAACTCTCTTCAGACGGCATTTGTTTTCATGACACATTCGCCGAGACATATAGCGTTCCCTATTATAGTGGATTAAATTTAAACCGGTACGGCGTTCGCTGCCCTGCC
GTACTATTGTACTGCTGCGGCTTCGCCGCTTCTGCT

SEQ ID 1226

MPSEPLFRRLFSLTHSRRLIAPVPTYSGLNLNRYGVASPCRTICTVCGFAALS

SEQ ID 1227

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CGCGCGCAAGCGTTTCAGATAGCGCGGACGGCGGCACTGGTGGCGAGGACGGTGCATCACTGCGGAATCGTATTGCGGCAAGCGGCAATCAAATCCTGATCGATGCCGAGCGCCAA
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SEQ ID 1228

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SEQ ID 1229

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GTTACCGGTTGTGCGAGCTTGCGCCACGGCGAAACAGGCGCGGGCGGAGGCG

SEQ ID 1230

MTLEPWAIEARRHIGLKEIPGAKNPTIVQMLKETGGFPGAASWYFDETPMCSLFGVGYCLKSGRAVIRDNWYRAKANSMSGLTKLEAPAYGCIJAVKPRGGGHVFPVVGKDAEGRILGL
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SEQ ID 1231

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SEQ ID 1232

VMSRHGAKLRRRYELGGIKFVIPGVPIR

SEQ ID 1233

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SEQ ID 1234

LTQLAGITAKAPRQQLYLRLPLCPTSGFVWVERQ

SEQ ID 1235

TTGTGCGAAGCGTTTATGCTGTTATGCCCGCAAGCTGTGTCAAATCGGAGGTTAAATTTTCTGAGGATATATCGGGAAGCGTTTTTTTGTCAATAAAGCAGGAACGGGCAACCATTTCC
GACAAATGCCGTCTGAACCGGCAAGGAGCGGTTCCGACCAAAACGGCAATGAT

SEQ ID 1236

LSERFSCYARKLCQIGRLIFVGYRESVFLSIKQEGNHFGQCLRKRAKAAVETQTAND

SEQ ID 1237

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SEQ ID 1238

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SEQ ID 1239

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SEQ ID 1240

HGYSAGKSTLLRLINLLERPDITGVNVCGQELTALDAAALRQARQNHGVFQQFNLLSNRTVAGNVAFPLEIAGWPSEKIKARVAECLEIVGLTERAGHPAQLSGGQKQRVGIARALAP
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SEQ ID 1241

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SEQ ID 1242

MADLTFEQAVSTVGMKDEIVRALGETFVHVLSTTFAVIFGTLLGVLLFVTSRRLQHYNKPVNFLNLNLNLMRAPFPVILMIAMI PATRAIVGSTIGPVAASLVLSVGLFYFARLVEQ
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SEQ ID 1243

ATGCCGTCTGAACGCCAAAAACCCCGCTATCCGAAAAATGCTATAAAATCCCTCTGTTCGCGGCAAAATGCCGTCTGAACGCCGAATCCGACGGCAGGACTCCCTGCCCTGTCATTTT
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SEQ ID 1244

HPSEKQKPRRYPKNAIKSPSRQMPSERRIRTAGLPACHFCLKPPQHQBKI

SEQ ID 1245

TTGAAGAAGGTTTTCATATTTTCTCTCATGTTGTGGCGTTTCAACAAAAATGACAGGCAGGAGTCTCCCTCCGGATTCCGCGTTACAGCGCATTTGCCCGAACAGGGGATTT
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SEQ ID 1246

LKKVFI FSPDVAVSVNKNDRQGVLPSPGVQTAFANRGIL

SEQ ID 1247

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SEQ ID 1248

MKTFPKTLSAALALILAAACGGKDSAPAASAAAPSDNGAAKEIVFGTTVGDFGDMVKEQIQAELEKKGTTVKLVEFTDYVRPNLALAEGLDINVPQHKPYLDDFKKEHNLDTPEAQ
VPTAPLGLYPGKLSLEEVKDGSTVSAFNDP SNFARALVNLNLGWLKLDGINPLTASKADIAENLKNIKLVEBAQLPSRADVDFAVVNGNYAISSGMKLFEALFQEPSPFAYVNWSA
VKTADKDSQMLKDVTFAYNSDAFKAYAKRFEYTKYPAAMNEGAAK

SEQ ID 1249

ATGCCGATTATCAAGCGCGTACCATCATCCGCTTTCCCATAAACCCGCTGCAACCGCAACCGGCTATTATAGTGAATAAACAGAAATCCGATAAACACGGATACAAATTTGCGGCAA
CACCAATATCCGA

SEQ ID 1250

MPIIKRRTIIRLSHKTACNGKPAIIVKKQKSDKHGYKLSATPNIR

SEQ ID 1251

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CGGCATCAGCGGGCGAGCGGTTTCCAATACCGCTGAAAGCTTTTGAACTTTTCCGCCCGCAAGATGTCGAAACGCACTTGTGGTATCGAAAGCGCGGAGATGGCGCGCTTCCGAA
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SEQ ID 1252

LSAPLASSESKPRNPPTTFAIPPSRAYSDRLNRFVIRILGVADNLYPCLSDPCFTTIIAGLPLQAVLWERRMMVRRLIIGISGASGFQYGVKALELLRAQDVETHLVVSKGAZMARASE
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SEQ ID 1253

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ATTACCGGCT

SEQ ID 1254

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SEQ ID 1255

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GCGCG

SEQ ID 1256

VGNIIILTFPLLRVIVFLSFLIFEEDMTRINPTQLWVSA

ATGGATCCGATTCGTGTTGTATTCCACATTATTGCCGGTTGGCATGGGCGATTTCACATATTTGGTGATTACCCTCAGGCCATTATTTTCATGGCGTTGGCGTTCGTCTATATCGGGC
AGGCGCACGATGCCAC

SEQ ID 1272

SEQ ID 1272
MAGETITAADYIKHQLQSITSLSDVTQGGGLKNLADSPFINLDVFFAVLLGVIGSPFLMRGAKKATAGVPGRFQAAVEILFEFVDDMCKSLIHSKSKKAVAPLGLTLFVWIFLMNAMDM
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SEQ ID 1273

SEQ ID 1273

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SEQ ID 1274

SEQ ID 1274
VRLPDDIDERQRHENKCLQGNHQNENRPGQTGNVVEYKQNRHDFNAAGSRPRATAKQGYQQEYQLARIHTAEQPHTVGYGFRKKLDVQQQKVRRCFCTERRTEQLVKPAAQSDFDVID
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SEQ ID 1275

SEQ ID 1275
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SEQ ID 1276

SEQ ID 1276
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SEQ ID 1277

SEQ ID 1277
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SEQ ID 1278

SEQ ID 1278
LIFTLLNLRLGVNQTGCTCTNGRIRPDYAPANGLTKANSSAMATPIKNAASIRPAIRNSLVCSPGISSGWRAEDSKYLEPTTIAIPIDAPNAPNATIKPHATAIKPIILNSLKKQRLNYKNKL
LGIKISGHRAPARYRRTPTP

SEQ ID 1279

[illegible]

SEQ ID 1280

SEQ ID 1280
VNINATLFAQIIVFFGLVWFTMKFVWPPIAKALDERAAKIAEGLAAAERGKSDFEQAEEKVAELLAEGRNQVSEMVANAERKAAKIVEEAKEQASSEAARTAAQAKADVBEQLFRARESLR
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SEQ ID 1281

SEQ ID 1281
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SEQ ID 1282

SEQ ID 1282
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SEQ ID 1283

SEQ ID 1283

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SEQ ID 1284

SEQ ID 1284
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SEQ ID 1285
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TGCCGAGTTTGAATTGAAATCACAAGTATTGCTGGACGAAGTGAACGGCGGCGCGTATCAACCTGATTATCGGTCGCGGTCTGACCGCCAAAGCGCGGAAGCCCTGAAACTGCTGCGCTCTACTGTCATTCGCCCTGCCGCAAGCGCCTGCCGGAAGACAAAGTCGGTTTATACCTTGGCGCAAAAAATGGTCGGTCGCGCTCTGCGGTCTGCGCCGAAGGACAAGCGCTGCGCTCCGGGTACTTACTGCGAACCCGCGCATGACGACGGTCGGCTCGCAAGATACGACCGGGCCGATGACCCGCGCAGAGTTGAAAGACTTTGGCTTGTTTGGGCTTCTCCGCCGATATGGTGATCGAGCTCTTCTGCCCACCCGTCTGCCAAACCTGTGCGATGTAAAAACCCATAAAGAACTGCCCGCCTTTATTTCTACCGCTGGCGCGGTGTCCTCGTCCGCGGCGACGGCGTCATCCACTCATGGCTAACCGCTCGCTGTTGTGCTGATACGCTGCTGATACGCTGGCGGACAGCCACACCCGTTTCCCATCGGTATTTCCCTTCGCCGAGGTTCAGGCTTGTCGCTCTTTGGCCGCGCAACCGCGGTAAATACCGCTCGATATGATCCCGAGTCCGATTGTATGTCCTTTCAGCGGCAAGTCGCAACCGGGCGTAACCTCGGCGATTGGTGGAACCGATCCCGCTTTACGCGATTAAACAAGGTTTGTCTGACCGTTCGTCGCAAGCGGTAAGAAAAACATCTTCTCCGGCCGCATCTTCGAAATCGAAGCGCTGCCGATTTGAAAGTGGAACAAGCCTTTGAATTGACGACGCATCCGCCGAACGCTTCGCGCGCGGCTGTACCGTGTAAGCTCAATAAAGAGCGGATTATCGAGTACATGAAATCCAACGCTGTGTGTATGAAAAATATGATTGCCAACCGCTATCAAGATCCGCGCGCTTTGGAACCGCGCATCAAGCTATGGAATAATGGCTGCGCAATCCCGAGTTGCTCGAAGCGGATAAAGATGCCGAATACGCGCGCGGTGATTGAAATCAACATGGACGACATCAAGAGCGCGATTATCGCTCGCCGACGACCCGCGACGAGTATGCTTTATGTCCGAACGCTCCGCGCACCAAAATCGACGAAGTGTTCATCGGTTCTTGATGACCAACATCGGCCACTTCGCGCGCCTCCAAACTTTTGGAAGGCAAGAGCGACATCCCGCTCCGCTGTGGGTAGCGCGCGCGCAAAATGACGCGCAAGAGTGTTCGCGCAAGCTCACTACCGCGTACTCGCGCGCGCGCGCGCTGTGAAATGCGCGGCTGTTTGGTTGTGTGTATGGCTTAACCAAGCCAAAGTACGCGGAGGTGCAATGTATGTCCTATTCGACCGCAAGTTCGCGAAGTCTGGGTGTAACCAAGCTCTGTTTACTTCGCGCTCGCGAGTTCGCGCGGATTATGCTTCCAACTGGGTGAAAATCCGACCGTTGAAGAATATCAAGCCAATATCGGCATCATCAAGAACAGGCGGATAAAATCTACCGCTATATGAACCTCAACGAAATCGACAGCTACAACGAAGTAGCCGAGACCGTGAATGTT

SEQ ID 1286

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KQSDIPVRLVWAPPTKMDAKELSDGHYGVLGRAGARMEMPGCSLCMGNQAOVREGATVMTSTRNFPNRLKGNTPFVYLGSAELAATCSKLGKPIFVEEYQANIGIENQDQKTIYRYHFN
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SEQ ID 1287

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SEQ ID 1288

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 CTMGFFDRDGEDALIVYDDL SKQAVAYTROI SILLRRPPGREATPGDVFYLHSLRLLEAARVNEHEV EKL TNGEVKGKTCGSLTALPIETQAGVSAFVPWNVISITD GQIPLFETDLFNAG
 IRPAINAGISVSRVGGAAQTRVKVLKGGIRLALAQYRELAAFSPQASDLDEATRQLHEGVETELMRQKQFSTLANAEMLTLWAINNGSYSDVPVAKALAFSEPLSFVRTQHPVELE
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SEQ ID 1289

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SEQ ID 1290

MAVGKELLTKIRSVNTQKTKTKAMQMVSTSKMRKTQERMSLARPYAEKVRVMVMSHLAQTNTHDGIPLLESHREIRRVGFIILITSDKGLCGGLNANVLKFLAQVQEYRNRQGTTEERIVCLGS
KGLMACQSIGLNVVASAVNLGDPPEKHEMLGQPLTELFRYEKHEKIDRIHLVYSGFVNTMRQEPMEVLLPIGENVIGDSAPKSPFSWEYTRYEPALAVLEYLVRRYLESVVYQALSDNEAS
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SEQ ID 1291

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SEQ ID 1304

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SEQ ID 1305

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SEQ ID 1306

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SEQ ID 1307

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SEQ ID 1308

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SEQ ID 1309

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SEQ ID 1310

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SEQ ID 1311

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SEQ ID 1312

MDIVFAADNYAATLCVAASVEAAHPDTEIRFVLDAGISENRAAANAANLRGGG

SEQ ID 1313

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SEQ ID 1314

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SEQ ID 1315

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SEQ ID 1316

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SEQ ID 1317

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SEQ ID 1318

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SEQ ID 1319

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AGAAAACCCGGATTTC

SEQ ID 1320

SEQ ID 1320
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RKPGFA

SEQ ID 1321

SEQ ID 1321

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SEQ ID 1322

SEQ ID 1322

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SEQ ID 1323

SEQ ID 1323

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GGTAATGGTCCGCGCTCTGGGCGAC

SEQ ID 1324

SEQ ID 1324
VNLNKHPLKLLDFTPEEITTYLDLAAELDAKAKAGREIQRMKGNIALIFEKTSRTRCAFEVAARDQGADATYLEPSASQIGHKESIKDTARVLGRMYDAIEYRGPAQETVEELAKYAG
VPVFNGLTNEFHPTQLADALTMREHSGKPLNQTAFAVGDARYNMGNSLLILGAKLGMDVRIGAQPSLWPSSEGI AAAAAAAKETGAKITLTENAHEAVKVGCFITDVTWVSMGEKPEW
QERIDLLKDYRVTPPELMAASGNPQVKMHCLPAPHNRETKVGEWIIYETPLNGVEVTEEVFSPAGIVFDQAEINRMHTIKAVMVAALGD

SEQ ID 1325

SEQ ID 1325

ATGCAAAACCCAGCTTATCAGCTTGGCTTCGCGCGCAGAGCGCAGGGCGCACATTGCCCGAACCTTCGGCAGTCGCGGCATCCCGTTCAGCTTTTCGACGCAGCTGATGCCGCTGTGAAAGGC
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ACCGATATATTGCCGTATTTGAGGATGATGTTCTGCTGGCAAAGACGCAGAAAAGTTCCTTGC CGAAGATCTTGGTGGAAAGAGCGTTTGAATAAGGATCCCGCTTTATCGCTCCGTTG
GAAACGATGTTTGGCGAAAGTATTGTCAGACCGGATAAAGCTCGAATTATGAAACACCGGTGATTCTTCTTGTGAGAGAGCGAACATTCTGGGACGTCGCTATATCATTTCCGCTGAGG
CGATGCGGTTTTTCTTGGACAGGTTTGGCGTTTTCGCCCGCAGCGGAATAAAGCGGTGATTTGATGATGCTTTACTTATTTCTTTGATAAGGAGGGGATGCCGTGTTATCAGGTTAGTCC
CGCTTATGTATCCCAAGAAATTTGCTTGGCAAGTTCTTCAGTCAAAACAGTATGTTGGGTAGCGATTGTGAAAAAGATAGGGAACAAGGAAGAAGACACCGCGTTGCTTGAAGGTGATG
TTTGACTTGAACGCGTCTTTGGGTAATTCGATAGGGAAGAAAGAAAGATGGAGCGTCAAAGCGAGCGGAGCTTGAGAAAGTTTACCGCAGCGCGGTCTATATTGTTCAA

SEQ ID 1326

SEQ ID 1326

NONHVISLSAAERRHAHTAATFGSRGIPFOFFDALMPSERLQAMAEIVPGLSAHPYLSGVEKACFMSHAVLWKQALDEGLFYIAVFEDDVLLGKDAERFLAEDTWLEERFDKDSAFIVRL
ETMFAKVIIVRPDKVLNLYENRSPFLLESEHCGTAGYIISREAHRFPLDRPAVLPPERIKAVDLMFTFYFFDKEGMPYVQVSPALCTQELHYAKFLSQNSMIGSDLEKDRQGRRRHRSRLKVM
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SEQ ID 1327

SEQ ID 1327
TTGGGGCGATTTTACCTAGCAGATGAAAAACACGGGATTTTATCCGAAAAAGCAACAATCCCCCGCGTCATCCCCGGAAGCGGGAATCTGGAAATTTAATCGCGCAAGAATTTATC
GGAAAAAACCGAAGTTTAAAGACCTAGATTCCCCCTCGCGGGGAATGACAGTGTCTCCATTTCTGATTTTAATCCCTATATTTACACAACTATT

SEQ ID 1328

SEQ ID 1328
LGRFYLADEKTRDFIRKSNNPPAVIPAKAGIWNFWNAARIYRKPKPKDLDSRLRGNDSVSLSDFNPLYFTYTI

SEQ ID 1329

SEQ ID 1329
ATGCCAGATTCTACCTGCCGAAACCTTTCCGTCGGACAACCGTCGACCTTCCCGACAACATCGTCCGCCACCTCAAGCTCCGCGCTCCGCCCAACGAAACATCACCTCTTTG
ACGGCAAAAGGCCAGGCACATACCGCAGCGCTGACCGTTTGGAAAAACACCGCGCCGAAGCCGAAATCTGACACGAGACACACACGCAACAGAGTCCCGCTCAACATCAGCTCATCCA
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GCCAAACGCCCTCGCAGCTGGCAGGAAATCGTCATCTCCGCGTCGCAAAAGCGCGCAGGAACACCGTTCCCCCGTACTGCCCATCATCGGTACCGTGAAGCACTCGACAAATATGCCGT
CTGAAACCAACAGCTGATTATGAGCATCAACCGCGCTGCAAACTCGCGCAGATCCGCGACCCGTCGGCGCAATCGTCTTATGCTGGGCGCCGAGGCGGCTGGACGAGACAGGAAGA
ACAAACAGGCATTGAAGCGCGCTTTCAGCGGTTACACTCGGAAAAACGGATTTTACGCAAGAAACCGCCCACTCGCGCCATCGCGCGCATGCAGACGCTTTGGGGCGATTTTACC

SEQ ID 1330

SEQ ID 1330
MPRFYLPENLSVGGTVDLFDNIVRHLNVLVRPNENITLFDGKGKAHTARLTVLEKHRAEATLHEEDTTNESPLNITLIQSISSGDRMDFTLQKSVELGYTAIQPVISERCIVRLDGERA
AKRLARQOEIVISACEQSGRNVTVPVPLPIGYREALDKMPSNWKLLMSINRACKLGDINHPSGAIVFVVGPEGGWTEQEEQAFRAGQAVTTLGKRILRTETAPLAAIAANQTLMGDFT

SEQ ID 1331

[illegible]

TGCGTTTCGGGCAAACTTCCAGCCGATGAGTACGCTCGCGCTTTCGGGACGATACGAGTATGGGACGACGCTGGACTGGTGTATCTGGGTCGGGGCTTATGATGTTTATGT
CCACGGCGGGCAGAGCTGTGGGATTTATGCTGCGGGTGGCTTGAATTTTCAGGAGGCGGGCGGAGGCTGACGACTTTGGAAGGCGAGGGTTTGGAGTGGTGAACCGTGTTCAAACGC
TCGGTCGTGCGCGCTGCAACCGAAGCTGTTTGAACGCTGGGTCGGTGGATACGGGAAAAACG

SEQ ID 1332

VLHRLQVVRHIAQTETNPRFLNTPSRKEDGSHLSEADIAAQTAFAAALFLLIDCPMLGEEMSRQEQSALHEQYSGERGLWIDPIDGTNNFVNLPHFAVSVAPVRNGRAELGVITYNPV
SGBCFYAERGGGAFNLNTRLPLRLVDKKNLEAIGVEIKYLSGLSSRMSTLAPFGTIRSMSSSTLDWYLCAGRYDVYVHGGQKLDYAAALIFEEAGGRLATLEGGDFWSGHEVFR
SVVALEPKLFERNVGVIRENQ

SEQ ID 1333

TTGGCTAAGTCTTCCACCTACCGGCTTAAACAAGCTATTCCACAGCTTGCCAACCTAACCTTCTCGGTCGCCACATCGCATTTGAATCAAGTACAGGAATATTAACTGTTTCCCATCGA
CTACGCACTTTCTGCTCGCTTAGGGGGCGACTCACTTACGCGGATGAACGTTGCGTAGGAAACCTTGGGCTTTCGGCGAGCGGGCTTTTCACCCGCTTTATCGCTACTCATGTCACAT
TCGCACTTCTGATACCTCCAGCACACTTTACAATGCACCTTCATCAGCCTACAGAACGCTCCCTTACCATGCGGTAAACCGGCATCCGAGCTTCGGTTATAGATTTGAGCCCCGTTCAC
TCTTCCGCGCAGGAGCTCGACAGTGAGCTATTACGCTTCTT

SEQ ID 1334

LPKSSYRLKQATPACQFNLLRPHLAPESSTGILTCFPTTHFCLALGADSPYADERCVNGLSASGLFTRFIATHVNI RTSSTLYNAPSAYRTLPHYAGKPAASAVIDLSPVT
SSAQDSTSELLRL

SEQ ID 1335

ATGAAGTTCGGCTTAAAGCGCACACTCTGTTTAAACCGTCCGAAGCGCTCAACATTTTAAAGCTTCGACAAACATTTACCTTAAAGGAAATCAATGCAAGTCTATTACGATAAAGATG
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GCCGAAGTTGACCAATTTGAAGAAGCGCGACGCTGGCATTTGACACAGGCTTCAACGCTGCTACAAACAAATCGTTCCGCGTCCGACTTGGACGTTGATTTGTTGGTTCGCCCAAG
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CGCGCGCACCAAGGCGGTGATTGAAACCACTTTCCGCGAAGAAACCGAAACCGATGCTGTCGCGAAGCAAGCGGATTTGTCGCGTGGCGTGGCGGAGTTGATCAAGCAGGTTTGA
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ACAATGCGGAGTACGCGGAAATACGTTACGCGCTGAAATGGTCAATGCTTCCAGCAAGAGCCATGCGCAATGCCCTGAAACGCAATCAACCGCGGAAATACGCAAAATGTTTATCCA
AGAGGGTAATGTCAACTACGCGCTATGATGCTGCCCGCGCGCTTGAATGCGGACCAACAGTTGAAAGTCCGCGCAGACTGCGTGCCATGATGCCCTTGGATTACGCGCAACAAATG
GTTGACCAAGACAAAAC

SEQ ID 1336

MKLPFRHRLFPNSEAAHQFKASTTYYLKGQMVVYDKDADLSLIGKTVIIGYSGQHAAHANLDSGVNVVIGLRHGSWKKAEAGHVVKTVAEATKADVVHLLPDETMPAVYH
AEVAANLEKATLAPAHGPNVHYNQIVPRADLDVINVA PKGPHTVRSEYKRGGVPSLIATVYQNSKARDIALSYAANGGTGGVITFTFREBTBTLDFGQAVLCGGVARELIKAGFE
TLTEAGYAPENATFECLHEMKLIVDLIFGGIANNMYISINNAEYGEYVTGPEVVNASSKEAMRNALRKIQTEYAKMFIQEGNVNYSMTARRRINADHQUEVKGARLRAMPHITANKL
VDQDKH

SEQ ID 1337

ATGAACACTCACCACCAACCCGCCCTGCCCTGCGGTTACGGCACAAGCTATGCCGGCTGCTGCCAGCGCTTCATCTGCGGCAATCTGCGGCCACCGCGCAAGCCCTCATACGTTCCG
GGTACGCGCATATGCTGCACTTATCGACTACATCATGCTACTACGTTCCGCGCACAACAACTTCTCGATGCCCGCAACTGATGCGAGTGGAGCAGAGAGCCGAATGGCTGGG
CTTGAATGTCATCGCACCCCAACCTCGGCAACAGCAGCGCCCAAGTGAATTTGAAGCTACTTCCAGACGCGCGAACCAGACAGTGCATACGAGCTGTCGCGCATTCGTGAAATA
CGGAGCAATGTTATTCATCGATCCGACTGTTCCGCTGCCATCATGAACAGCCCTGCATTTGCGGTTCCGGCAAAAAATTCAGAGCTGCTGCGGCAAAATATCTGCAACCTGTCGCA

SEQ ID 1338

MNTHHPPCPGSGTSYAGCCRP LHLRLPPTAALIRSRGAYVLHLDIYIATTPVAQQTFLDAARLQWRSRAEHLGLNVLIAHRLNKQHAQVEFAYFDQGNRTVHHLZSAFVKI
AEQWYFIDPTVPLPMKQFCICGSGKFKACCGKYLQFVA

SEQ ID 1339

GTGGTGGTGAAGTGTTCATTTTGTGTTGGGAATGCAATGCCGTGTAAGAGGGCTTCAGACGGCATGGTTGAAAGCCTGTCCGTTAGGGCATCAGCATGCCGCCGT

SEQ ID 1340

VVSVHFVWECKRLKGLQTAWLKSLSVRASACRR

SEQ ID 1341

ATGTCACGCGCAAAACCGCCGCCACCATCGAGTGGGAATAAAGCAGCAACAGGGCTGCACCGTCCGGCGCAGTCTTCGATTATCGGAAAAAGGAAAAATATGAGCACACAAGATTAA
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GATTAGCAAAACGTCGCGCACATGGGCGCGCAAGCGCGCTATTAAATTCGCGCAACCGCGAACCCTGAAACCTGATTGCGCGACATGAAAAAACGTTCCGCGCAACTCGACATTCG
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GCATGATGAAGCAGCGCGCGCGCGCATCATCAACATCACTCCGTGTCGCGGTGATGGGCAATCGCGGCAAAACCAATTAATGCGCGCAAGAGCGGCTTGAATCGGTTTTCGCAAAATC
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SEQ ID 1342

MSAANRPPSSGNKQQTGLHRPAQSFYDRKKGKMSQDLSGKIALVTGASRGIGAAIADTLAAAGAKIIGTATGESGAAAIKRLAQWGGEGRVLSNAEPETVENLIADIKTFGLDIL
VNNAGITRDNLLMRKREEDDIMGVNLKSVFRASKAVLRGMKQRAIRIINTSVGVGMNAGQWYAAKAGLIGFAKSHAREVSGRITVNCVAPGFIIDTETRALPESTRQTTAQT
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SEQ ID 1343

ATGACCCAGACAAAATCTCATCTCGACTTCGGTTCTCAAGTTACCGGGCTGATGCCCCGCGGTGCGCGAAGCCACGTTTACTCGGAATGCACTTCTTCGATATGCCTTTGGACG
AAATCAAGCGCTTCAACCCCAAAGGCATCATCTTTCGCGCGGCTTAATTCGTTTACGAATCCGACTATCAAGCGATACCGGTATTTTGAATTTGGGCAATCCGGTTTGGCATCTG
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TGCCGTATTCTCGCCGTCAAATCCGTGGCGTGATGGGCGACGGCCGCACTTTACGACTACGTCGTGCGACTGCGCGCAGTCATCACCAGGCATTTATGACTGCACACTGGGCAGAGCTG
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SEQ ID 1344

MTQDKLILDLFGSQVTRLTARRVREAHVYCELHSDMPLDEIKAFNPKGILSGSGPNSVYESDYQADTGIFDLGIPVLGICYGQPMAHRLGGEVQPGNQRFGYQVKRTDSGLTRGIQD
DAPNTLDVWMSHGDKVSKLPDGFVITGIDTPSCPJAMMENAEKQFVGIGQFHPVTHTKGGRALLNRFLIDICGAPQWTPMPTYIEEAVAKIRQVGVGSEVILGLSGGVDSVAALIHRAIG
DQMTCFVDEHGLRLNEGKQVMDMPARNLGKVKVITHVDAEQGFMAKLGVTDPEKKRKIIIGAEFIEVFDAAEKKLTNAKWLAQGTYTPDVTESAGAKTKKAHAKSHHNVGGLPENMKLKL
EPLRLDLFDNDEGLVAGLGLPREMVTYPPGGLGVRILGSEVKKKEYADLLRQADDIFIQELRNTDENGTSWYDLTSQAFVFLPVKSVGVGMGDRGTIDYVVALRAVITSDPFAHWAEL
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SEQ ID 1345

[illegible]

SEQ ID 1346

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LMTVWSVMTLSKIRKDMFARMLTLSRYHQETPSPGTLMNMLNLTQSVSNASDIFTVLTRDTMTVGLTFLVLLYNWQLSLIIVVLMFPLLSLSRYTRDRLKHVIDSQKSGTGMNVIA
ETHQGHVRVKLFNGQAQANRFDAVNRTIVRLSKITQATAHSPFSELIASIALAVVIFIALWQSQNGYTTIGFMAPIVANLQMYAPIKSLANISIPMQTWMFLAADGVCAFLDTPPEQD
KGTLAQRVEGRISFRNVVDVEYRSDGIKALDNFNLDIRQGERVALVGRSGSGKSTVVNLLPRFVPSAGNICIDGIDIADIKLCLRAQFALVSDQVFLFDDTLFENVYRSRPDAGEAEL
SLQANMLQSLISDASIPGLHQPIGSGNSLGGQQRVVALARAALKDAPILLDEATSALEDNESERLVQQAELRLMERTGTIIVAHRLTFTVESADRIIVMDGGKILBQTHDQLMFQNGY
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SEQ ID 1347

TTGACTTCGTTCCGCAAAAAGCAGCGCTCCCTCTTCAGGCTGCTTTTTCACGTCCGAACGGCAAAACAGCGCATATTTGCGCTATAATCCATCCCTACCAAACACCGACAGCGGCTCGCGT
TGCAGTTCCTCCGCCCTACCGATATGATAGAAAACTGACTTTCCGGACTGTT

SEQ ID 1348

LTSPKKPALFRLLFTSERQTAAYLRYNPSLPNHRQRLPLQFPFYRYDRKTDFTV

SEQ ID 1349

ATGTCCTTTCCGCAATCTCTCTCCCGCGGACAAGGTTCCCAAAGCCTCGGCATGATGAACGGCTTTGCCGGAACAGCTCATCGCTCAAAAACACATTTTGACGAAGCGCTCCGCCATATTGGGGCAGG
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SEQ ID 1350

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SEQ ID 1351

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SEQ ID 1352

VVDADLRLLDFNFGFECFKGVGGGPHQAAMGRNGYRQRQGAFGSGFGGSHGASGGGVACNHDLSGRVEVDGDFHFCALCGFGTNLPDLFTFQTONGRHCAYALRYGGLHQFGAQADEFDG
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SEQ ID 1353

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SEQ ID 1354

LWVGITQAAGSHRRVVDITLLDKHFCVPAGLDAFQGLAHGFFAGSIDHFRAGNVFAVLRIVGNVGVHIGNTAFENQVNDQPHFVQAEVSHFRFVTPGQGFKTCFDQLGHATAQYGLFAE
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GRFSNGFNMMAGCPGFFPRRAVAQTDEHVYTRIPQVSGMGTLTRTVTDGNGFAFDQOQIGITPVIDLHLISPKVNGCRSLKMLSGFGVRVQSVPLKQRLSSIRFPTLRFRRRTGRRRLG
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SEQ ID 1355

AGTAAGCAAAC TTGAAATCCCTACTTTGATAAAGCTTACTGCTTTGTTGTGTCTTAATCCTGCCCTTTGTGTTTCAGGATTAAGTCGATACAA

SEQ ID 1356

SKQT*NPYFDKAYCFVVS*SCLLCFRIKSIQ

SEQ ID 1357

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CATCTC

SEQ ID 1358

MKRQAPFKPHCAAFLSAVSLRLPVLGACTATLSLYAFALYGIDKRRRAVRGKRRIPEHRLLLPALPGGHTGAYLGSRHPEHKTAKKRPVVLFRITVSGNVLATCILIDYFVPPPELFVKLGQ
 HL

SEQ ID 1359

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SEQ ID 1360

SEQ ID: 1556
 MOYAKISGSGSYLPANRVNSDDLAQKVDTSDEHTARTGKIFRHIAAENEKTSDLAAEARRALADAKIANINDIDLIIVATATPDHFPSTATIVQQRKLGITNGCPAFDQVQACGAFHYAL
 TTNAYTKSGMAKNAKALVIGAEFTSRIVDNDRTTCVLPDGDAGAVVLSASDKPGITHSKLKADGNLYKLINVPQGILACGKVGSGSPYISMDGPGVVKFAVRMLSKLADDVIEEAGYTAEQID
 NIVPHOANRRIESTAKHLGLSDEKVVLPVODKFTSAASIPALDAGIRSGQIKRGQWILLLEGIGGGFAMGAVLLQY

SEQ ID 1361

ATGCGGCTCGAAGCAGCTTGGGCTTTCAGACGGCATTTCCCTTCACTTAAACACGCGTATCGGCAACCCGCCGCCCGCTCCACGGCAATCCGCATCTGAAACCAATCTGTATGCCAAAC

SEQ ID 1362

MPSEAAWAFRRHFLHLKORIGNPAPPVKGNDPLKTCIPNHTPIPVSVICTLPVLGNHFFAYNSRI

SEQ ID 1363

ATGCCGTCCTGAAAGCCCAAGCTGCTTCAGACGGCATCTTGATGTGTGGGTTTCCATCAAAATTTATATTGTGTCGGGTGTTTGTGTTTTTGTCGTGATAAAATTCGGAAATGATATTTTGGAATGTGTA
GAAATATTTTATAGAGATATCTGTTCAATAGGGTAGGAATATCCCAAGATTTCCCTTACCTTCCCGCTGTAATTTTCCTGTTTTTAAGGTTTTTTTACTTTTAAATATCCCGCGCTTC

SEQ ID 1364

MPSPSPSCFRHLDCNVSTKLYWCRCFLSDKFGNDILNCRNIFRLMFNRVGISODFPYLPVAVPCPKVFYFNIPAK

SEQ ID 1365

PTGCCAATAATACAAACAATTTTGAAGGGCGGGGATATTAAGTAAAAAAACCTTAAAAACAGAAAAATTACAGCGGGAAGGTAAGGGGAATCTTGGGAGATTCCTACCCATTGMCATATCT
CTAAAAATAATTTCTACAATTCAAAAATATCAATTTCCGAATTTATCAGACAAAAACAAACACCGGCCACCANTA

SEQ ID 1368

1P110TLEGGDIKVNLA TENYSKVRKILGDSYPIEHLKNI STIONILSKFIROKOTPAPI

SEQ ID 1367

TTGATAGAAATGAAAACATCGACGGTCGTTTFTGGCGGATTTTTATGGCAGACAACGGGGAGCGAATCCAAATCCCGGTTTGGAAAAATCTGCACATTAGGGAATCAATCGCTTTTTT
CGGTATCAAAATTTGAGAAAAAAGCCGGCGTCTTGTTTCAGAAATCATCCCCGAGCCGGAATTTGGCAATACCGAATTAACGTGTATTTTGAAAAAGGATATTATAGTGGATTACCAA
AACCGGTACGGCGCTGGCCCGGCTTAGCTCAAGAGAACGATCCC

SEQ ID 1368

1.IIPNKTSTVVEGGFFMADNGERTOTIPVLNPDIRINRFFSVSNFEKKAGVLVFRLLPEPEFGNTLTVYFEKGYSSGLTKTGTALPRLSSKRTIP

SEQ ID 1369

TTGTGTCCTTAATCCTGCCTTTTGTGTTTCAGGATTAAAGTCGATACAATCATCACCCAAATACTATGTTTGTGTTTCTTTTCTCTTGCGAGAGGTTTTTATCCTTTGCAAAGAAATAAAAAATC
AAAAACAACATCTGTGCTTTGTGTTGT

SEQ ID 1370

LCINPAFCVSGLSBYNHHPNTMFVFFSLARGFYPLORIKNONKLIVFVC

SEQ ID 1371

GTGTCGCCCTTAAACGGCAACTTCATTTCATCAATACGATTTCACAACGCTTCGGTTTGCCGCTGCAGGACGGAGCAAGGCTTGGAAATGCGCGCTGGCATTATGTTGTCATAAGCTGCT
TGGGATTTCCAATTTCACAGAAAAAACAACGGTTTCGGTTTGCCGGAATTCCTGATGGAGATGTAGCTGATGTGCOCTCTTCCGCAACGCTGGCTTTGACCAAGTCTTTAAACTGTGCTG
CAACGCTTCGAGTATTCGGTTTGACGGTAACCAAGTCGACAAATTTAATGTTGACATAAATCTCTCCGCGCTTCGTTTTCAGACGGCATTCAAAATACCATGCGGTC

SEQ ID 1372

WCRI NGNPTIHOYDFORPGFAVDGLDEGLEMRAGIMFVNSCLGFPPIPHENKTVRFADFLMEIVADVALFRTAGFDQFFKLCCQCFRVFRFDGNQCDNFNVRHKSLLPFVFGTAPKYHAV

SEQ ID 1373

SEQ ID 1373
ATGCCGTTTCTCAACCATAGACGACAACTGGACATATTGATGAAGATTGCGATTACGCTACGAAAGCTATGACGCGGAACATTTTACCCGCGCCCAACCGGCATTTCGGCTTCGAGCTGG
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CGTGAAAACTGTGGCGTTTGGCTTTGTGCCGGCTTCAATAATGTGATATTTGAAGCGCGCTGAAGAGTTGGCGTTGAAAGTCTGTCGCGGTGCTGCTATTTCGCCCGCAATCGGTTGGGAAACAT
ACGGTCGGTCTGATGCTGAACTTTGAAACCGCGCTATCCCAAAAGCTACCAAGCGTACCAGCGTACCCGCGATGCGAATTTTTCGCTGGAAGGCTGACCGCGCTTCAATATGTACGGCAAAACGCGGGCG
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ACAATACCAGCCGGGGCGGGCTGATTGACAGCGCCGCCCATCGAGCGGTGAAATGCCGGAAAAATCGGTGCAATTGGGCATGGATGTGTACGAGAACGAGCGCGAGCTGTTTTTGAAG
ACAAATCCAACGATGTGATTACCGACGACGCTGTTCCGCCGCTGTGCTCTTGTCATAACGTACTGTTTACCGGACATCAGGCATTTTTCGACGGAAGAGCGGTGGGTAAATATTTCGGAAGT
TACGCTGTCCAATATCCGCGAGGTTCGACAGACCGCGGATTCGCGGCAAGCGGTTCTGTCGCGACGGT

SEQ ID 1374

SEQ ID 1374

MPFFLNHRRLQDILMKIAITYGTSYDREHFTFRANRHFGFELEFFDFMLDAKTAKMAEGEAACIPVNDASRPVLEKLAQIGVKTVALRCAGFNVDLKAAREGLKVVRVPAYSPEVAEH
TVGLMFLNLRTHIKAYORTDANFSLGLELGFNMVYGTAGVIGTKIGIATNRILKGFQGNMILLADYPPCNPEVEKLGGRYVDLDELARSDIITLHCPATPNENHYMLNEAAFDKMDGVMIL
DFTFQNLIDCSAATRALEKCRITGALGVVYVNERELFFEDKSNVDITVDVFRRLSSCHNVFLTGHQAFITREALGNISFVTLNIREVGQVDCGNVVRADG

SEQ ID 1375

SEQ ID 1375
ATGTTTTTCATCTTATCAAATCATGGCTTTATGGTTAATCGGACGTGCTTCTATCTCAAATTCCTGTGTGATAAAGAAATTTCCCGGATTCCTGTTCCTGCAGCCGGATATCGAAA
TCTTCGATATAAGTACACAGGATGTCAAAAGCCAAAACGTTCCGAATPAATGAATATAATCCAATCGCGATTCAATCAGACGGGCATCAAGCCTGCCTTCAGGGGATTTCCGAATCTCA
TCATCCGTTTGTCT

SEQ ID 1376

SEQ ID 1376
MPCPLGNNLWVILIGRAEYVLEFLVDKRNFGGFLPROPDIKIFDLSODVKSQKTFRRIMNIIQCGFNQGLKPAFKGFSLEHHPFV

SEQ ID 1377

SEQ ID 1377
ATGAAGACATTAGAAAAACGGATGAAAGCTCTAGACAAACGGATGATGAAGTTTCGGAAAAATCCCTTGAAGGCAGGCTTGATGCCCTCTGATTGAATCCGCATTGGATTATATTCATTATT
CGGAACGTTTTTTGGCTTTTGACATCCTGTGTACTTATATCGAAGATTTTCGATATCCGGCTCGACGGAACAAGATCCCGGAAATTTCTTTTATCAACAAGGAATTTGAGATAGAAAGCAC
GTCCGAT

SEQ ID 1378

SEQ ID 1378
MKTLEKRMKALDKRMKPGKSLGRLDARLTESALDYIHYSERFLAFDILCTTYIEDFDIRLTEQESRELSFINKEFEIESTSD

SEQ ID 1379

SEQ ID 1379
ATGACCGCGCAGCAAAACCGCAGCTCCGCCAAGCCCTGAACCGCGCAGGCGCGCGATGGAACGCATCGCATCTGCCATACCAACCCAAAGTTGCGCAGGATGAATCCCTCAGTCCGCC
TAAAGAACCAAAAAATCTCTCCATFCGCGGTGGCCATCAACCAAGTTAAAGAAAGCAAAAGCCCAAGCGCGCGTATCCGAGGCAACAACGGGCGCGCTCATGGCAACCGCAGGTTTGCTCT
CAAGACATATACCCGCATCGAACGCCCGCCATCGCCAAATCTCTCTCCGACACCGACCACTGTTACCTTCGCCCTCGCATCTCGGCGCAAAACGTCGATGCAACCCGAAACAGCTTGCC
CAATTTGCGCTCATCGGCAGCGAACTCGTCCACGGCTCCATCTCTCAAAAGGACAGCCGCGCGCTCGGCTGGTCAACGTCGGCAGCAAGACATCAAAAGTACGGTAACCGTCAAAACAA
CCTACAACTGCTGCAAAACAGCAAACTCAACTTATCGGCAACATCGAAAGCAACCGCATCTCTGTGCGCGAAGCAGATGTGTGTGTCGCGACGGCTTTGTTCGCGAACGTCATGCTCAA
AACCATCGAAGGCGCAATCAAAATCTGATGAGCGAGCATTCCGCGCGAATTCGCGCGCACTGTGTCAACAACTCTGTCGCGCGCTTGCGCGCTTACCGCGCTCAAAGGCTTGAAAAACAA
CTCGATCCGCGCGAGTTCAACGGGCGCATCTCGCTCGGGCTTCGCGCGCATCTCATAAAGCCACGGCGGCACAGACAAAACGGTTTCCGCTACGACCTGGAAGAGCCTTACCACGAAG
CCAAGTCCGCGCGCTTTCCAAAATCGAACAAAGGCTTGCCGAACAACTCGCGCATCTGGAAGCCGCCAAAACGAAACCGCGCGCAGTCTG

SEQ ID 1380

SEQ ID 1380
 MTGDETQLRQALNAAGAFMERIDICHTTQVVGMDESPQSALKNNKYSSMRVALNQVKEGAQAASAGNTGALMATARFVLKTIPTGIERPAIAKFLPSDTHVTLALDLGANVDCTPEQLA
 QFAVIGSELVHALHPQKGQPRVGLNVGCTEDIKGTDTVKQTYKLLQNSKLNFIIGNIESNGILYGRADVVDGFGVGNVLIATLEGAVKFMGSAIRREFQSILFNKLAVAALPAKGLKNNK
 LDPKRFNGAILGLAGIVIKSHGCTDKTGFRYALKEAYHRAKSAGLSKIBQGVABQLAALAAQNETAASL

SEQ ID 1381

SEQ ID 1381
TTGGGGCTTTTGAATATTTTCACGGGGTATTATACGGAACGCTTTGCCCTTGTTGTTGACGTATGGCGGAAGCTTTGGACGGATGGTGCCCTCCAAATCAAAAAAGCCAG

SEQ ID 1382

SEQ ID 1382
LGLLEYFHGVLYGTLCPCVLTYGESLDGWCVOCKKSQ

SEQ ID 1383

SEQ ID 1383
ATGAACAGAAAAATCTGGTACACCTACGATGACATCCACCGCGTCATCAAAGCATTTGGCAGAAAAAATCCGGAACCCGGCGTCAAATACGATGCCATGCTATCGGCGGGCGGCT
TTATTTCGGCAGCGCATGCTGCGCTGTTTTCTGGAATATCCGATTATTCGCGTAAACACCGCTATTACGACAGCAGCAGCGAAGGACAAGTTACCGAAGAAGTCAAAAAAGTCCAAATGGCT
AGACCCCGTCCCGAAGTCTCTGGGGGGCAAAAACGCTGCTGCTGCTGATGAAGTGGACGACAGCCGCTAACCATGGAGTTCTGCTGAAAGAACTGCTCAAGGAAGACTTCGACACTGTC
GGCGTCGCGCTCTTGACGAAAAAATCAAAGCCAAAGCAGGCAAAATCCCGAAGCGATTCCCTATTTCAGCGGCATTACCGTAGAAGACTGGTGATCAACTATCCGTGGGACGCACTCG
ACATCGACGAACAACACGCGCTTGCCGAAGCCGATCGAGGC

SEQ ID 1384

SEQ ID 1384
MKQKIWYTPYDDIHRVKALAEKIRNAGVKYDAMIAIGGGFI¹PARMLRCFLEIPIYAVTTAYYDS²SEGQVTEVKKVQNLDPVPEVL³AGKNVLVVDVDSRVTFE⁴PCLEKLLKEDFTV⁵
GVAVLHEKIKAKAGKIPEGIPYFSGITVEDWNIYPWDALDIDHNRLAEADRG

SEQ ID 1385

SEQ ID 1385
TTGCTTTGTTTGTGATTTCGGCTTCCAAATTGTTAAAGATCGATGCGTCGTATTCTACTTCGCAAAATCAAAATAAGCTGCTAAAAACAGCAAACTGCTTTCATTGTAAAGTTTG
GTGAGGCAAACGGGATCGAACCGATGACCCCTGCTTGCAAAGCAGGTGCTCTACCAA

SEQ ID 1386

SEQ ID 1386
LSLFVDFGFPIC*RSMRRYSTSQIKISC*KQOTCFHL*SPFGGKDRDTDDPILLAKQVLYQ

SEQ ID 1387

SEQ ID 1387
TTTGTGTTTTGAAATGCGAATGCCGTGCATGAAATCAATTTTAATCGCCATATTCTACTGATTTGTTTGAATTCGGTGTATTATGCCGTTTCTCAACA

SEQ ID 1388

SEQ ID 1388

SEQ ID 1389

SEQ ID 1389
ATGGTATTTGAAATGCCGCTCGAAAAACGAACGGCAGGAGAGATTATGTGCAACATTAAAAATGTGCGCACTGGTTACCGTCAAAACCGGAATACACGGAAACATCGGCAGCACAGTTTAAAG
AACTGGTCAAAAGCCAGCGGTCCGGGAAGAGGGCACAATCAGCTACAATCTCCATCAGGAATCGGCAAAACCGGTTTTGTTTTCGTGGAAAAATGGAAATCCCAAGCAGCTATTGACGA

SEQ ID 1390

SEQ ID 1390
MYFCECRKNRQERFMSNIKIVALVTVKPEYETELAAQFKELVKASRAEEGNTSYNLHQEIGKPNRFVFPVENWKSQAADENHASAHTQAPVQSVDGKTEALIVLMNEVAV

SEQ ID 1391

GTGTACACGATTTCTGTTTCATCGGAATTTCTTGGTGGTTGGGGCTTTTGAATAATTTTACCGGGTATTATACCGAACGCTTTGCCCTGTGTGTGACGTATGGCGAAAGTTTGGAC
GGATGGTGGCTGCTCAATGCAAAAAAGCCAGTAATTCATGGCAATGTTCTGGCTTTTTCAGTCAGTCGAATAGGGATTTATGCGCTTTGGCTTTTGACCATTTTGGCGCGCGGTACATACC
GTTGGGGAGATGTGGTGGCGGGGTGTACTTCCCGGTGTGCTGTCGACAAACAGTGGCGGGCGGTGAGTGGTGTGCGAACGGTGATACCGCGTTTGAAGGGGATTTTGTGTT
TGT

SEQ ID 1392

VYQIFCFIGISLVVGFIFSRGIIRNALPLCVDWVRKFGRMVRPMQKPVIAWQCSGFFSQSNRDYSPLALTTLRPRYIPLGEHWGCRCTSPVVLSTNSAGAVSASCERCIPRLEGDFL
C

SEQ ID 1393

ATGCACCGTTCCGACGACGCACTGACCGCGCCCGCACTGTTTGTGACAGCACAAACCGGGAAGTACACCGCCGACCACATCTCCCCAACGGTATGTACCGCGCCGCAAGAGTGTC
AAGCCAAAGGCGAA

SEQ ID 1394

MHRSHDALFAPALFVDSSTGEVHRPHHSFNGHYRGRKVVKAERG

SEQ ID 1395

ATGTCAGACCTTAATTTGATTGACCGGAAATTTTGGCGCCGAAAGCGAGAACCTGCAAGGCACTTTTCTGCTGGAAGAAATGGACGAGCGAGTCAGTTTGCACGATTATCCCGCCGACA
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GTTTCATGCTCGATGAAAGCAGCGGTATCATCTGTTTTCGACGAAGAGTCTTGGACGAATCCATGCTTGGCGACGAAGAACTCGAAGGCATACGTGATTGAAAAAGAACTCGACGTGCC
GCATTTGTAGAGACCAAACTCTGATGTCCTGCCCTTTTGGCGCGACGACGACACTGCGCAATACCTTCCGGAATCCGCCAACAGACAAACCAACCCCTTTGCTGTTTGGCGG
GTTTGAAGACGAT

SEQ ID 1396

MSDNLIDPELFAERQNLQGSFLLEELDERVSLHDYPADRRNKISFTLTGGRDLRLFLDLNVKADHPLICQRCIKPHFPHLDESSRIILFSDEESLDESHLADDELEGILIEKELDVR
ALVEDQILMSLFFSPRHGCHGNTLPESANQDKFPFAVLAGLKSS

SEQ ID 1397

GTGTTTCGGCGCATGGCTGGATTTTACCGCCCTTCGGGGCTGTTTCAACGGTAAGGAGGATGGGATGGGTTTGGAACTGCTTTGGTATTGGGTACGAGTTTCGGTTTCCCGCCGCAAC
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GCTATTTGGAGCGCGAGCGGATGCGGTTTATTTGTTCTGTTGCGCGGAAAGCGAGGGCTTGGGCGCGCTGTTGATCGAACGGATTGAAAGTACCGATCCGAATGCGCTTGAATGCTCGC
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SEQ ID 1398

VFRMAGFYRPFGRVFNKEDGMLFLVLGTSSVFRREQMERLGIAPQASPDFDETFLGESAPQALRLAEGKARSLTGRPPGALIVGADQVWCDGRQWKGPMNLANAQKMLHLS
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SEQ ID 1399

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GAAACCTTTGCAAGAGGGCGCATATGGGATTTGTCAGCGAGCGGGTTGCCCGCTGTTCCCGATCCGGGCGCAATTTGGTGGCATTTGGCGCATAAACACGGTTTGAAGTACGGCT
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TACGGATTGACGTTGCCGACTCAGTTGGTGGTCAATAAACGGTTGCGGATTTGGCGAGGATGAAGGAAATGCCAATCTGAAAAACCGCGAGCATTTTGTGATGTATGCGGT

SEQ ID 1400

MSGMSFVLYLIPITPLGTFDTPCLLQHEQRAVVGITDFVVEAKTARAHKLHGIITPIREINLQTLNEHTDLKTLPELLKPLQEGRSNGIVSEAGCPAVADPGANLVALAHKHGFVVRP
LVGPSSLLALLAMASGANQNFAPNGYLPSEKNERIQSLNALEQRSQCGETQIFITETPYNDALLADAVENLHPETRLCTADTLPLTQLVSVKTVADWRHREKPNLKKRPTIFVMYAG

SEQ ID 1401

TTGGCGCAGGATGAAGAAATGCCAATCTGAAAAACGCGGACGATTTTGTGATGATATCGGGTTGAAGATTTCCGCCCGATAGGGGGTGAACAA

SEQ ID 1402

LAQDEGNAQSEKTPDDFCVCGLKISAFIGGEQ

SEQ ID 1403

ATCGAGGTTTCCACCGCATCGGCAAGCAGCGCATCATTCGGTAAGGCGTTTCAATAAAAACTGCGTCTCGCGCACTGCGCGGAACGTTGCTCCAAAGCATTCAAACTCTGAATGCGC
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SEQ ID 1404

MQVFHRIKQRIIAVRFPKNLRLAALPRTLLQSIQTLNALIFFRQITIKRKVLPIRTSRHQQQAGRADQRPYFKTVFHRQCHQIRARIGNSRATRLADNPHTAPFLQRFQFQSLQ
IRVFIQRLQIQFAYRRYPQLQMRTRRFPFDKIRQDNRPLFMLQARRVRRTOQRNNOIQNRHSLTHRLKMPSEPPRRHKRAVTKHPRPRPSKNRPGKPADQSRHSRDYFQSVR
STARPSPRFSPHTNNKPHPARAPNSGCCAARPTASSRPPSTRYADASC

SEQ ID 1405

ATGCCCGACGATGAAAAATGCGCTGAAACCTGTTTCAGACGGCATTTTATTTGTTACCCCTATCGGGCGGAAATCTTCAACCCGCATACATCAAAAAATCGTGGGCGTTTTC
GATTTGGCAITTTCTTCTCATCTGCGCAATCCGCAACCGTTTACTGACCAAC

SEQ ID 1406

MPQHEKCLRPVQTAFLFTPTTGGMLQPAYITKIVGRFFRLGISFLRQSATVLLTIN

SEQ ID 1407

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SEQ ID 1408

MDFKRLTAFPAIALVIMIGWEKMFPTPKVPAPQQAQQAATASAAALAPATITVTITVQAVIDEKSGDLRLRLTLKYKATGDNKPFVLPDQKEYTYVAQSELLDAQNNILKGI
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IVKAVLPIPTNASTRSNAKMAAPKLQTIKEKYGDHMAQQMMQLYKDEKINPLGGCLPMLLIQVPIGLYWLFPASVELRQAPWLGWITDLSRADPYITLPIIMAAHMFQYTLNPP
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SEQ ID 1409

CGACACGAGCTGACGACAGCCATGACGACCTGTGTGTACGCTCCCGAAGGCACTCTCCGCTCCGAGGATTCGCCACATGTCAAAACCAAGGTAGGTTCTTCGCGTTCATCGAATTA
ATCCACATCAT

SEQ ID 1410

RHELITAMQHLVCGSRHSSVSGGFRTCQNVRFALHRINPHH

SEQ ID 1411

ATGCGACATATCTTATCTGTCTGATCGAAAAACGAATCAGGTGCGATGAGCGCGTGTGCTGCTTCTGTCACGCGATTACAATATCGAATCTTTGGCGGTTCGCCGCGACCGGAAGCA
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TGTGCAAGCGCAACTGATGTGTGTAAGTCCGTGCCGCGGCAAGACCGGACGAAATTTTACGCTTGACCGAAATCTACCGGGGCGCATCATGACGTAACCGACCGCAGCTATATGA
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AAATT

SEQ ID 1412

MRHILSVLIENESGAMSRVVGLFSARDYNIDSLAVAPTEDKTLRMTIVTHGDEQVIEQITKQLNKLIEVIVVDLINESRPFVERELMLVKVRAAGKDRDEFRLITETIRGSIIDVIDRSTT
TEITGSTDKLDSFLETVGRAQILETVRTGAAGIGRGERILKI

SEQ ID 1413

ATGATGGGGCTTTGCTGAAAAATTGGAAGCCGCTGCTTATTTGTCCGCAATCGCGTCTTTCGCGCTTCTTGGCAGCTGGACAGGCGCGCGCAATACCGTCCGCGATACGGTCCGCGG
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TGTGCAACCGCTTAAATCATPTGAAACCTGTGTACCGCAATGCTGTTTGTGATGCTGACGCGGTGCGCGAACTCAACCGCGCGTTCGACGACGCGGT

SEQ ID 1414

MTGALLKNWKLILLSAIAFFAVSWQLDRAAQYRRGYGAANVSEVSERLKAAAVEHAZHARKSSAAYQAQKAAREEKERVYVQTLKIIEKPVYRNACPDAGVRELNAAVDDGG

SEQ ID 1415

GTGCAAACTCCGCGTCGATGAACTCTTGGCGGAATCAAGCTGTATCCCGGAGTACCTTTTATCCGTTGAGCGATGGCCCTTCCATACAGAACCCGATCACTATGTCTGCT
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ACCGGCCCACTCAAACTGCTTACCATGACGCTCCCGACCGGATGACGGGTGCGGTAGAACCTCAAGACACACGAGGTGGTATTTTCAGGACGACTCCACAGAGACTGGCGTCTT
GCTTCAAGCTTCCACTATCTTACACAACTGACTTCAAGTCCAATGCAAGCTACAG

SEQ ID 1416

VPNSAVDMNSWAESSLLSPEYLLSVERMPFHTPEPDHYVLLSHLPDLVSQSLSYLLPLHYQSDFRPDLGNLRTPLRFRGRRPQSNCLPCTVPDPDGGSGLEPQRHQGGIFKDDSTETGVF
ASKPSTYPTQVTSKNALQ

SEQ ID 1417

ATGGGACAGTACAAGAAGCTGTGCTACTTGTGTTTGGCGTTCGCGGTATGCTTTACCATTTCTGGCTATATGGGACGAGGTTTATAAGAAAGCCCGCTTACCCGCAACAGGTG
TTTCCGCACTCCGCAAGTCTGATGACGAAAGACGATATTTTGGCAGGTCACTGCGTGGCAGATACCGCGCATGGAAGTCGTTTCGATTCTGGGTACCGCGCATATCAGGCTCC
GACTGGACGCGCGCATGGCTGATCTGTGATTTGCCCTGTTGGATTGACCGCGCAACAGACTTACGGCAAAAAATTCGATGAAGTTTCCCTGAAGAACAGCCGTTCTGAAACCC
CGCTTGGCGGATGANTACCGCAATCAAGCCGTATTAAGAGACGCGCAGCTGCTGATCAAGGATGAGGCGGTGAAAGCATGCAAGGATCTGCTCTTACTATACCGCGTTTACGCGG
ATGATCCCAAGTTCGCAACCAACCGCGAACACTTTGCAATGAAAAACACACATTTGCCAAGCCAAAGAGCGCGTGAAGAACTGTTCGACTTCTTCTTCTGACTTCTTGTCTGCTTCGAC
CAACCGTCCCGCGCAGGTCTTTTACCTACACCAACAACTGGCGCGCAGGCTTTGATCAACAATGTACCGACTACTGAAATACATGTGTTGCTGTTTACCAAGTGTCTGCTTGTATG
GGCATCGTTTGTGATGTTGGGTTATTCCTTCTGACCAACACGAGGAAGTGAAGTGGCGTCTGAAGACCCGATTTCGAAATCAACTGACCCCTTCGCAAAAAGCAATTGGGCAAT
ACGCTTCTCTGACGCTGCGCTGTTGTGTTGATACAGTATTTGCTGGCGCGCTGACCGCGCACTACACCGTCAAGGTGAGGTTTCTACGGCATTGACGAGGCGTTGGCGTTTGAATGTC
CGACTGTTTCCCTTACGCTGACCGGTACTTGGCACATCCAATCCGCACTCTTCTGATGTTGCAACCGGCTTTTTCGCGGAGGTTTGTCTCGCGCGGATTTGCAACGCGCGCAAGAT
CCCAAGTTCACAGTGCAGGCGTGAATCTCTCTATATCGCCCTCTTCTGATGTTGCAACCGGCTTCTTACGCGGCGCACTTCTGCGTTGACGACATCTCTCTCCCGAATTAACCTCT
GGTTCGGACACCAAGGTACGAATACCTCGATTGCGGACGTTTCTGCACTGCTGCGCGGTTCTTACGCGGCGCACTTCTGCGTTGACGACATCTCTCTCCCGAATTAACCTCT
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TGGCGCGCTGCGCGCTTCTTGTGTTGGCGCGGTTCCGCGGACGCTGACCAACCTGACTTCTTCCGCTTCTTACCTTCGCGCTTATGCGCGGCTTCTTCTCCCGAATTAACCTCT
GCCGCTGGTGTGCTGGCGCGGAGGACATGAGCACTGCTTACCAACCTGACTTACCGGCTTCTTACCTTCGCGCTTATGCGCGGCTTCTTCTCCCGAATTAACCTCT
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CATTGGGCTTCTGATTTGTGTTGTTGCGCGTACTTGAACCAAGCGCGGTTTACGACAACTGATGACTTGGGCTTCTGCGTCTCAACGCGCGCTTGTGCGGTATGATGCAATGCA
CTGCTGCTGCTGCGGCTGATTCAGGCAATGCGCTTATCAGCAGCGGTTTGTGATGCGCGCGGAGGATTTCTGCAATGGAATCTCGACACCTGCGCTGGGTACGCACTGCG
CCGACTTAACTTTATCGCGGTGCAATCTGCTTGCATCAAGCCACTAAAATCGTATTCGCGCGGACAAA

SEQ ID 1418

MGQYKILWYLLFAVLAVCTILGYMGSEVYKAPPYEPQVVSASGKVLMTKDDILAQSAWQSTGGNEVSGILHGAQYAPDWTADWLHRELSAWLILTAQQTYGKKFDEVSPBQAVLKT
RLADEYRNQSRKEDGSVVISDTRVKALESILPYTHGVYDDPKLQTTREHFAMKNWLPQEQAREKLDFPFWTSWASSTNRPEGVFTTNNWPHRLINNVPTTENYWNSTSVLLIM

GIGLLMNGYSFLTKREBEVSEDPISKIQLTPSQKALGKYVFLTVALFVVQVLLGGLTAHYTVBEGQFVGIIDEALGFHSDWFPYALTRTWIHSALFWIATGFLTAGLFLAPIVNGKD
PKFQAGVNFYIALFIVVGGSYAGNFPALTHILPEFNFVFGHQGYEYLDLGRFWQLLLMVGLLLMLFLMLRCTVSAFKEKGVDEKLLAIFVASMVGVGVFYAPGLFYGEKSPIAVHEYW
RWWVHLWVEGFFTEVFAATAFAFVYINMGFVRRSTATASTLAAAIFMLGGVPGTILHLYFSGSTSASMAIGACFSALEVVPLVLLGREAYEHSYQHLSDWAKRLRPLMCFVAVAFHMH
IGAGVPGFLINPPLISLYIQLMNTSAVHAHAALFGVYGLALGFLVLLVARYLKPNARFDDKLTWNGFHLNGGLVGMTAISLLPVGVTQAYASITHGLMYARSEFLQMEILDTRWVRTA
PDLIFIGGAICVAIQATKRVFGRDK

SEQ ID 1419

ATGCCGACGGTTCGCTGTCCGATAGACGGGGAATAAGGCGGGCTTCATACCGACGGCGCTGCCGACGCCGGAAGGTTACAGCGCATTTATAGAAACCGATGGGAAATAAAGGAA
AGCGTCAATT

SEQ ID 1420

MPQVACSDRRGIRAGFIPDGRAASPKVQYALYRNRHRIKGRKRAI

SEQ ID 1421

ATGAACCTCTCTATTGTCCAACTGCTGCTGGGGCTGATAAGGTTTACCAATCTGCATCAGCCGCTGAFTCCGCGCGCTGCCGTTATACGCGACCTGTTCGCAATACGCGTGAAG
CGGTCAAAAAATACGGCGCATTTCAAAGGCTCCGGCTCGCCATCAAGCGCATTCACGCTGCCACCTTTTCGGCGGACACGGACACGACCCCGTTCC

SEQ ID 1422

MFLLSKLLGLLIRFYQYICISPLIPFRCRYTPTCSQYAVEAVKYGAFKGLRLAIKRIARCHFPFGHGHDPVP

SEQ ID 1423

ATGAAACGCATTTATCAACCTTCGGTTACCAACGCAAAACGACCCACGGCTTCCTCGTCCGCTCCAAAACACGCGCGGACGCGAGTATTGGCGCACGCGGTGCCAAAGCGCGCAAC
GCCTGGCAGTG

SEQ ID 1424

MKRTYQPSVTKRKTHGFLVRSKTRGGRAVLAARRAKGRKRLAV

SEQ ID 1425

TTGCAAAAGCGGCAATTTGGAGTGTAATTCACGGTTTAAATTATCTACCAATCTTATTTTAGGAACCATCATGAAACGCATTTATCAACCTTCGGTTACCAACGCAAAACGACCCACGGC
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TCGACAGGCTCAGCAAAACAGGCAAGGCGGAACCTGCCAATCATGTTCGGCAACCCGCAACCGGATGCGGGAACAGGTA

SEQ ID 1426

LTKAANWVINGLIYPPYFRNHETHLSTFRYQYQTHPRLPALQNRTRTSIGRTPCQRPQTGVSGLDYRFRQYRLKTDFFSSVFAFNRRSRDLQVSRNNGNLDHPRIGLVVG
KTKAKRANERNYMKRVIRDWFLNKNRLPPQDFVVRVRKFRDRAKQARAEALQIMFNPATGCGKQV

SEQ ID 1427

TGCGCTCGGATTTCTGCCGCTTTCTGTGGATAAATTTTGCACGGGTGTGGATAAAATATCGCGAGTCCGTATATCGGTTGCTGCGTTTGAACCGACGCGTATTCAACAGATT
GTTTTCCTTTTGAATAATATATATTTCTTTGTTTCGATTCATTTTACGATTTCGAGCCTATCCA

SEQ ID 1428

LPADFRLSVDFLHGLWKYRRVGIIGSLRFEPTRIQQICPLFENLIFSLFISPLIRAYP

SEQ ID 1429

TTGAATACGAAAGCGGACGCGCGGACGCCAATCTTCCCTTACCGCTTCTATTTTCGCGCAAACTGGCTTCTGAGCATATTGCAGGCAAACTGCTTCTTCCGTACACCCCATACG
CCACCTTCTTCAACCGTAAGGGGCGCAATCCATTGCGCAAACTGCCGCTGAGGCAACATATCGTGAAGACGCGGAGGACAGCGGCAAACTCTGC

SEQ ID 1430

LNTKGTAGSQFLPYRFPYSGKLALEHLAGKLVLAVHHFYATLLTNRKGRNPLRLKLPVRQHVKTAEARPELILC

SEQ ID 1431

ATGACATTAGCAGAGTTTGGCGCTGTGCTCCGCGCTTCTACGATATGTTGCCCTACGGGCAAGTTTCGCAATGGATTGCGCCCTTACGGTTGGTGAAGAGGGTGGCGTATGGGTGG
TGTACGCGCAAGCAACAGTTTGGCTGCAATATGCTCAAGAGCCAGTTTGGCGGAAAAATAGAAGCGGTAAAGGAAGAGTTGGCTGCCGCGCTCCCGCTTTCGTATTCAAACCGGAGAG
CGTGGCTTA

SEQ ID 1432

MTLAEFNPICLRLRLDMLPHGQFAQNIAPLTVGEEGVWVYVGNQFACNMLKSQFAGKIEAVREELAAGRPAFRIQTGRERAL

SEQ ID 1433

ATGCGCGCGGTGAAGGTGCTGTGCAACCTGCCGAGCGCTCTTGCAACGCGGGTTCGAGGAGATGCCGCTGACGAGGTTCTGTGGACGAGCTGCCGCTGAAAAGCCTGTCAAAACCG
CTGCGTCGAAAACGCGCGCGGATATTTGGCGGAACGTATGAAAACCTGCCGCGAGCGCGCTCAGGCTGCCGCGCTGCTTCCGCGCGGAATCGGCGCGAGTTGCCAAAGCGCGGAC
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TGCACGCGCATCAGGCGGTGCCAACTGCCGAGGAGAGCCCGAGTTGGCGGAGATTACGAGAACTGCTGATTCTGATTCAAAAC

SEQ ID 1434

MAAVEGAVEPAEPLSHAGSEEMVQEVLLDELSEPKVPKPAASKTAADILAEKMLPHEPRQAAGPASRPESAATAVARTDAQRDAEAREYBQYNLSFDYTFDTLVEKGNRLAAAAQA
IAENPGQSYNPFYLGSTGLKTHLVQAVGNELKNRPDAKVRVYHSDDYIRSPKAVRNWYDVFKQYQYDLIIIDDIQFIRKDRTHREFFLYLNHFNHKKQLILFCDVLPKIEG
MDDLKSRFSWGLTLELEPPELEMRILAIQKAEAGISIEDEALFIANLIRSNVRELEGAPNVRGASSRPMNRFPVIDIDLARTALQDIIAEKHVITADIIIDAVAKYTRIKISDVLGK
KTRNRIARPRQVANSILKELFTLSLPSIGDSFGGRDHTTVMHGRIVAKLREEDPELAQDYKELLILIQN

SEQ ID 1435

TGGTAATCTGTTTGTGTAAGAGCGCTTGGAAATATATAAGTATCCCTTCCGCTGTCTAAGATATCTCTCGATATTTCCGACATTCCGCTATATCTTTTCAGTTTCGTCGCGCTTCG
GCAGCGCGAAGAACCGAATATACGCCCGCAGGGGAAACAGTCAATATCTTTCAGCGGATTTTTTCGGGAAATTCGTCAT

SEQ ID 1436

SVICPVKERCEIIXPFLSKISLIDIPCYTTFQVRRFGSGEENYTPAGENSQYFQDFPFGIIRH

SEQ ID 1437

SEQ ID 1437

ATGAAGCCGCTCTATCTTAGAAAACTGCAACAACCTCGGCCACCGGTTGGAAGAAGTTACCCACCTTTTAGGGCAACCCGAAGCCACATCCGATATGGACAACCTACCGCAAGCTCAGCGCG
AACACGCGCAACTGACCCCCGCTGCTGAAGATATCCAAACATATCGGCTTGCCCAAAGCACTGCGCGGATGCGGAAGAAATGTTGTCGACCCCCGAAATGAAAGACTTTGCCGCGGAAGA
AATCGAAGCGCGGAAGCCAAAATCGACGAACCTGGATACCGAATTCGAAAACATGCTGCTGCCCAAGATGCCGACGACGACAAAACATCTTTATCGAAATACGCGCGCGGACGCGGCGGC
GACGAAGCCGCGCTGTTTGCCGCGGATTTGCTGCGTATGTACACGCCCTACGCCGAACGCAACCCGCTGGCAGGTTGAAATCGTGTCCGCCAACGAAGCGGAATTTGGCGGGCTATATAAGAAG
TCATCGCCCGTATCTGCGGACCTGCGGCGCGTACACCGCTGCGAAATTTGAATCGGGCGGACACCGCTGCAGCGGTCGCCGCGCAGGAAGCCGAAGCGCGCATCCACACCTCGCGCTGTAC
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CGCGTCCGATATACCCACTTGCCGACAGGCATGGTGGTGAATGCCAAGACGGCGCAGCCAAACGCCAACGAAGCGCAGGCGGATGAAAGTCTCGCGCGCGGCTGAAACGACGCGCGCAA
AACCGGAAGTCCAAGCCAAAGAAGCCGCGGAACGCAAAATCCCTCATCGGCAGCGGCGGACCGCAGCGAACGCATCCGCACCTTACAACATATCCCAAAGCGAGGCTAACACGACCCACGCGATCAA
CCTCACCTGACACAAGCTGGAATTTGTGATGACGGCGGATTGGCGAGAAATCACCGATGCCCTGATTGCCGAACATCAGCGCGAGCTTCTGCGCGCGGATGGCGGAT

SEQ ID 1438

SEQ ID 1438
MKPFSILEKQLQIGDRLEEVTHLLGQPEATSDMDNYRKLTRHAELTPVVEVPQNYRLAQSDLADEAEMLSDPEMKFAAEETEAAKAKIDELEDTLQKLLPKDADDCKNIFTIRAGTGG
DEAALPAGDILLRMYSRYAERNRWQVEIVSANESLEGGYKEVJARIVGLGAYSRKLPFSGGHRVQVRPATESQGRHTSACTVAVMPEADELEDIELNPADLRTDTPFASGAGGQHINKTIS
ATVTHLWGLMTEGCGDPSCHANKAOMAKVLAARLINDAOKREVQAKEAEERKSLIGSGDRSERINTYNPQGRWTDHRIINTLHKLDFVMDGLDAKITDALLAEHQAEILLAMGD

SEQ ID 1439

SEQ ID 1439

ATGTTGATTTTACAAAGCGAGCGGACAGCCTGCTCAAGCCGCTGCAAGCCTTTACCGGCATCTGTGGAACGCCTACACACCCCTGCCATCTCTTCCAATGTGCTGATTGAGGGCAGGGGCG
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GCTGCCCTCCGGGTCGCGTGTGCTGTGATTTGGGACGACAACCGCTTGACGCTGAAGGCGGGCAAAATCGCGTTTTCGCCCTGCAAAACCGCTGCCCTGCCGCCGATTTTCOGATGATGAATGT
GCGCAGGACATTCAGCGCGACTTTCTCGCTGGGGCAGGAGCGTTTCAAAACCATGCTGTGCGAAGTGCAGTACAGCATGGCGGTGACGAGCATCCGCTATTATCTCAACGGCTGTGCTGATCG
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GGAATCTGTTCAAATCTGTGGAACAACCCGACGATCCGATTCAAATTCGAGCTGTCTGGCAACGACAGTGCCTTTCCAAATGCACCGACGACGACCATTCGTCAGGCAAGGTTCATCGACGGCAAAATTC
CCCGATTTCACACCGCGTGATTCCTTTGGACAACGACAAAGATTTTCGCTGTGTCCTGTCGCGAACTTTTGGCGCGCTGGAACGCTGTGTCCATTCTTGCCAACGAAAAATTCGCTGCGCGC
GCTGTTCTTCAACCCGGCCTGTTGAGCGTGTGTCGACGAACAACGAGCGAGGAGGAAGCGCGGAAGAAATCGAANTCGCCTATCAGGGCGGCGAATCGAAGTTCGCTTCAATATCG
CTATTGTGATGAGCTGTGCGCAACATCCATTCCGACGATATGCAGCTTGCCCTTCGCGGACGCGCAACCGCTCGACGCTGTTACCGTGGCGCAACATTCGAATTTCAATATATTTGTGATG
CCGATGCGGATTT

SEQ ID 1440

SEQ ID 1440

MLILQAERDLSLKLPLQAPTGIIVERLHTPLPILSNVLIEGRGGQFKLLATDLEIQITDAGPEGGAGDFRITTNAKKFPQDILRALPAGALVSLWDNDNRLTLKAGKSRFALQTLPAADFFMNV
GEDI SATPFLSGQERFKTMLSQVQYMAVDQDIRYLLNGLLMQVBSGQLRLVATDGHRLAYAACAIADLPAEVEVLPRKTVLELFLKLLNVPDDPIQIELLDKQVRFQCNQTTIVSKVIDGKF
PDFNRVPLDNDKIPVLSRAELLGALERVSILANEKFRGARLFLPQGLLSVVCSSNNEQEEAREEIEIAYQGGELEVGFNIGYLMQVLRNTHSDMLQAFGDANRSTLFTVPNNPNFKITVM
PMRI

SEQ ID 1441

SEQ ID 1441

TTGCCCCGATGCCCTGAACACAGACCGTCCGTCACGTCATGCCGCCTGAAACCCGGCGCAGATGCCGCCAAGCCTTCAGACGCATTTGTCCGCCGCTCCGACCGAACACAAACCATCTTTGGG
AGAACCTTATGACCGAACAAACCCGATCTCTCTGCCGGAATCGAGCCTTCAACCGCGCGGTGTGGCAAGCGGAAGACAAAACGTCCCCCTTTTGGAAACGCCCTGCGCTT
CCTGTGTCATCGTGTCCAATCTTGACGAGTTTTTGAAGTCGCGATCGGCTGGCTCAAGCGTGAAACAAAGCTGCACCCCGCGCGAGGCCGGAACAGCGCAAAATGCCGTCTGHAACC
ATCGCCGACGCTTACCGAAGCGCGCGCCCTCCGTATACCGCACACAGTACGACCTGTTCAACAACGCTCTTCAGCCCGAGTGTGGCGCGGAAAGCATTCATTTTACCGCCGCCGCAATTGGA
CGGGCACCGCAGAAATATGATCTGAAGACTATTTCGACCCGGAATGCTGCCGATCTTGACCCCATTCGGACTCGACCCCTTCCACACCTTTCCCGCGCCGCTGAACAAATCGCTCAACTT
CGGCGTAGAATCTGACGGCACGGACGCGCTTCGGCAGGCCCTTCGGGTATGGCGATTGTCTCAAGCACCCGCGCATCTGCCGCGCGTGTGTCCTTCCGCTCGGCTGCGATCTGGCGGACAC
GGCTTCGTCTCTCTGTCGTCCATCTCTCACGCCACGTCGGCAAATCTTCCGGGCATGAACGTCAAGGCTGCCACCAGTTTCGTCCTCGGCTGCGATCTGGCGGACGAGCTGTGCGGCGGACAC
AAGACGTACAAAACCTCCGCGCCGCCATTCAAAACGAATGCAACCGCCGAATACGGCGACGCGGTGCGGCTCGAAGTCCGCTCCAGCGGACAGAGCTTGACCGTTCGACGAAG
GCAATTCAGGCTGACCGACGCGCAATCTCATGCTCAAGGTCAAAGGCGGCTCAACTCTGCGGCTCAACCGCGTCCCGGACCTAGTCAACCGCCCGATTGAAATTTCCGCGCCACACGCG
GGCGGTCTGAAAGCCTTTGGGCAAAAACGCCCGATPCTTGCAATTTGGTGGCCCAATCGCCCATCTCTGCTGCACCAACCTTACCAATCTTTCGATTCGCGGTGCGATATGATACGCGAAGCG
CCGCGCATTCGCGGCTCTGTGCGCTCAAATGACGATTACCGCACCGGCACGCGCTCCGAATCTGTCCCGCCCTGATGAAGGCGGCACTCGCGGACAAACAAAGTAACCGTGTCTCGTA
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CGAACACGCAAAAGCGCGCAACCGCGCGGATTACCGCCAAGATGAATTCGCTCATCGAACCGACTGCTGATAGAAAGCCCTGTATCGGCGAAGCGCGGACGCGTCAAAATCGATTGTGAT
GTGCGCGGTATGTGTACCTTGCGCCCGGTTGTAAGAGCTTTGTCGGAACATCTCCGCTCCGCTCCATCGTCCGCGAGGACGCTGAACACGCGCGGTATATTGTTTCCACAAACACGCG
CGGACGACACCTTTATTTCACGCGCGGATTGGAATGGGCGCAATTTCTTCGCGCGCATCGAAACCGCCACCCCGATTACCGCGCCGGAATCTCAAAAACGCGTCAATCCGCGAAGGTTTGG
AATGGCATCGGCACGAATCAACACGCGTGGCTGATGACGCCGACGCGCGCTATATCCGCGCGCGCCCGCGAAGCGAAGCGGACCTGCAAAAACGATTATTGGGATTTGCTC
CAGGCG

SEQ ID 1442

SEQ ID 1442

LPRCLQKQTVRHVPFETGADAAKPSDGIVRPLRPNNHNLWENLWTEQNRILCRELSLAFNRRVLAQAEKDPVLLERLRFICTVSSNLDEFVEVMWMLKRENKLHPRRRPDNGKMPSET
IADVTEAARSLIRHQYDLFNNVVLQPELARESLHPYRRRNRWGTQKKNIWEDYFDRELLPIITPIGLDPSHPFPPLAPKLNSLNFVAVELDGTAFGRPSGMAIVQAPRILPRVVFLPSELGGGH
GFVFLSSILHAHVKGKLPFGMNVKGCBFRLTRDSDLTVDEEDVQNLRAAQNELHLDREYGDGVRLEVADTCPAYIRDFLLAQFRLTDAELQYVKGFPVNLVRLNAVVDLVNRPDLKFPFPTF
GRLLKALGKNSPIDFLVRQSPILLHHYPQSFDPVMTNREAAADPAVLAVKMTYRTGTSELVPMALKAALADKQTVVVELMARFDEANNVWNAQLEEGAEAVVYGVFGYKVHAKMALV
IRREDGVLKRYAHLGTGNVHQTSRIYTFDGLTLTADQETIADVNTLFMEITGLGKPGRLNKLYQSFFTLLHKMVGIRLARETEHAKAGKPARITAKMNSLIRPTTVI EALYRASAAGVQIDLI
VRGMCTLRPGVKGLSENIRVRSIVGRQLEHARVYCFHNNGADDTF ISSADWGMGRNFFRRIETATPTIAPELAKKRVIREGLEMALADNTHAMLMQPDGGYIRAAPBEGSEADLQNLMDLL
RG

SEQ ID 1443

SEQ ID 1443
GTGACGGACGGTCTGTGTTTCAGGCATCGGGGCAATGTGAAACCGGATACCGGTACGTCGGGTATCGTCTGTTTCAAATCACTTCCAAACAAAAAATATGACGCAGTTTTTTCGTACACCGCA
TCGCTCAGCTTGTGATGACGCCGTGTGGTCATAATCTCTGTCGGACACGGACCGGGACCGGATCGCTTCTGTTTCGCTTTCGGACGGTATCTGATTTCCAAACCGCGGTGCAGGGCGAAAAAGAAAAAT
CGCCCTCCTGCTTGAAACCGATGACTTGCGCCGCGTAAACCGGGCTGTGCGGTACTGTCTCAGCGCTCAGTCCGAACGTCGCCCTTGGGTGTGGCAGTGCAGATAGGACAGGGGTGGCAGTGAAG
GTCTGTGGCAAAAAACAGATTTCCGCTTGTGATGTGTGACGATGACTTTTTTCTTTTGAATATAGGCAGTACCGCATCCGGCTGCCCCGTGTCGGAATACGGGGGACGTCTGTACAGCGGCAG
CAACAATATCCC

SEQ ID 1444

SEQ ID 1444
VTDLFQASGQCEGYRYVYPSVSNHPQHKTPTFFVHRIADVDAAVGHNPVGHGRGGDAFVSPFGKYLIPNAVQGEKKIALLETDDFAAVTGLVGTVQRQSERFLGCGSADEGVALP
VWGKTEFLGCVDDFFILNIGTDIRLRPLCEYGGSRQQAQYP

SEQ ID 1445

ATGCCGCCCTCGCTGCTTCAGGGATATTGTGCTGCGCTGCTGACGACTGCCCCCGTATTGCGCAGGGGCGAGCGGATGCGGTGAGTGCCATATATTCAAAGAAAAAGTCATCGTCGACA
CCTCCACCGCGGAACTCTGCTTTGCGGAGCAGCGCTCAGTGCCACCCCGTCTCATCGGCACTGCCACACCCAAAGGGGAGCTTCGGACTGACGCTGAACAGTACCGACAGCCCGGTTCAGG
CGCGGAAGTCATCGGTTTCAAGCAGGAGGGCGATTTTCTTTTCGCCCTGCAACGCGCTTTGGAATCAGATACCGTCCGAAAGGCCGAAACGAAACGATCGCTCCCGCTCCGTGTCGACAGG
ATTATGACCAACGCGCTGCATCAACGTCAGCGATGCGGTGTACGAAAAATGCGCTCATTTATTGTGTGGAAGTGATT

SEQ ID 1446

MPFRLISGLILCCLLTAPVFAQGPDAVSAYIQKKKVVIVDTSKAELCFADDRQCHPVLIGITATPKOTFGLTFLNSTDKPGYGGEVIGFKQEGDFLALHRVWNQIPSERRNERIASPSVSDR
TFRNGCINVSADVAYEKLRYHFVLEVI

SEQ ID 1447

ATGCGCCCGCTGTGACCAAGACGACATCTCAAAAATCCCGGGCCGCCGCATTACGACGAAGGTATGTACGGCGTGCGCANTGGGATTACCTGTTCCACTTCCACACCCCGGGCGTGG
GTATFCGACCTGAAAAACATTCGGCGTGGAAAGCGGTACTACCTGCCAATACAAGTGATTTTCGTATAAAGACAAATTTGCCCGCAGCTTCTACTGGAACCCCGTCTTCCCGAAAGATGC
CGTCTGCCCGCCCGCACCCAAAGCCGAGCCGCAAGTCATCATCCCGAAATCGTCCCGCAAAACCGAAACGTAATCCGCCAA

SEQ ID 1448

MRPGLTKDDIYKIPGRPHYDEGMYGVREWDYLFHFHTPGVGIDPEVTSVGEVVTTCQYKVI FDKDKFARSFYNNPVFPKDAVCPPPAKAEQVI IREIVPAKPKRIRQ

SEQ ID 1449

TTGCGCGGATGACGTTTCGGTTCCTGCGCGGACGATTTTCGGGCTCGGCTTTGGTTCGGGGCGGGCGGCAGACGGCATCTTTTCGGGAAGACGGGGTTCACGATGAAAGCTG
CGGGCAAAATTTGCTTTATCGAAAAATCATTTGTATTCGGCAGTAGTAACGCCCTCCACGCCGGGAAGTGTTCACGGGTGATACCCACGCCCGGGGTGTGGAAGTGGAAACAGGTAATCC
ATTGCGCGACGCCGTACATACCTTCGTCGTAATCGCGCGCGGCCGGGATTTGTAGATGTCGCTTTGGTTCAGACCGGGCGCATCTGATCCAGTTCGTCAATAGTCGGGAATGTGCGCG
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GCTTCGGT

SEQ ID 1450

LADTFRCRHDPADDDLRLCFCGRRADGIFREDGVFVEAAKGFVFIENHFLVLAGSNAFHAGSVFVEDTHARGVEVEQVIPPFAHAHVHTFVVERAARDFVDVVPFGQTAHLIQFVISRCAA
LVVERYGIGFRENRIVGRVAGFVDVALMLRRQTECLPPLTPSSV

SEQ ID 1451

ATGAAATCAACAAATCGTCAAAACCGAGCTTGGCAGTATTGGCGGCAGGCATTCTGTCTGCCTGGCAACCATAAAGCAACGTCAAAGCCGACGGCACGACCGACAATCCGGTTTCCCG
GAACCCCTATCCGTAACGCTCGACAACAAGCGCGGCACATTCCCGACTTA

SEQ ID 1452

MKIKQIVKPSLAVLAAGILSACATTKQRQSRRHDRQSGFPGTLFRNARQQARHIPDL

SEQ ID 1453

ATGAGGGCGCGAGCGGGGTGAACACAGCACTGACAGCGGTGGGGCTGCTGTGAAGATGAGGCTGACCGACACACATTTGCCATTCTTGCCGATTTCGGTTCGCGCGGCAATCTGGCGCAGGTGC
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GCTGGGCATCCATCTTGTTTCAGACGGCAATTGCGGAACAGGATTTTCCCGGTTTGAAGACCGTATTGTTGCGTTATACCCCGAGCGTGGGTGCGGGAATCCGGCTTGGATTTTACGAC
AAACCCCAAAACGCCGCGCAGCGTGAACGGCAAAATCAAGTTTPTAGCCCGCAGCTTGCATTCGCGCAAACTTCGCGCGCGCGGTGATGATTATCAATCTCAAAGCCACCGCCGACATCG
CCGCGCGCTCAAAACAGACAGGCTTTACTCAAGCGCGCATGPTCACGCTTCTTCAGGCAGCGCGGAAGAAGCGCGGTGCTGTCGACAAATCCCGGTCAAAATCCGCAATCGGTTCCGCTGCT
GCTCAATCCGAACCGCGCTTAAAGCTGCGCGATAGCTTAAAGCGCTTGAACGATTCGCTGATTGGAACCGGATAGCCCGTTTCATGTTGGAAAAACCGCTCAATAGCGCTGCCAACATT
CTTCGGGATTCGCGAAATTCCTCGGGAATACGCGGTACCGCGCGCGGAAATCGCCGCGATACCGGAACGCAATGCGGACAGCTCTGCTCCGTC

SEQ ID 1454

SEQ ID: 1454
MGRGRGETRVAAGAGVGMRLTDTHCHLADSVLRGNLAQVLAEARQAGVWRFTVPATCPQDNQVAKSEMPSEHGQIRIALGITHWPSDGLAEQDFSGLEAVLVRYFRANVVGIGLDFYD
KTQTPPQREHQIQVFSRQLALAQTLRRVLIHNLKATADIAAAVKQTGFTQGGIVHAFSGSAEEARVLTKLGFKIGISLLNPARKVRDITKALNDGDFVLETDSPFMLENTVNTPANL
LRIRIAAEIRGTGAETAATERNADSLLRP

SEQ ID 1455

SGAAGCAGTATGACGGCGCGCAAAATCATAGTGCACAGATCTCAAAGCCGAAGGCGTCGAGTACGTTTCGCGTTATCCCGCGGGTCGGTTATCGAAATCTACGATGCCCTGTTCCAACCTCAATA
 AATTCAAACACATTTCTTACCGCCCATGAGCAGGCGGCAGTACACGCGCAGATCGGTATGCGCGCGCTCAGCGGTAAAGGTGGCGCTGGCATTGGTTACATCCGCGCCCGCGGTTACCAATGC
 GCTGACCGGTTATGCTACTGCCATATACGGATTTCGATTCGGATGGGTGCATCAGCGGCACAGGTAGGCAATTCCTCGATTGGTACGGATCGGCTTCCAAGAGCTGTACCGTGGGATTATAC
 CGTCCGTGCGTCAAACACAATTTCTTGGTTACGGACATCAATGATGTGGTGGAAACCAATTAAGAAAGGCGTTCCAAATTTGCCGACGCGCGGACGCGGGCGGTCGATGATGATGTCGCGA
 AAGATGTTACGACGCGGATGCGGAAATTCAGCTATCTCTCAGGAAGACATTTTATTCCTGTTGCTATCAACCGGCTGGTTTCAAGGCGATATCGGTCAGATTAAAGAGCCGTCGACAGTGTGGC
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 GAAATATATTACCGCGGTCGAGAGTCGGAACCATTTTCGATTCTTTGCGCGGATTTCGTCAAACCTTGCCGAGGCATACGGCCATATCGCATCCCGCTGGACAAATAAATCTGATGTGGAAG
 GTGCCCTTGTGGAAGCAITGAACCAAAAAGCAGGCTGGTGTATTATCGACTTCTTGACCGACACAGAAATGATGCTTATGCTCGGCAACGGCAAGGTTTGGACGGAATGCTGACT

SEQ ID 1456

SEQ ID 1456
 MQLSGAQIIVQSLKABGVYVYFGPGGAVIETVDALFQLNKKPHILTRHEQAAVHAADAYARVSGKVGVALVTSGPVGTNALTGIATAYTDSI PMVVISGQGVNSLIGTDAFQEVDTVGIT
 RPCVKHNFVLPDINELVETIKKAFQIAASGRGPPVVLVDPKDVQAMAKFSYPQEDIFIRSTYQPVVQGHIGQIKKAVQMLASAKRPVVYFGGGVVLGNASEELTRFVMTGAPCTGTGLGL
 GATPSGDRQFLGHLGMHGTYEANLALQNAADVLLAVGARFDORVVVSPSKFFEAKKVIHIDVDPSSITAKRVADIPIVGDVKNLSLQMLVWQKQESVPSEDALQKWKWKTIEBWRSDRLH
 PDNGSEKIKPQYVQIKLAEITGNSALITSDVGQHQMPFAQYGFALFEPKRWLNSGGLTGKVLPTAIGAKLAAPDQDVMFCITGDSEIOMHILQELSTCFQYTRIPVNVITLNGWILGAVRQD
 FVNGGRSSTFVDSIPDFVILAEAYGHIIGRLVNLKSDVEGALLALNKKDLRFLVIFDITDCKGVNPPVGVNGKGLDVMFLPHMRTDGA

SEQ ID 1457

SEQ ID 1457

TTCTTTGATTTTCATATGCAGAAATCCTTTTITTAACCGATGCCCGCTCGCCTTTTGTTCGGAAGAGCCGCATCAGGAGAGTTTAAACGTT

SEQ ID 1458

LFDFHMONPFLPDARLPFVRKSRIIRVLNV

SEQ ID 1459

ATGCGTAAATTCGACGCGCATCATTCGTATGCCGTACAAATACACCGCTTTTACTGATACGACGTTTTTATGCTAATATTACGAACCAAAATCAACGTTTAAACTCTCTGTATGC
GGCTCTTCGGAACAAAAGGCAGACGGGCATCGGGTAAAAAGGATTCTGCATA

SEQ ID 1460

MRKPARASPMFYKYTAFTDTHVFYANITNQNYTKTLLMLRFRKGRASGKKGFCI

SEQ ID 1461

ATGCGCGTGCAGATTATACGCATCCTGCCGCGCAATTTGCCGATTTCGCGGCATCGGCAACCTGTTATAATTCCTCCTTTAAATTCCTAACGTTTCAAGCGAAAAACAAATGACCATGCAA
GAACATTACACGCCCGCGCCATCGAGCCTGCCGCGCAGAAAAATGGGACGACGCCGATTTTCCAACTGCTCCGAAGACGCTTCCAAACCCAAATATTATTGCTTTGATGTTTCCCTT
ACCC

SEQ ID 1462

MRVRIYASCRQFADSPTSATCYNSSFKFLTPSSSEKQNDHARTLPARRHRACGAEMGRFPYQRLRRRFQTLILLPFDVPLP

SEQ ID 1463

ATGTTTCCTTACCCTTAGCGCGCAAGCTGCATATGGGGCATGTACGCAACTACACCATCGGCGACGATTAGAGCCGCTTCAAACCTTTAAACGGCTTCAACGTTATGCAGCCTATGGGTTGGG
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CTGGGAACCGCGAAGTTCGCCACCTGCAAAACCCGAATACTACCTGCGGAACAAATGGCTGTTTACCAAGCTGTTTGA AAAAGGCATCGTCTATCGCAAAAACCGGAACGGTGAACCTGGGACCCG
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AGCTGCTCAACGATTTCGCAAGCTGGAACACTGGCCGGAACAGTCAAACCATGACGCGCAACTGGATCGGCAATCTCGCGCATGACCGTGGCTTTCGCGCTTCAGACGACAGCAA
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TCAACCGCGCAAGCTGGAAGTGTGGATTGCCAACTATGTCTTGTGGGCTACGCGCGACGCGCGGTGATGGCTGTTCGCGCGCACGACGAACCGGATTTCGAGTTTCGCGCGCAATACAA
TCTGCGCAAAAACCAAGTCATTGCCCTGCGCGACACGCAATTCGACGCAAAACCGATGGCAAGAAATGGTACGCGGACAAAGAAAAACGGCGTATTTGCTCAACGACGGCGACTTGGACGGCTTG
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CACCACCGCAAGTTCAGCGACGACTACGCGCGCGCGCGGCAAGCTTCAACACCGCATTCGCGCGCGTGTGGAACGCTCAACCAATACGACAAAAACCGACACCGCGGCAACAGGCGCG
GCCGTCGCCCAAGAGTATTGGAAGCGCGCTGACGCTGTTGTGGCCATCTGCGCGCACATCTGCGAAACCTGCGGAGCGAATTGAACGCGCGCAACTGTGGGAAGCAGGCTGGCGCG
CACTGCGCAACGAAGCGCGCATGAAATTCATGGAAGCGCAAGCTCGCAAGAAAAATCATCGTCTGACCGCGGACGCTGGTGAACATCTGCTGCT

SEQ ID 1464

HPYPSPGLKHGHVRYNTTIGDVLSRPKLLNGFNVMPQWDPAGNPAENAAKNVAPAAWYDNIYMKPTQLKSLGFAIDWEREVATCKPEYRWEPWLFKLFKGIYVRKNGTVNWD
VDQTVLANEQVWDGRGWSGALIEKREIFMYFYKIDYAEELLNDLKLHWPQVKTQMRNIGKSRGHTVRFVSDSDSKQLEBDYAKFLQVYTTPTDLMGATTVAVAAEHPLATAAA
ADKPELQAFIAECKAGSVAEADMATMEKKGVPTGRYVNVPLNGDKLEWLVNIYVNLGWDGAVMAVPAHDERDFEPAKYNLPKQVLA VGDNAFDANRWQEWYGDKNGLVNSGDLDGL
DPYTAFDAVAAKIQSGAGRPFTQYRLRDWGISRQRYWGPPIPIVHCEKCGVDFVPADQLPVLVPEHVVDPDGMGSPFLAKMPEFYETSCPCCGGAARETDTMDTFHSSWYFFRYMSPKFS
DGMVSAESAKEYWAGVQYIGGIEHALEHLLYARFTTKLMRDEGLVNVDEPFERLLTQGMVVCETTYRENDKGGKWINPADVELTTFDDKGRPVSAVLKADGLPVVLSGTERKMSKNNGV
PQELINAYGADTARLPMFAAPPEQSLWSDSGVEGAHRFLRLNRVVEYELKQGA VPAAGNQDGLSKELKDLRHLHSTTAKVSDDYGRQQFNTAIAAVMELLNQYDRTDTGSEQGR
AVAQEVLEAVRLLWPIVPHLCETLWSELNGAKLWEAGWPTVDEALVXSEIEVMVQVNGKLRGKITVAADASKADLEAALANEGAVKPMEGPKAKKIIVVPGRLVNTIV

SEQ ID 1465

TGCCCCGCTGCTGCGCGCTTCGCTCTCTTGTCTGATTTTGTGTAATCTACTAAAAATTAATCTCAAAATCCAAATATGAATTTATTTTCGATACCCAATTTGGGAAGCAACAAAA
AAGCAACCCCAAAAATTCCTGTGTAATGAGCGAGGCTTGGCTGGA AAAACCGCTATTGCCCTGTTGCGGAAGCAAGCCGATGCAGAGATTTCGCAATAACAACTGTTGCGACCTCTT
TTGCCAAATTTGCCAGAGCAATATGAATTAAGAGTAAAAATCAAAAACCATAGGCAACAGCGTGCTGACGCTGCATATCGCACTATGTTGGAGCGCATCGGTCAGATACCAACCCC
AACTTTTCTTCTTGTGATATATAAAAAGCGGATTACTCCATACGGCAATTTGTGCTGTGTACCCAAATTTTCATACGCCGGATATGATTTATCCGAGAAATTAAGGCATTAAAAACCGAC
CGACCAACATATGTTGTTCCATCAATCTCGCCCCCTTGCCTGAAAGCGGAAAAATATTCCTTAATAGACGATTCCCGCATTTATCGAACCCGAAACCGTTCTGAAAAATGCGAATCCAACCT
GTTTTTACGCAACCAAAATGCGGAGCGCAAGACTGGCTTTTGGCTGTTATGAAATGATACGACCACTACCGAAGAAATTCATATTGTCGCAATGTTGCAAAATGTTGAAATGATATCC
ATCCAAATTTCCCAAAACCAACATATCAAGACAAAAATCCGCCAACAGTTGCAAAATTTGCGGTGATCAAAATATGATCGAATTCATTTGGTTCGCGACTTTTCAAAAAAATCGCAAAATG
CACCCAACTCCCAAGCGTTTGTATTCAATCATGATACTGAATTTACGAGAAATATTTATTTCTTCTGCCATTTCAAAAACGGTTGAAGTACACGCAATATTGCCGCAAGGCGCAGCAG
TCGTA AAAAGTCGAGAAATTTATGGCAATTTATGAT

SEQ ID 1466

LPCCLRLRLVLIFVNLKIKINLKIQNNLFFDTQLGKQNKATHKIRVMSEANLEKNYCPCCGSKPMQRFANNKPVADLFCPNCHEQYELKSKNKTIGNSVPDGA YRTMLERISRDTNP
NFFFLAYKADYSTRLVLVPRHPIPTDMLIPRNKGIKNRPHHMCINSINLAPLPSGKIPLIDDSRIIEPETVLKWKQSNLFLRNQNAERKMDLLAVMKCIDQLTEFTLSQMYEFENKLS
IQFPQNNHKKIRQLQILRDQNMIEFTGRGLYKKNRQIAPNSQGVLLSNHDTFTNTYSSAILTKVTEVQRNIAAGSSRRKVVGELLATYD

SEQ ID 1467

TCTTTTCAGAAATGATTTCGAATACGAATTCGCTGCCATATAGGCAATCATAGGCTGACAAATCOGATGATGGTCCACACGGCGGCTTTTTCGCGCGCATCGGTCATGCTGTGTTG
AGCAGCAGTCTCTGCTAAATACGCAATGACCAATATGCCGAATACGGTTTATGGGTAATGTCATGGGTTTTCGCGAATACCGGCTTCGCGCAAGAAATGTCGCGTACGACGGAATAGGTCA
GCAGGATGAACCTGCGCCATAGCTCGGAACATGAGTTTTCGCAACTGAGCAGCAGCGGAGGAATCTGCGAGCTTGGAGAAATTTTCGCGGTGACGAGCTCCGCTGACGACGCAAGCT
CAAAACGCAATTAATGTTGCGATGCCGAACGCGGATGCAAGCAGTGATGTCGCGATATGACGACATAAGGGAAGTGGTAAATTTTCAATATCCCGAATTTTCCGGAATAACCAAA
CCTGACAGCAGCATCAGTGGCGCAAGGATACGACGCACTGCACTCGCGCAGCGGATAAAAAGCTGCGCGCAAAATAAATAACAGCATCATCAAAACATCAGGCTGCCGGAAT
ACCGAAGCGCATATGATTTTGTGTTGAATGACCGCATCAGCAGTCCGCGCGCTGGACGCTCAATCGCGCGCCCAAAACCGGCAATTCGCTCTCCAGGGTAAATCCGCGCGCG
CCCCGCTGTTGGCAGTGCCATGCAATGACCAATCTGCGTAAACCGCGCTCAAAAAGATGAAAACCTGTCGGCAT

SEQ ID 1468

SPQNDQYELAAHIGNHKAADKSDDPHGFFAAPCGHAVFQQSSVNPQ*QYAEYGFMGKCHGFAEYFGKECAADDGIGQDDTCFPHGLEHEFFQTEBRRQESCELGESVAVQAFVQQA
QNGQ*CCDAEQPVCKQ*CADMQHKGKGVNFI SREFSRENQ*QHQCGARIQQQLHSAQRKKAAGKINKQHPNNQAAGIPEAHNDPVLNDRHQCRADVGCRAQNRQRLPRVIPA
PILLAVPCKCTQSCVNRQRQDENKRC

SEQ ID 1469

TTGGATAATCTGCTGTGTCCTGTTCCCCCAATGCGGTACCTTAAATCGCTGCTTGGTGAATTGCATTACAGTGTCTGGCAAGCGGTTTGTCCCTATTGGTT

SEQ ID 1470

LDNLSVAVFPQCAVFKSLGGLQVLWQSGLSLV

SEQ ID 1471

ATGATTGATTTTGACAAACCGGCTGAAGAAGCTGCCATTATCAAAGCTGTTTGAATAATCGTTTCAGACGACCTTGCTCTACAACGAAATCCCTTAACGTCATCGGGAAGATATT
GGAAAAACATCCAAACGGCTGTTTGATA

SEQ ID 1472

MIDFDKPAEEAIIYQSRLLKKSFTTLLSSTTKIPLTSCGRYHKNITQAVLI

SEQ ID 1473

ATGATTTTCGCAGACCCGCCCTTACTTCTTCCCAATGACGGTTTCACTTGTCAAAACGGGCAAAATGGTTCCGTCAATAAGGGCACTGGGATTAATCCAAAGGAATGGCGCAGATTGG
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CCATAATTTGAACAATATTACTTGGGAAAAACCAATCTCCCTTAAATTTGCTGCGGTTCTTTACCCATTCGACAGAAACAATCTTATGGGCAAGAAAAATAAAAAGCCAAACAT
ACGTTTCATATGAAATGATGAAGACAAAATAATGGCAACAGATGAAATGTGTTGGACATTCGCACCTCCAAATAAAACCGAAAAACATTCGGCAACATCCGACACAAAAACAC
TCCCTTACTTGAACGCTGCATATCTATCGCTTCAAATATCGGAGATTAAATTTTGACCTTTTATGGCGAGCGGCACAAACAGCGGTTGCCGCTTAAACATGGTCGGAGATTTCGGG
TTGCGAATCGAAGAAGATTTTTGAAT

SEQ ID 1474

MIPADPPYFLSNDGFSQNGQMVSVNKGWDSKGMADLEFYEWLRLCYALLKPNGTIWVCGTFPHNITLYLIGYLMQTVGYHILNNITWEKNPNNPNSCRFFTHSTETILWAKNKKAKH
TTHYEMKAQNNKQMKCVWTFAPPNKTERTFGKHPTQKPLILLERCILSASNIGDLIFDPMGSGTIGVAALKHGRFFCGCELEDFLN

SEQ ID 1475

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ATGCGGGTTATGAAGTTTGGTTTAAATGAGAAATGAAGGCTTATGTTTCAAAAAATATGAGTTTACCAGTTTGGAAAGACTGGAATACAAATTAATTTGGAAGACATCTGTCTAA
AAGATTACTCGCCGATAATGGCTTATTTATCATCATCGTGATACCTTATTTATTTAGATCAAAATCCAAACAACTCCCGGTTCACTAGATGAGAAATTAACAACTTCGGAATTTAAG
AGAAAAATATACAAAGTTAGTTCACCTTTAGGTTGGCGGGTGGATATGCTATGTTTGAATGATTGGTTTACAAAAACCGGAATAT

SEQ ID 1476

MIIIGIGGARTQTGLRFEERTDLRLFEIIPGYDLRKTDDNAGYEVWPNGLKAYCFKRYEYRFLERLEYNINWKDHLKRLPLDNLFIIRDTLFIIBIKPQQTGSGVDEKLQTCDFK
RKQYTKLVHSLGNKVGYYVVLNDWFTKPEY

SEQ ID 1477

ATGATTGGTTTACAAACCGGAATATTAAGATGTTTATGATTATATTATCAGTGTAACTGCCATTACCAATTTAAACAGATTCCCTTAAGGTGGTTTGGACTGCTGATGGTGAACAA
ATGAA

SEQ ID 1478

MIGLQNRNIKDVLDYIISVNCHYQNTIPLRWGLPDGETNB

SEQ ID 1479

TTGACAGATGCTGCATTACGTGTCGCGAATCCGCGTATTTTGAACAAAGGTGGGGTACTTTTATCACAATAGCAGAAAGATGGAAAAACGGCGGGGATTGG

SEQ ID 1480

LFDAAFSVAESAYFQKVGILLYHNSRKMEWGSDW

SEQ ID 1481

TTGTTCAAAATACGCGGATTCCGCGACACTGAATGCGACATCTGTCAAAGATTATTTGAAAAAGGTGAGTTAGACAAGTCTGCCGACAATGTGATACCATCCAAACATATCCGACG
GTTTAGGCGGTATTCAGAGTACGGTGTCTTATGC

SEQ ID 1482

LFKIRGPRDTBCSICQRLFENGRVRQRCQKYHIQNYPQGLGGIPEYGVLC

SEQ ID 1483

GTGTCTTATGCTGATGCTGTAAACAATGCCCGTATAGAAAACTAAAAAGGTTGTGCCGACCGTTATGCCGGTTTATGACCAAAGTGTGAGAAATAGGGGCGGTTAATAAAAAACGT
GGCGT

SEQ ID 1484

VSYADAVNNARIENLKRLLPTVHPVYEQSVRNKGRVKKRRR

SEQ ID 1485

TTGCGTAGCCGACTTGGCAACCGCAAAATCAGCAAGTTCACAATAGACCGCTGCTGAATATGCTGCCAAAAACAGGCAAGACCCGGAAGTGAATATCAGGGCTAGCCGACAAATGC
CCGACCGCATCAAAACAGCCGAAACCGCGCGGTACAGACGGCATAGCCCGACAGCAAGGACGCGCGCGGCAACCCGAAACATCCCGACCCGAGGACCGGGGATTTTTT
CGCGCGGTTCAGGGGGGATTTGGAATTAAGCGGACGGGCTTGAAGGCAAAACGGCGCGGCGGCGCAGAACTGTT

SEQ ID 1486

LRSRLGKRQNVHNRRAEYACQNRDRRTEYQVAAQMPDRIKPSRNGGTDGIARQQTAQTGAKPETSPTARHGDFLRPLQGLDLSGTGLKAKRAGRRTV

SEQ ID 1487

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CTT

SEQ ID 1488

MICAFLNCITTSFIRPQTNRDKPLCHSTCNAIPPSSDLGYAHWNTATDRLSNQLERNTEFVKSKNDNANRQFNQKSFIF

SEQ ID 1489

TGAAATATTGGAACCTTTTAAAGTTGGAATTGTAATAATCCCGTTTCGGGCAAGCCTTGACGGATTTCGGGATATGCTGTCCGGCACACAA

SEQ ID 1490

*NIGTFNVGIVKSPFRASLDGFADMLSGTQ

SEQ ID 1491

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SEQ ID 1492

NKQKIFVLYTGGTIGMTQSSAGLRPDALVQALAPFSDGMDFMHVCEPLIDSSAVQLQNWCAWLDIAAALPQYDGLVLRGDTDTLAYTANMFALALQGLDKPIVLTSQWFPYNAEGSD
APENLVTAVAAFPGLKQTLIAFDGLKLYPAVGSSKISTETAAGFNAHFALAEWDETRGWHNVRI PQDAADVSDGLEIRYPDPQAKIAVRPLIPGFAVQELADLGGQLPAQALILQSYG
HGMTSAGEGPIRAVDFTQOQKLLNLSQVPOGCAAVIAQGDALRRAGVNVNGKCNLEATATLAVSEGWADGVKHELQRLGLV

SEQ ID 1493

ATGCAGGGAATGCACGACATCGGCGCAATCGACAAAAGACTATGCGCGGCTTTGCAAGTCTTGCCTGACCGAAATCAAGCCGTTGAGCGCGGGGACATCAAGGCAATCAGGAGAAGG
AGGCATATCGCAAGCCGCTTTCGCCATCTATCTCAACGTTGGGAAAAATCAGCTTTCGCTTGGAGCGGGCGCTTAAAAAGCCGAGCGCGCGCTTGAAGCTGCTGACCATCTCAA
AAACAAGGCGATCGAAGCCATTCG

SEQ ID 1494

MOGLHDI GAIDKRTMRGFDKSLTEIKPLSGDIKAIKEALSOAFAIYLVNKGHVSAMERGKPSGAALKLITIVKNGIEALIA

SEQ ID 1495

GTGTATTGCTGCGAAAATCCCGCTTTTATATTTTCATGGCTGTATCTCCGTGAAAGTCCGCTTTGACTTCGCTTGTCTATGTGCGTTTCTGTCTATGCCAAGATGATGGCGCGGTTTTCT
TTAATTCGTGAAGTTCTTTATCAGTGATGTTTTCCGCTGCTCTTGGCAAAGCGGCTCATGAAAAACGCGCTTCCATGCTGAAAAATATCAGACTGCGA

SEQ ID 1496

VYCCBNFIFHGCISVKVFPDFACSMVSIVIAKMAAVFFNSVSSLVMSRSLAKAVMKNARSCLKNRLR

SEQ ID 1497

ATGACCGCTTTGCCAAGAACGACCGGAAAAACATCACTGATAAAGAACTTACAGAATTAAGAAAAACCGCCCATCATCTTGGCAATGACAGAAACGACATAGAGCAAGCGAAGTCAA
ACGGCACTTTCAGGAGATACAGCCA

SEQ ID 1498

MTAPAKNDRENITDKELTELKRTAAILAMTETDIEQAKSNGTTFETIQP

SEQ ID 1499

ATGCGGATATTCAAAACCAATGGATAGTGAAATTTGCCAAGAACCAAAAATCAGTGATTCAGAGCTGATAGAGCGGCTAGAGCGGGCAGATAACGGCTGATAGATGCAGATTGGCGG
CGCG

SEQ ID 1500

MRIFKNQWIVKPAKKHKSIDSELIEAVERADNGLIDADLGA

SEQ ID 1501

ATGCCGTGAAAAATATCAGACTGCGATAACCCCGCTTCTGCCCTTGCCTTGCCTTACGCTGCTTAATCACGCGCGCCCAATCTGCATCTATCAGCCGCTTATCTGCCCGCTCTA
CCGCTCTATCAGCTCTGAATCACTGATTTTGTGCTTCTTGGCAAATTTCACTATCCATTTGGTTTTTGAATATCCGATTTGTCAACCGTTACT

SEQ ID 1502

MPEKYQTATTAASALPLPCYTLLNHAPKASISPLSARSTASISSESLILCFIANFTIHMFLNIRIVQFFT

SEQ ID 1503

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SEQ ID 1504

LVFEYFHCATVYLVILGIIPKTGNTASRLFIPCNFSYAA

SEQ ID 1505

TTCGGGTTTTCCGTTTTTTTACCCTTGGCAGTGGGAGCGTAGCGGAATGAAAAAGCAAAACGCAAGGACCGGCTATTTTGAAGCAAGTGGGTTAAACCGGTTGGTTATATTC
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SEQ ID 1506

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SEQ ID 1507

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SEQ ID 1508

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SEQ ID 1509

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SEQ ID 1510

LRYFSDTVKNQVSSIRADWTGLHSQEGDGRITISLKSIV

SEQ ID 1511

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SEQ ID 1512

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SEQ ID 1513

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SEQ ID 1514

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SEQ ID 1515

GTGGCCGTAGGCTGTGCGAGTTCAAATCTCGCTGTGCGCACCAACACACAAAAACGCTTAGAAATCTAGGCGTTTTTTTCGTTAATCTGTCTGATGCCATCAACCAATCCCAATCAA
TACAAGGATTTCAGGCTGATGTTATCTCCGCTCCCTTCTGACTGTGAATCCCGTCAATCCGCTCAATCCGCTCAAT

SEQ ID 1516

VAVGCASNLAAGTNTQKRLKILGVFFRLILSDALINQSQIQGPDQCYPAVFFLTQVSRPIRPN

SEQ ID 1517

TTGAACCTCGCACAGCCTACGCCACTACCCCTCAAGATAGCGTGTCTACCAATTTCCACATGTGCGCATTGAAAAAAGTGTATTTCTGCTGCTGAGAACAGGGGAGAGGTTCCGTA
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TAC

SEQ ID 1518

LNSHSLRPLPQDSVSTNFTMSAFEKLLFLLLRNRGRFGLAYFGCLLSLYVAEVQTPVCRVGVNIHSHAGCKECCNGRAAEZEVVAGRAEYALRAAASRSEGRAGIRAFVLEQ
Y

SEQ ID 1519

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CAGCAAAAACAGCGTTTGGACTTCAGCAACATACGACAGCTCAGCAAGCACCAACCGGTAAAGCAATACCGAACCTTCTGCCCTGTTCTCAGCAGCAGAA

SEQ ID 1520

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SEQ ID 1521

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SEQ ID 1522

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SEQ ID 1523

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SEQ ID 1524

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SEQ ID 1525

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SEQ ID 1526

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SEQ ID 1527

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CCATCAGGTATCCGACGCTGCATACGCGCATGTATTTGGCGGAGCGGGTTTGAACCTGTACAACTTCAGGGCGGATCGACGCGTGGCGGTTGAGTTGACGCGGAATGGCG
CGTAT

SEQ ID 1528

LGLQATFCLVFFGGFVMDIVQLPSAALKAMWDEGRMFLDVRTDEBAAVCSLPAHHPNLILPLRQNELPDDVPLVVYCHHGIRSLHTAMYLAEAGFENLYLQGGIDAMAVEVDAEHA
RY

SEQ ID 1529

TTTTAACAAAGATGCCCTGATGGGCAAGCTATCTTATTCAGACCAAGGAACAGTATGTAGACAATTTAACCAGCGCGCTTCAGCAATGTCTTCAAAACAT

SEQ ID 1530

F*QRMPLAGQAILIQTQDYVRFNRPLQOCLQKH

SEQ ID 1531

TTGCTCGCCTTGGGTACCATCTGACTGTCTGCGGCTTCGCTGTTTTGCTGATTTAAATTTAATCCACTATACAATCAATATATTTAAGTCGTTGTAGCCCTCTTGTCTGTCAA
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SEQ ID 1532

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SEQ ID 1533

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SEQ ID 1534

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SEQ ID 1535

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SEQ ID 1536

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SEQ ID 1537

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SEQ ID 1538

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SEQ ID 1539

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SEQ ID 1540

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SEQ ID 1541

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SEQ ID 1542

LERKRSRVSFQTFPSVSGICFVSGILRFAANFLQVVCILINILIRMQNRTP

SEQ ID 1543

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SEQ ID 1544

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SEQ ID 1545

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SEQ ID 1546

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SEQ ID 1547

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ACGCTTTGGCGCAACTGATGCGCTTGGCGCAAGGATGAAGGGAATAAGGGAATGTTTCCCGCTTC

SEQ ID 1548

LREVRLLLEADVALPVVKEFVNVKEKALGQEVAGSLTPDQFTGVVQALVELMGENKNTLDLVSPPAIILMAGIQAGKTTTGVKLARLLKNDQKKVLVSDAVYRPAIEQLRL
AEQVGVDFPSPDTHQKPVETATAVDYAKKHFDVLMVDTAGRLAIDEEMNETKALHAVNVNVEITFVIDAMLGQDAVNTAQAFNEALPLNGVVLKMDGSDRGAALSVRHVTKPIK
IGVGEKINGLEFFPHRDLASRLTGMGDLVLTIEDVQKGI DEEAAAKMAKLLQKKGFLDNDFKEQIQMRNHGLENLMSKMPGELGQISKQIPBGTAEKMGKVEALINSNTPKERANPA
LLKAGRRRIAMGAGTTVQEVNKLKQFEQMQNMKMFSGNLGKLMRLAKGMKIGKMPFGL

SEQ ID 1549

TTGTCGAGATAAAAGTCAAGCAAGCCGAAACATTTTCGCGCGAAGCGGCAATTCATCAAGATTATGCGCTTCGAAAGCGCGAGGGGGGCGAGATTCGCGCGCGCGCGGACGTTACG
ACGCGATT

SEQ ID 1550

LSEIKSQNKPHRLRFATFYQLRCLKAAGGADSRPAGRSOGI

SEQ ID 1551

TTGTTTTGATTTTAAATAGAAATTTTATTATTTTAACTTACTGTTCTTTCCGCTCCAAGATTCTGTATGATTCGCGCAATTCCTGCGGTACGCGACAGCTAAAAAATACTACAT

SEQ ID 1552

LFLLILNRIFLILILFFPLQRFCHIRQLPYGQRKILH

SEQ ID 1553

ATGCAAGACACGCGCGAGATTCGTTTTGTCAGGAACACCGCGCGGATGATACCATTTCCATCAGAATCGCGAATATTCGAAGGGCGGTACCGCATGTGTACGCGCGCGGACCTACCGTT
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CGCGCAAACTCCCTCGCTGCTGCTGTTTTTGAAGAAATTTTGGGA

SEQ ID 1554

MQDTRQIPPCQEHARMYHFQNAEYPRGVYRMCTAATYRSGYPENKILFSVADFDELIGDQVYLVGVSHLVEQPNRALLTLNKGSDTATYTLVLEAGELVEGGPHFPAGKNHVSWRDE
NSVWVCNPDWDRQLPESGYPREVWLVERGKSPESLPAYQIDKGMVNVNARYLDPGSPFDLIEASDGYTKYTLQVSEGGAKPLNLPNDQVVGVLGHLILLRLKDWHRANQSYPSG
ALVAVKLNRLGELGAQLLPAPDETQALSVETTKRPVVASILENVQRLKAWRPADSKYQAEPLPHLPSGALERTDQPHGGDVVYLAASDFTPLPLPALDLNRELTVMLRQPPQVSDG
IEVRQFNAVSSDGERIPYFHVGNKNAAPDTPLVYAYGGFIPILPHYLGSVGKYWLEBNAFVLNIRGGGEFGRPHWAAQGISKHSVDDLLAVVRDLSEGMSSPKHIGLQGSNGGL

ITAAAFVREPQSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGNPQKYEACKRRRLGELSPYHMLSDGIDYPPALITTSLSDDRVRHPAHALKIFYAKLRETSQSWLYSPDGGGHTGNGTQRES
ADKLACVLLFLKKEFLG

SEQ ID 1555

SEQ ID 1555
TTGTGCGCAACTGAGGCATCCGATCGTCTCATCCAGCGCGTACCATTCTCGACGCGCTGCGCGCCGCGCAAGCGCCGACGCCGCATTATTGCGGGGGTTTGC GCGTTACCGACGAA
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CCCGAAACGCGCGCAAGACTACCGCAGCAACGGACGAAACCGGCATATTCTGGTGCGTGCCTGCACCGC

SEQ ID 1556

SEQ ID 1556
LSQLGIRLVLIINGAYHFLDRLAAAGQRTPHYCRGLRVTDETSLGQAQQFAGTVRSRFEALCGSVSGFARAPSVPLVSGNFLTARPIGVIDGTDMEYAGVIRKTTDTAALRFQOLDAGNIWVM
PPLGHSYGGKTFNLDWQAAASVAVSLQAELVYVLTSLDGISRFDTGLAETLSAQEAQSLAEHAASETRRLISSAVAALEGGVHRVQILNGAAGSLQLQLFTFRNGIGTSLIAKEAFVSTIQ
AHSQDIPHIAALTRPLKEQGVLLHRSREYLENHISEFSILEHDDGLYGCAALKTFEAEDCGEIACLAVSPQAQDGGYGERLLAHIIDKARGIGISRLFALSTNTGFWFAERGFQTASEDEL
PTRRKDYRSNGRNPILVRRLLHR

SEQ ID 1557

ATGCCCGCCCTGTTCTCTGCGCACTGCAAAACCCGCCCTCGGGTCAAGAAGCCGAGCTCAACGTCGCCCAAGGCTCGTCGCTGCCAAAAATGCGAAGGGCTGTTTAAAGCCAAAGACC
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CGCGGATATCCTCAACGGCGGTACAACCTGCACGATACGCCGCCCGCAACCGCGCTGCCGCACTGCCCGCCGACCGCAGGTTTCGCTACCGCCGCCCGCTCAGGAAGGGCTCAACTGG
ACTATTGCAACCTGTTTCGCACTTATCGTCTCTCATATGACAGCTTTCCTACCTCTTCATCTTA

SEQ ID 1558

SEQ ID 1558
NPACPCPHCKTRTLNWKETQLNVAQGVVQCEGLFKAKDHLASTKEPIFNDLPEAVSDVKLVHRIGTHAISKKQISRDEIADILNGGTLHDTPTATAAAAAAAAPQVSVPPARQEGLNW
TIATLFAILVLIHOLSYLFIIL

SEQ ID 1559

SEQ ID 1559
ATGCGCGTCCGAACCACTGCGCGTTTCAGACGGCATCAAACCGACACACACCGAGAAACATCATGCCCGCGCTGTTTCTGTCCGCACTGCAAAACCCGCGCTTGGGTCAAAGAAACCCGACT
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AAACTCGTCCACCGCATCGGCACGCACGCATTAGCAAGAAACAGATTTCCCGCGACGAAATCGCGGATPATCCTCAACGGCGGTACAACCTTGACGATACGCGCGCCGCAACCGCGCGCTG
CGGCACTTGC CGCGC CACCGCAGGTTTCGCTACCGCGCGCGCGCTCAGGAAGGGCTCAACTGGACTATTGCAACCGCTGTTTCGCACTTATGCTCCTCATATTGCAAGTTTCCCTACCTCTTCAT
CCTATGAACGCGCCCGACAGCTTTGTGCCCACTTCCGCGAAGCGCGCCCTTACATCCGCGAAATGCGCGGCAAGCACTTGGTTCGCGCGGATAGACGCGCGCGCTTCTGCAAGGCGGCACT
TAAA

SEQ ID 1560

SEQ ID 1560
MPSEPPAASDGIKPTTTEKTSCTPPVSVRIKAPASGSKPSSSTPKASSAKNAKGCLKPKTIWQARKNLYSTICPKLFMSNCSSTASARTPLARNRPATKSPISSTAVQPCITRRPQPPL
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SEQ ID 1561

SEQ ID 1567
ATGACTGATTTTCGCCCAAGATTTCCTCAAATTCCTCCCTCGCCCCAAATGTTTTGAAATTTCGGCGAAATTTACCAACCAAGCCGAGCGCGGTCCGCCCTATTTCCTCAATGCCGGCCTCTTCA
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CGCGATGATGCTGGCGGAAAAAGCGGTGAACGTCGCGTTTGCTTACAACCGCAAGAAGCCAAAGAACCGCGCGCAAGCGCGCGTGTGGTTCGGCGCGCGCTTAAAGGGCGCGTGTCTGATT
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AATTGTCTCGCGCTTCAGGAAGTGAAGAAACAATACGCGCTGCGCGTCCGCCCATCGCCAGCCTGAACGATTTGTTTCTCTGTCGCAAAACACACCCGAAATCGACAGTCTCTCGAACC
CGTCCGACCTACCGCGCGGACATCGCGCTAGGA

SEQ ID 1562

SEQ ID 1562

MTDFRQDFLPKFLSLAQNVLPKFGFTTKAGRRSPYFFNAGLFNDGASTLQLAKFYAQSIIESGIRFDMFLGFPAYKGIILAAATAMMLEAKGVNVFPFAYNRKEAKDRGEGGVLPGLKGRVLI
IDDVLSAGTSVRESIKLIEAGGATPAGVAIALDRMEKGTGKLSAVQEVKEQYGLFPVAPTASLNDLFIILLQNNPEFGQFLFPVRTYRRQYGVVE

SEQ ID 1563

SEQ ID 1563

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TTGCGCGCCCGCGAGCATTCGACCGGCATTTAAACAGGAAACCGCGCGTGTGAAACGGTTTTCGCTGATTTTGGC

SEQ ID 1564

SEQ ID 1564

ICAVKLMSAFAPPEPRQRRRQHAQCDEARLQAVHFRHQPIDVVRVLAQVNPNGHGNRGQFVHNKQAKIIRYFAADAGGNENGSPQTRQETGDKQNFVAVVFEFLMLRVTFTRHRDARN
RFELEDLPDPAAGGKHAVARQHAETTRKKNMRIGITHTRNHAARYQQIFGNRHAETADDQNEKHGRIAVFDKKGFGQKHKSGYSIVGDKKSQEAETFSABNGILSKIMPSESGRGGR
FAPRRFTFRHRLNRKTAAVETVLPDFA

SEQ ID 1565

SEQ ID 1565

ATGCTTTTCGCTACCGCGCTTCCTTTTTCGCGGGCGTTTTCGTACTTGCCGCGCTTGCCGCTCGAAACCTCAAGACAACAGTGGCGCGCAAGCCGCTTCTCAAGTGCATCCGGCGCGGGCTG
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GGTGTGATCTGTGCTTTTCGGCTTTACGCATGTGCCGATGTCTGCCGACAGGGCTTTTGACGTACAGGCACACTTTGAAGCAGATTGGCGGGCAGGCTAAGGACGTGAAAGTGGTGTTC
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AATACCCCGTGTCTCTCGCAAAATCAATCAAAAAGACGACAGCAAGAAACTATTGGTCGACCACTTCTCCGTGGCTATCTTATCGATAAAAACGGTGAGGTGGCCATTTTCTCGCCTTA
CGGAACTGACGCTGGAAACGATTTGCTGCGCATCTAAGGACCTGCTC

SEQ ID 1566

SEQ ID 1566
MFSPVPSRFLPGVFLAALAAACKPQDNESAQAASSASAPAAENAACKPQTGTFDMRKEDIIGDFTLFDGEGKPFSLSDLKGVVLLSPFGFTHCPDVCPTGLLITYSDFLLKQLGGQAKDKVKVF
VSLDPERDPTPEITIGKYAKQFNDFPIGLITATGGQNLFPVIKQOYRVVSAKINKDDSENLYLDHSSGAYLIDKNGEVAIPSPFGSEPETIAADVRTL

SEQ ID 1567

TTTCAAAACAGGTTGATGCACCTTCCTCGAATTTCGAATAGCTAAACATGCCTGCTCGTGCGACAATTCACACCTGCCAAATCAAGCAA

SEQ ID 1568

FQNR LMHPSSNFRIAKTCLLVRFHTCKIKQ

SEQ ID 1569

ATGTTTAAGCGCGCGCTACCTCCACCTGCACGAGGCTTTGGGCTTGGGTTCGATGTGGCTGAAAACAGGCCGCGCGCGTCTTGCGCCCAAAAACACACCCGCAACCCCGGCACAGGCACGTC
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TTCACGGCAAGCGGGCATCTCTCTCGACAACATCTCTAAAGCCGACAGGATGGATGCGCGCTATGTTCACAAAACCTGTGGGTGAAAACCGCGCGCTCGGTAAACCGATGCGCTGTG
AACAGGCGCTCGCGGATGCGCTGGGTCAAATCGCCAGGGAATCGACGGCTCGCGCGCCCCCGCGCTCTATTCTTCGGACAGCGCTTTGTCAACCTGGAACCGCGAGCGGATGATTGAAAC
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GGCGCAGT

SEQ ID 1570

NL SARYLHLHEALGLCPMMLKQAAAVLPKNPATPAQARPQTVRAATIRPSQPHNVQTRLETHKALETAAVHTRKPAPEFETETPPGLSDGLIAPVPAASGITKLAVVSLCPPIEDAVYQGL
 FHCKAGILLDNILKAAGLDAAYVHKTWCVKTAAVGNMHPSEQAVADALGQIARELDGCRAPAVLFLGQAVPNLNRQAMHETLCGSRPFFIIDHPARLLRQPELKARNWQVLKQLKRALRQG
 GGS

SEQ ID 1571

ATGAACATCCGCCAGCCTCACCGTCCGACTGCGCGCACTGGCCGCGCTCGATACCGCTCGCAACCCGTCGCGTGGAGCAACACGCCAATTGAGTCCGCGCTGTGTTCCGCGTCCGAAC
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GTCCGCCCTGCTCGAATTATGGTACGCACATCTGCCGAAGGCACGCAAGCCTGCTGCTCGAAGTTCGCGCAGGCAACGCCGCCGACAGGCACCTGTATACCAAAACACGGCTTCAGCATT
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SEQ ID 1572

MNIRPASPSDCAALALDTVCNPSAWTORQFESALVSPSEQVFLAEKDGRIAAFIVWQNLPEDESLHLIATAPECRRRGVASALLEYTHAHLPECTORLILLEVRAGNAAAQALYTKHGFST
 AGRRRKNYYCAADGOTEDAIVLEKIC

SEQ ID 1573

TTGGTATACAGTGCCCTGTGTCGGCGGGCGTTGCTTCGGCGGACCTTCGAGCAGCAGGCGTTTGGCTGCTCTTCGGGCAGATGTGCGCTACCAATATTTCGAGCAGGGCGGAGCGCAACGCCCGCTCGCG
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SEQ ID 1574

LVYSACAAALPARTSSSSRCVPSGRCAVQYSSRADATPRRRHSGAVAIRCSSDSSGRFCQYTIKAAILPSPSARKTCSDGETSADSNWRCHVADGLQTVSSAASAAQSDGEAGRMFHFVPSV
PPVLWQSGRFCCGRRAVRVRPQLRDSRRRGRARENRRRSAYRVCLRRADGFPVTRHCRCRLKRRTPRGGQCLPPYRLDNRNNGGGSACRTTHKTLRPYARPOBRVCSFAAAAARRRHRAW
GCRLKACRTALENLAPRCRYAVE

SEQ ID 1575

ATGCAAGCCGATTTCAACCGCCGCCGCTCTCGCCGTGCATACCGGAATCTCTATTGTGCGCTCGCGCTGCGCGCCGACGGCGAAATCCGTCTGTGTCCATCAGGAAGTCGGCATCCGCCAGT
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SEQ ID 1576

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MGEVFFYAMFDTLNRRLSDSYOVGRAADIALPEGYVSDGIGSAPALENRPPFSGKPDMPATAADFLALALGGYPATGAHAELLYVRNKIALTAKEOAEKART

SEQ ID 1577

TTGAAATCGGCTGCATGGTGTGGTTCTCGTTGGTTTCAGACGGCATTTATATAGTGAAATCGGCTTGCCCTGCCGTGTCGTCTGTGTCCTAGGGCGGTATGGCGCAAAAATGCCGTCCGAACGG
TAAATTATCGTGTTCGGACGGCATTTTTCAAATACTACTGTGTGTGCGCCGATCCCGAATTCG

SEQ ID 1578

LKSACMVWFSLVQTALYSEIGLPAVSSCPRAVWRKNAVRTVNYKVRTAFPKYYCLSAMPIS

SEQ ID 1579

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TTTCAAT

SEQ ID 1580

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 ET

SEQ ID 1581

CACTCAGCAAAATCAAGCAATATTTCAGAAAAATCGTACCGATCCGCCAGGGCAGTATGGTAAGTGTGTACCTTATGCCGGACCTGCATGTTGAACAATAAAGGAAAAAATCATGAACCCGC
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CAGCCCGCTCCGCAAACTGCCGCACACTGTCTGGATCCGGACAGGTTTGGCTGACCCAC

SEQ ID 1582

HLONDAIIOKIVPIRPGQYGKCVPYAGPAC*NIKEKIMNRROFLGSAAAVSLASAASFARAHGHADYHHHHIMQPAAASAYTAVRQTAHFCLDAGQVCLTH

SEQ ID 1583

SEQID 1583

ATGATGCGCAAAATAATTTCGGCAGCGAGCGGTGCGCGCGGAAGTCGGTCAGTTTCGGATTACGCCCGATTTTGTATTGAACTCGGCTATCGCGCGGGCAGGTGCTGGTGCAGCACG
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ACCGTTCGCGCGACTGGCAGCCGATATCGCAACAGATGATTAACGTGCGCATTCAAAAGGGTCAGAAATGCGAGGAGCTTCGAAAGACGCTGTTGGCCGAAGTGGAAAAAGAACTCGAAG
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SEQ ID 1584

SEQ ID 1584

MMAKKYPFGTDGVRGEVGQFPITPDPVLKLGTYAAGQVLVQHDTDQKPTVLIGKIDTRISGYMLAEALVAGFTAAGVNVVQGPLPTPGVAYLTRALRLSAGVMISASHNTYSDNGIKFPAEGG
VKLSDEVELRIEAKIDEEMKTPQSARLGRARRISGADDRYIEPKCKSTFPGHSDLRGLKLVITDANGAGYVAPKVFHELGAQVVSIGNEPNGYINIEKCGATHTKTLQAAVLQNEADYGLIA
LDGDEDRLLMVDKRNQVVDGSDSLIVYLAKARAREGINIGGVGVTFVTNMAETALKKQGVDFCRKAVGDRYVLEQLNQRGWLIGGEASCHILCHDKHNFGDGIISALQVLAALQLLNQDLA
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SEQ ID 1585

SEQ ID 1585
TTGATTCCTCTCTGACCTGCCATATTGATCGAGATATGCAAAAAAGATACCTAAACCCAAACGTTTATATATTATCTATCTGTGTATGACTAGGAGTAAACCTGTGAACCGAACTA
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SEQ ID 1586

SEQ ID 1586

LIFASLTCLIDAVCKKRYHYNQNYVILSCMTRSKPVRNRTTFCCLSLTAGPDSDRLQRRGGGGGVAADIGTGLADALTAPLDHDKGLKSLTLEASIPQNGTTLTSLAQGAKEFTKAGGD
NSLNTGKLNKDKSRFDVQRIEVDGQTITLASGEFQIYKQDHSVAVALRIEKNNDPKIDSLINQRSFLVSLDGEHTAFNQLPDGKAIEYHGKAFSSDDADGKLTYYTIDFAAKQGHGKIE
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SEQ ID 1587

SEQ ID 1587

ATGAGCCGCTTATGCGTTTTCCTGCCGTAAAAAACATTATAATCCGCTTATTACCTATTGCCCAAGGAGACACAAATGGCACTCGTATCCATGCGCCAACTGCTTGACCACGCGCCGAA
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SEQ ID 1588

MSRLNFFAVKNITIIRLIYLLPKETQMALVSMRQLLDHAAENSYGLPAFNVNNLEQMRAMEAADQVNPAPVIVQASAGARKYAGAPFLRLHLILAEEFPHIPVVMHQDHGASPDVQCRSTQ
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KMASRYAKGELNOIVE

SEQ ID 1589

[illegible]

SEQ ID 1590

SEQ ID 1590

LCGTVMVLGFAAYFDAYLHENIVREGKSEHTVAAYRRDLEELFALLAQMPSEDAGVQPDLSRRDPTAALRRLSQRGLDGRTLARKLSAMRQYCAWLVRKGLMRADPTADIKPKQPQPERVP
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SEQ ID 1591

SEQ ID 1591
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CGCGTTTGACAGCCAGGCGCAATACTGCCGCCAGCCGACAGCTTGCGGCCAGCGTCCGACCGTCCAAACCGCGCTGCGACAGCCGCGCAACGCGCGGTAATAATCGCGCCGACAA
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SEQ ID 1592

VGFVIEAGDVVEIEIGINLRKRAVSEQLHRPDVARSLQVAVGVAHMMRRNPVAVAVLRRPFEAFDLALAQARAVPAGKQGFVAVRCLTQRIQIVFGPHAFAGQNLITLAPFAG
NVYPRPVIYIICIQAVYLAHAQTAAVHQLERVVAHRQVAAVHGQIQHPVQPFRLRQFGYALGLLRFDVGGRVGAHQPAFDQPGAILPPRQLARQPTVQTLARQPPQRRRIAPRQ
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SEQ ID 1593

ATGAACCCAAAGCCCTACTCCACCTGATTGACAGCCCGCAAGATTTCGCCCGCTGGCAAAAAACAGTCCGCCCGCTTCGCCGGGAGTTGCCGCCCTTCTGCTGGAATCTGTCCGGC
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SEQ ID 1594

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VEFEQRFPDRYFDVGAIEQHAFTVAGGLACBGMKPVVAIYSTFLQRAYDQLVHDIALQNLVPLFAVDRAIGVADGPHAGLYDLSFLRCVPMNIVAAPSDENECRLISTCYQADAPAAV
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SEQ ID 1595

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SEQ ID 1596

VLGVFLRVWKFIPILVRITAAVPSADTRQNAV

SEQ ID 1597

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SEQ ID 1598

LPCIGRRHRRYTDKRNKFPNAQRHTKHPKAAARTLPAACGVSIIKKPKQTPFKNAAR

SEQ ID 1599

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SEQ ID 1600

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SEQ ID 1601

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SEQ ID 1602

VCTLCRTMLKHGKNHPESSIFGQRRCLFGFRRLFRACARTRLFPSSRYAACRRIRLHRRPNCRTLSCGRTGLPDPLFVPAHSGRHVVRLCGCRAPDACLMRRGARPCRTKFPST
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SEQ ID 1603

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AGCGAAGAGTATTAGCCAACTCGGTCTGCAACAAATGCTGCCGAATTAAGTTTGGTAGCGGGGAGGAAACCGTATATCAGACCCAAACCGAGCAAGAGAGCTTCAGACGA
TCCCAAGTCCCAATAACAAAGGAGATCCCAATCA

SEQ ID 1604

MVAKIKFSDSTLSVLNNGERRFVYVCLFDLKKDKILYIGKCGNRIFEHENVASRQDPVSGEIIDRLKALSKCKLGRYIISYHLTEVEALAESALIHVKSVLGKKLKNKIAGBGP
GGISVEBLDRRFPGSSLPSEINPDGLILAIKHNAPDLDTDEELDYLPDNDQDANLKSRTLGNNVIGKDVASKVKYVIGVHTGLQNAVVSATBVDGFTWTEETKNGRKQTRVRFRTSR
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SEQ ID 1605

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SEQ ID 1606

LSCQPEVCNRTVGSGLAASGEVSAFPPIFYISGGRGKFLPFCLREGGVIQNYQAHQ

SEQ ID 1607

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SEQ ID 1608

MIIVIIYVFLYVSLFEQMFICAVNHATIFNIHIL

SEQ ID 1609

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SEQ ID 1610

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SEQ ID 1611

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SEQ ID 1612

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SEQ ID 1613

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SEQ ID 1614

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SEQ ID 1615

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SEQ ID 1616

VCMKPVVWALLLCACTSNFGDREHOFRLYSGLNLNOYSVASPCRTICTVCGFVALS

SEQ ID 1617

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SEQ ID 1618

LPTNFTYMKSERHNEWCADYDGEVVRDYRFTHKVEKDERSVIRDTVGIVIRKEAGKSLSOPEK

SEQ ID 1619

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SEQ ID 1620

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SEQ ID 1621

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GCAAGACATCATGGAATGTATTTCCCGCTTGGGCGGCGTGTATCAGGCAGGTACATTAACAGGCAACCGGATGCGCGTCCGCGCGCTTGAAAGATCGGAATATCATCAGCGCGAAGG
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SEQ ID 1622

LRINMNRNELFDRAKAIIPGVNSPVRAFGSVGGVPRFIKKAEBGAYVMDENGTRYTYDVYGSWGAIPAIVGHAHPVEVVEAVREAALGGLSFGAPTEGETIAIEAQIAEIMPVSVERLRLVSSGTE
 VMTATAIRLARGGTGRDKIIKFEGCYGHHSDSLVIVAGSGLLITGFNPSSAGVPADPTKHTLVLEYNNIAQLEEAFAQSGDEIACVIVEPFGVNNMLVRPTEAFVKALRGLTERKHAVLIYDE
 AHTGFRVALGGAQSLHGITPDLTTMGKVIYGGMPLAAPGGRKDIMECISPLGGVYQAGTLSGNPIAIVAGLKTLEIIQREGFYENLTALTQRLANGIAAAKANGIEPAADSVGGHFGLYFA
 AHVPRNYADMARSNIDAFKRFPHGLMDRGIAFGPSAYEAGFVSAHTPELIDETVAIVAVEVFKAAEA

SEQ ID 1623

SEQ ID 1623
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GAAAC

SEQ ID 1624

LTTYFRRHFYSRLKSKMYTPVIPAQAGIRKVGLAVIFNHYRN

SEQ ID 1625

SEQ ID 1625
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SEQ ID 1626

MSDCAVAVROMLAICGAVHDLAAONSPLTRDAAKVCL EACKQCAKACKEHSAHHAECKACVYESCLDCIKECEKLA

SEQ ID 1627

SEQ ID 1627

ATGAAAAAACTCAACACCCAATCGCCCGATTTCCAAGCCGGACTCAAAGCCCTGCTGGCTTTTGAAACCGCGCAAAACCCCGAAACCGAAGCATGCTGCGCGACATTTGCGCGCAGCTGC
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SEQ ID 1628

SEQ ID 1628
MKKLNTQSPDFQAGLKALLAFETAQNPETERIVADICADVQKRGDAALIEVTNKPFDQTNAKSIDDLILTQADLNAAPERLXXXXXXXXXTAARRVESYHQQRKMSWSYTTDEGTLGQQQI
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SEQ ID 1629

SEQ ID 1629

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SEQ ID 1630

SEQ ID 1630
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RGAOIVRVHDVKATADALKVNEALGVNR

SEQ ID 1631

SEQ ID 1631

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CAACCGCGATGAGACAATGTCGGCGGAATTAAGCGGATTTCGCGACCGCTTTTGTGTCGATACGCGCGGATTTGACGATCGACTACTGCTGCTATTTTGATTTTAA

SEQ ID 1632

SEQ ID 1632
LYGSRRLPCAOTDADGAQKRTAAYKGQDPAKVTHYLTRPAGPSCQRCVCPDETGFDRRLFRPYARSLKQNAKARISGKRYRRLSLVSAQVGNRPAPNVQNTVAGVFFEARFQCLLPA
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SEQ ID 1633

SEQ ID 1633
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SEQ ID 1634

SEQ ID 1634
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SEQ ID 1635

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AGCCGAAGTCGACAGAACTGCTGGACTTTATGTGGAATGGATACCCGGACGCGCCACACCGATGTGCGGCACTCCATCCACCAAGACCGCGTTTATGTGTCAAAATATATGCGGAA
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SEQ ID 1636

VQDKNNLCWLDMEHTGLNPETDRIIEVAMIITDSLNVLQSEVYAIHQSDLLDNDEWNTATHGRTGLTQVRRESSITEAEVEQKLLDFMSEWIPGRATPMCGNSIHQDRRFHVKYMPK
LENYFHYRLNDVSTLKEIAKRNWPIAKSVVKRGSHKALDDILLESIEMRHYREHFLISAPKBAQ

SEQ ID 1637

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SEQ ID 1638

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SQPDIPIRISDRILWITPSWHPAPEGCAVNLRLDPGLAFGTGSHPTTRILCLKWLDLQKNGESVLDYCGSGILTIAALKLAGSAVGVVIDEQAVERSGRDNQENNVDAQFFLPDLSLPQGF
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SEQ ID 1639

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SEQ ID 1640

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SEQ ID 1641

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SEQ ID 1642

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SEQ ID 1643

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ATCGCTATGTTGCGGACGTTCTACCGCGCGCGCGCGGAAATGCGCGCGCATTTGTCGAAGTCGCTCAACAGGTCAAGCGCGGACACGCTGTGATCATCGAAGCATGAAGTGTATG
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SEQ ID 1644

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SEQ ID 1645

GTGCGCAAAATCAAACTTCTGCAATTTCCCCAAAAACCGCGTTTGTGATATTACTGGAACATTTACCGCAACTTCGCGGAAATGAACACAATTTACGGTCTGTTCCCAACACA
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GATTTCGCGCAAT

SEQ ID 1646

VRKIKLPAHFPPKPPFDILLDIYRQLRENEHNTVSSHRTKTVSEHSARFAPLPQAGCFLKNQRNPPPEHRQPLKEQKWCAN

SEQ ID 1647

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SEQ ID 1648

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SEQ ID 1649

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SEQ ID 1650

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SEQ ID 1651

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SEQ ID 1652

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SEQ ID 1653

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SEQ ID 1654

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 PFEPAAADRLATOMKSGVEGVAAMAGRTIQESQKALRGELTGLCPNPFEDKATIRRELANPGERMLFVADAFAPGTPPEETHEICHAIDPFLWQIATIDMLKKEYSDSQGLQDLVLAAL
 RLRLKRGFSDKRLAQLLNVSEKEVREHRYALKLHPVYKRVDTCAAEFATETAYLSTYEEBCESRPSDRKKVMILGGGPNRIGQGI EFDYCCVHAALALRESGFETLMVNCNPETVSTDFD
 TSDRLYPEPLTLEDVLEIVRTENPMGWIVHYGGQTPLKLANALVENGVNIIGTSADSIDAAEDRERFQKVLNDILGRQPPFNRIAHNEEEALVAAEIGIYPLVVRPSYVLGGRAMQI IHSAR
 QLOKYMREAYQVSDSEPTLDFFLNATIEVDVDCVSDGKDVVITGGIMQHVEQAGIHSNGSGCSLPYYSISEEIQDETRTKAMAYALGVGLVLMNVQFVADGVGVVLEVNPRASRTVPFV
 SKATGVPLAKVGRACMAGI SLKEQGVKEVKEPFAVYKAEVFPFIKPGVDTILGPMERSTGEVWVGASFGAEYTKAQILGAGERLNTGVGKIFLSVREKGRVIRKTAKNFQALGYGICAT
 RGTAYOYLTEHGLIVOLANKVPEGRPHI GDAKNGEALILVNTVSTSDPSVDSHII ROSALQORVQOYTTTAGEMAMSEGAKSRYDLGVSVSYVLEHGLRKNRH

SEQ ID 1655

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TTGGACATATCAACGATGACATTTGACGACACGGCATAGGTCGGCAA

SEQ ID 1656

CAEHFQTFRRNGFKDLFTCPFPFTTDNHLRAQQPVFGNIPRFSNRHIGQGVVMLQICTCTDRGKCRPDGILYHVSVELVRPNKGVGGISRELLIQTFDDILIFIKONGCRARLKQLQFLRGRF
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SEQ ID 1657

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SEQ ID 1658

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SEQ ID 1659

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SEQ ID 1660

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SEQ ID 1661

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SEQ ID 1662

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SEQ ID 1663

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SEQ ID 1664

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ELEKQPAR

SEQ ID 1665

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SEQ ID 1666

MPADRYAPLETVLQELSAHGKPLSGIVARTGAMGKIQSVYLRDPGNLLEISSY

SEQ ID 1667

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ACGGTTTACAGGAATTATCCGCACACGGCATCAAACTT

SEQ ID 1668

MKISALDHLVLTADIDRTIAYFTQVLGMEVSPGNRKLFLGSKINLHGRGAETQPNQAHAACGTADLCLLTDTPHNKRFRYNYPTASNL

SEQ ID 1669

ATGGTCGAGTGGCTAATTTTCAATTTCCAGCTTTCTTTTTTCAGACGGCAGCAGCATACTGTTGCGGCTCTGAAATCATTATGCTTTTTCAGACCTTCATATTGCCAATGAATTTGTCGA
ACAAA

SEQ ID 1670

MVECANFHFQLSFSGSSILLPSENHYACFAAFILPMNLSNK

SEQ ID 1671

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SEQ ID 1672

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DYLVRNETVAIADIDTRRLTMLLREKGAQGGAILTGADATVEKAQELIAAFGSMVKGDLAKEVSCETETVEMTEGEMELGKGFVTPDKQPYHVVAIDFGVKTNILRLMLASRGRLTVVPAQT
SAEDVLALNPDGVFLSNPGDPPECTYALAEAVQKLMESGKPIFGICLGHQLISLAIGAKTLKMRFSHHGANHPVQDLDSGKVITTSQNHGFAVDADTLPANARITHKSLFDWTLQGIETD
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SEQ ID 1673

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SEQ ID 1674

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SEQ ID 1675

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SEQ ID 1676

MSVRSFIRINDILANSAYKITDVPFPAKLIDAMESPAHPFEGHEALMREWRALASAPILHYPNPSGGLQELALSAFIDIPDCAVALGNGSDELQIQTITLAKPGAAMLAEPGFIHYR
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SEQ ID 1677

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SEQ ID 1678

MPVTHFPTSARRNYGNTRTVI PAQAGIRFFEFQSPFINCLSEICLDSRLRGNDGAVSVFSDKFLKIKISSFLQKQTKIRNLKSRSHESGNPVRVSIVLVSFG

SEQ ID 1679

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SEQ ID 1680

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SEQ ID 1681

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SEQ ID 1682

MYRFLDSNPDKMSVRTI FEGDKPITSAPAVSRLADKRVVIFGTGSDLTEDDVLNTGBOYIYGIFDDDKGTVKVTVQNGTGGGLLEQVLKEENKTLFLNKGSDGSGSKGWVVKLBQQRV
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SEQ ID 1683

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SEQ ID 1684

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SEQ ID 1685

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SEQ ID 1686

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SEQ ID 1687

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SEQ ID 1688

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SEQ ID 1689

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SEQ ID 1690

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SEQ ID 1691

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SEQ ID 1692

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SEQ ID 1693

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SEQ ID 1694

MYRVAASFLRAYPWQSFQWQSATVCPARHCLRGNGGPRRHPSCGNLSQQLNRLNTSLAACPLSSSLPQBERTGRLLGLRFAARKTCAGCTPLFRRPETTAANLSCLSNRLQPKHL
PQSAPSPVGEGRGGILQVAATFPNNSTAPIQAFRLVALSPALSHGERGRGGCM

SEQ ID 1695

TTGGGCGGTTGAGTTGTGGGAAAGGTTGCCGCAACTTGGAGAAATGCCCGCTCCCGGCGCTCCCGCACGGGGAGGGAGCGGATTCGCGCAGATTTTTCGCTTCAGGCGATTTGAAAG
GCAACTTAAATTTGAGCTGTGTTCAGGTCGT

SEQ ID 1696

LGRLSCWERLPQLGSECLPGPPRGRERIAADFSVAGDLKGNLNLQLLPQVV

SEQ ID 1697

TTGGGAAAGGTTGCCCAACTTGGAGAAATGCCCTCTCCCGGCGCTCCCGCACGGGGAGGGAGTGGTTTCGCGCAGATTTTTCGCTTCAGGCGATTTGAAAGGCAACTTAGATTGCGAG
CTGTTGTTTCAGGTCGTCTGAAAGCAAAAGCAGCTGCACAACCTGAT

SEQ ID 1698

LGKVAATWRMPSPRPSPTGEGVGFGRFPGRFRERQLRFAAVVSGRLKSKQPAQPD

SEQ ID 1699

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GTCGTCGAA

SEQ ID 1700

LRTEAHIMNIQNIITLLDVAVPNTARTLGGEKAVRSVGQSDGIHIALHFGFVFAHIAALADAVQETLMPETGGAHILGIDTEIGTHKVRPGVTTIKGVKNIIVASGKGVGKSTTT
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VVE

SEQ ID 1701

TTGTGCGAACTTTTACAGGTATGCGGCGGATTTGAAATCCGTTGCCAAATATCCCGTGCAACAGCAGTCTGCAATTAAAGCTGTAAAAATTGCT

SEQ ID 1702

LCELLHGMRRIRKIQNTIPCKQQAIFVKIA

SEQ ID 1703

TTGGTGTGTTTGTCTGGTGTCTGCTGTTTGGATTGGGTACGCAAGCCCGACGAACCTGCCGGGGGGCAGGGCGGCTTTGACCTGCTGTGCGGGCAGCGGCTGACTTTGGACAGTTTA
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SEQ ID 1704

LVFLVLSFLDVRKPFDEPAGAAGRPLTLLSGQRLTGLQFSRDRTVLVYFWGSMGVCRYQSPILIDLAADGVFVGVAVRSGSASEVAAYMAKRLGLFPTVSDDEGLARSMRIATPAV
VLVKNKGVRYTTGISSTWGLRARIQADFFG

SEQ ID 1705

TTGATTCTCTACATAGCGGAAAGTTTGACAAAAACAAAGTTAACCGAAAAATCCGCTGAAAAATTCGTCCGCGCAAGCCCAATAACTGC

SEQ ID 1706

LILYIAESLTKTKVNRKNPPEKFVRASPHNC

SEQ ID 1707

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SEQ ID 1708

LGRHCLSLQVTEHTFKPSGKPVGVIFDATVI

SEQ ID 1709

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SEQ ID 1710

NPSSTLSAGSTDKPNIPIWTKTQLHLNFLTLAGSAGSLPKLAKLCYRTPVALYKQRLKQAEQDPARGIRPSIMAKLEKHTGPKGWLDRKHRRTVPETAESTGTAEIRIAETAS
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SEQ ID 1711

AAGTAGTATCTCGTCATGCTCTTCGCCAAACAGCAGACACGCGGCGAGATTGGGAATTGAAAGAAAAGGTGTGCAAAACCGCGTGTTCGACGATTGGACGATTTCATCTTTGCCA
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SEQ ID 1712

K*YLVMLFAKQHDHAGRLGIERKRCVQNGVFDLDDFIPANGQVFI*RINGTAAFGSLLOGLTAH

SEQ ID 1713

TTGGCGGGCGCTCTCTGTGTGTCAGGAGGAAATATGATTATTGTCTAGCAGCGCTGCCCGGAGGCGGACATTGCCGCGTGTGCGCTTCATCCGAGCAGAGGCTGCGGAGACACA
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SEQ ID 1714

LGGPSLVSGNMIVMSRRAEADIAGVVAFIRSRGLREHISHGDERTVIGAIGDDRVLVSREVQTLPEVEKAVRILDTWTKTVSRNRAEDSRVAAGVAPGGGTIVRIAAEPSVSNADA
VFLDPPTTANLYDLFSADEGRGRCRLAEQAAAHGAGKPVLRVVRNVRHVEAALNAGADILYLGGLMSDLAVLNEAGSLNIPVLICKDKHSAEDWLNAAEYVVSGRNRLHLLGESGV
LGHFKGHPYRLDVESTVKVRQISHLFVIANITGLMSRDMPQEIYGLAKAAGACGIVGTCFEKAGG

SEQ ID 1715

ATGACCAATTCAGGCCATTCTGAATCAGGCGAATATTACCGATCAGCAATGCGGATTATCCGCTCTTTGGCGGAAACGGCATTGGATTTCAGGATTGGCGAATCAGGCGTGCA
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GCTGTATGAGGAATCCGCGAAGAGTGGACGAGCGTTACGACGCTATCGAGGAAGTCTGGCGCGGAGAAATGCTGCTTAAAGACCTGTGCGCAGAACTTGCCAAAATCGAGGAT
CGTTGAACCTG

SEQ ID 1716

HTQFRPILNQANTIDQWRIRLLAENGTLDFQDLANQACILRPSLTGILTRLEKAGLVRLKPSNDQRRVYLKLTSEGEKLYEIEIGEVDERYDAIEVILGREKMLLLKOLLAEAKIED
ALNS

SEQ ID 1717

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TT

SEQ ID 1718

MCSSSDSKSRSDVSAHYGLRVQRILDFGKFCQQVFKQHFLLAAQHFLDSVVTLVHFFADFLIQLLALGSQLQINAPLVVGRFQADDQPRFFKAGQDTGAGAQNARLIRQILKIQCAVF
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SEQ ID 1719

TTGAAAGTTTCTGCAATCCGCCATTTTCCCTTTTAAACCGTCCCTATATAGAATGCTGCACACAGGCNTCCCCCATGTGCAGCAGTTC

SEQ ID 1720

LKSFQIRHFSPLNRPYKNAHKAAPHVQF

SEQ ID 1721

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SEQ ID 1722

MADLQKTFQTSFRDAMASCAAGVHVITTDGAAGRYGIMTAVAPVTEPPTVMLCINRSARIIPILSENGSLCINMLADEHQDVAEHFAGLTGLSPEERFAYHIWHERGTGQLEKREGALAH
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SEQ ID 1723

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SEQ ID 1724

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SEQ ID 1725

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SEQ ID 1726

LTAVFAKMLQGISDFATFIRTLVILAAALVLFUTYTGKQGVNGFTGRNRTLVLSGLATGASWLAIFYKALQLGKAPQVAPVDKFSVLVLVALMAVIFLDERPNTQEWIDLGLVTAAC

SEQ ID 1727

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SEQ ID 1728

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SEQ ID 1729

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SEQ ID 1730

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SEQ ID 1731

TTGTTGCTGCGTCAAAAATTTCACTGCGGGTTTGGTGCAGATAACGTTATAATATGCTGATATTTTTCATCCACCTGTTTGTGCGC

SEQ ID 1732

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SEQ ID 1733

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SEQ ID 1734

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SEQ ID 1735

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SEQ ID 1736

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LADIEFTIGTELALADLASVEKAIVREKRASGDKAQKLVLDLCKKLPHLDGKGPVRSFGLDAEERALLKPLFLITAKPAMYVGNVAEDGFENNPHLDRLKELAAKENAPVVAACAHE
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SEQ ID 1737

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ATTA

SEQ ID 1738

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SEQ ID 1739

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SEQ ID 1740

MSQALPYPRDIDTLRAAAVLSVIVFHIEKDWLPGGFLGVDIFFVVISGFLMTAILLREMSGGRFLKTYFIRRIKRILPAPFAVLAATLAGGFFLTQDDFFLLWKSALTALGFASNLTYFAR
GKDYFDPDAQBEKPLLHIWISLVEEQFYFVFFILLLVARKSLRVQPGFLAALCALSAASPMSALDKYTLPHLRACELVGSILTAVRMRYRQQRNPVAGKRYAAVAGLFSACILSACILFA
YSEQYAYFPGPAALIPCLVAALITYFNHYEHLKPKFFQWKITVAAGLISYSYLWNHWPILAPMRYTGPDNLPYPSPAALIVTLAFSLISYHCIEKFPKKWKGSFPAQSVLWITYALFMLVLG
AGSFFAMRLPFMAQYDRGLGTRTSNTSCHNNNTGKQCLWGDTEKQPELLVLGDSHADHYKTFDFAVGKKKEWSATMVSADACATVEGYASRVFQNWAAACRAVYRYAEHLPRYPKVVLAHNRG
SOMPENRSRLAYDAGFPQKDFRMLHLSSEKQAVYLMADNLASSYNVQRATILSSRI PGCKORFLRPDDSTLKANARIRELAAKYPNVYIIDAAYIPADQFGGLPVYSDKDHINPYGGT
ELAKRFSEKQORFLTRHNH

SEQ ID 1741

SEQ ID 1741

ATGACGGCTGATCCAAGACTCGCAATCGCGGGCGCTTATCGCGCAAAACCAACGACATCGAAGCGCTTAGACGCTTTGCTGTAAGCAACAAAAATCGCCCTTTACTGCGGTTTCGACCCGACAG
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CAAAGCCGCCGAACCGCAGCTTGAATTCGCGCAAAACCGTTGCCGGCTGGGTAGGAAGCATACGACGCAATTAACCCCTTTCTTGAGCTTTGAAGGCGGAAACGCCGCCATTATGCGCAAC
AATGCCGACATGTTTCGGCAGCATGAATGCTCTGACTTCTTGCGCACATCGCAAGCATTTCTCGGTCACGCGCATGCTGAACAAAGAAATCCGTCAAACAGCGCATCGACCGCGACGGG
CAGGCATTTCCTTCACCGAGTTGCGCTATTCCCTGCTGCAAGGCTACGACTTTCGCGGAGTTGAACAAACGCCACGGCGCGGTTTGTGAAATCGGCGGTTCCGACCATGCGGCGCAACATCAC
CGCGGGTATCGACTTGACCCGCGCGCTGAACAAAAACAAGTGTTCGGTCTGACCCCTGCCCTTTGGTTACCAAAATCCGACGGTACCAAAATTCGGCAAAACCGAAGGCGCGCGGTGTGGCTG
AACCGGAAAAAAACCTTCGCGGTACCAAGTTCTACCAAGTTCTGGCTGAAAGTCGCCGATGCCGATGTGTATAAATTCCTGAAATAGTTTACCTTCTCTGTCATCGAAGAAATCGGTGTGCTG
AAGCCAABAGCAAGGCAAGCGGCAGCAAGCCCGAAGCGCAACGCATCTTCGCCGAAGAAATGACCGGCTGATTCACCGGCGAAGACGCTTACCGCGCGGCAACGATTTCCGTAAGCGCT
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TTGGCAGCGTCCAAACAAGAGCGCGCGCTTTGTCAATGTCAAAAGCGGTTTCTGCTCAACGGCAACACCGGCTGAAGCCAAACAACCCCAACACGCGCGCAAGCGCCGACGATGCCTATC
TGTGTGATAGGCGAATACAAACGTTTCGGCAAAATACACCATCTCTCGGCGCGGCAACGCAACCAACGCGCTTTTGGTTTGGAAA

SEQ ID 1742

MSVIGDLSNGLIAQTTIDRALDALLNEBQKIALYCGFDPDTADSLHIGHLLPVLALRRFPQAGHTPIALVGGATGHIGDPSFKAAERSLSNAETVAGWVGSIQSQTPTPFLSFBEGGNAADMAN
NADWFGSNGCLDPLARDIGKHFPSNAHLNKESVQRIDRIDGAGISFTPEFAYSLLQGYDPAELNKRHGAIVLEIGSDQWGNITAGIDLTRRLNOKQVFGFLTPLVPTKSDGTKFGKTEGGAVHL
NAKTSFPHYQYQFWLKVADADVYKFLKYPTFLSIEEIGVVEAKDKASGSKPEAQITLAEFTRLTHGERALAAQRISESFLPBDQSRLTESDFEQALDGLPAFEVSDGINAVEALVKTG
LAASNKEARGFVNKAVLNGKPAEANNENHAAPERDDAYLLIGEYKRFQKYPITLRRGKRNHALLVVK

SEQ ID 1743

TTGGAAATAATCCGATTTCGCCAGAAATGCCGCTCTGAAGCTTTTCAGACGGCATTTTATCAAAATGCAAAACACCTCGCGCTGTCGATATGTCGTCATTTCCATGCAGGGGGGAATTCAAACCTTGTCCCGCAGGAAACTTATCGGGGAAAAACGGTTTCTTCAGTTCTACGTTCTAGATTCCCGCCTGCGCGGGAA

SEQ ID 1744

SEQ ID 1744
LEIIRLPQKCRKLSDGTFIKCTPCACRYVVISNOAGIOTCPHGNSGKTVSSVLRSRFPARE

SEQ ID 1745

ATGATGATTATTATTCGGTTTTCCACAAATACCGTCTGAAATATGCGGTGGCGGTGCTGCAGATGCTGCTTTTGGCGGCAGTCGGGCTGCACGCTTCGGTATATCGCACTTCACGCCCGAA
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CGAACCCGACGGCGCGCGGTTCGCCGTTTCGGTCAAGAAACCAAATCGGATTTGAGCTTGGAAAAAAGCTTGGTCGGATCGGATACAGGTTGAAAAATGGGTGGTTTCGGGTGCGGATCT
GCCCTGACGCGTACAGAAACGGCGCTTGGAACATCCAGACCTGTTTCGACGGCGGAAACAGCTGCCCTCAGCTCAACCGATTATCGTGCAGAACAGCAGCCGTCGCCCTCAATTTCTCG
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TTCAACGCCGCGGAGCGGATGCCGCCGCTCGGCTCGGTGCAGACACTTCCTTCGCAACCTCCACCTGACCGCGCAATCCCGGCACTGGCACTCAAAAACACAGCATCAAAACCG
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CAGCTTCAAAAACACCGCGCTTCAAAACCAATTTCTCCCTCGGCTCGCGCTGGTTTGGAGTCGGGACAAACCGGCTGGACGCCCGCGCTGCACATATCGACCCCTTCAGGATACCGCTCGAC
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AGCGCGCATCGATACCGAATCTTCTCCGACAGCTCTATGTTACGAGCAACCGCTATACCTGGAATACGAGGAATTTGCTGAAGATGTCCTTATCCGCAACCGCGTCCATCCGA
AAAAACAAACCGCTTCCCTGAAAATCACCGGTACCGTGGACAAGCGCTCATACCGTCGATTACCGGAGGCTGACCGCGCATCAATTCGCGCAAGAGAAACAGAAATCTCTGAAGA
CACCTGCTGGAACATGGCAGTGGCTCAAACTAAAGAACCG

SEQ ID 1746

MDLLSVFHKYRLKYAVAVLWMLLLAAVGLHASVYRTFTPENIRSLQSIATHRKISPDADIRRRLLPRPTVILKNLITTEPDGGRVAVSVKTKIGLSWKNLWSDRIQVEKWVVSADL
ALTRDRNGAWNQIDLPAGKXASVNRITVENSTVRLNFLQQLILKEISLNQSPSSGQQFESSGILVWRKLSVPWKSRLFLSDGIGTPEISPFHFEASTSLDGHGITISTGSPSVR
FNAGGADAAGLGRADTSFRNLHLTAQIPALALKNNISIKTGVNQTTFAGGEYARWDSFKLDKANLHSGIANIGNAEISGSFPTPRLQTNFSLGSLVWSRDNLDAAPRLHISTLQDITV
RLPQFRPI SRLDGLSIPNLQWNNAELNGTTFDRQPVAAKPKYTRBGA PHLEAAAALQKLNLAPLYLDEFQNGKIFPDILGRLSGNVEAHLKIGISQILPGLQLDMDMETYLHADKDHIALSR
FKSLYGGHTGGISIANTRPATYRLQNASNTIQIPLLQLDLPFGHSPSGNDVIDLTSAGENRKLQIRLSLQSLSLNLSNAGHIDHDSILKNGLSGKISGTPPYRFTLNSEISDGI
SRHIDTFLPSDSLYVTSNGYTNLDTQELSEDLIRNAVHPKNKPIPLKITGTVDKPSITVDYGRLTGGINSRKEKQKILEDTLLEQWNLKPKPE

SEQ ID 1747

ATGCTTCCAACGGTTTCAGACGGCATTTTTTACACAATTCGCCCATTTTTCATCATTTCCCGACAACACCGCAATCTCGAAACCCGTCATTCCCGCGCAGCGGGAATCTAGATCTGTCCAG
TGCAGAACTTATCGGGCAAAACGGTTTCTTGAGATT

SEQ ID 1748

MLPTVSDGIFPTTIPALPHHSRQHNRNLETRHSRAGNLDLSVQELIGQNGFLRP

SEQ ID 1749

TTGGAGTCGATGAATCGGTGGGCTTCAGTCCGCCATTCOCATCAATCCAACATTTCTACCGTTTTTCATCGAATCCATCGAATCCGCCCTTTTCGAATCTGACCTATGCAACCGAACCG
TCATTCACCGGAATGGGAATC

SEQ ID 1750

LESNNKASVVRHSQSNISTVFIESIESAPFNLTLNRTVIPTEVGI

SEQ ID 1751

ATGCCGTCTGAACCTTCAGACGGCATTTTGTATGCACCTGCCGTTTACGGGCGCGGGCGGGCGCAGTAAATACCCGAACCGTCATTCCCGACAACACCGTAATCTCGAAACCCGTCATT
CCCGCGCAGCGGAAATCCGACCCCGGACCGCGCGGGAATCTATCGGAAATGACTGAAACCCCGCTCTAGATTCCCACTCCCGTGGGAA

SEQ ID 1752

MPSEPSDGI FDPAPVYGRGAGAVKYPNRHSRQHNRNLETRHSRAGNPDPRRGNLSEMTETPRPRPPLPWE

SEQ ID 1753

GTGACGGCGGATTAGCTACGCCCGCGAACGCATTACCCAGGATTATCGGGAACCAACCGGTGCAAAAAAGGCAAAATAGCACGGTAAGCGATTATTTTCAGAAACATCCGTAAGCAT
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CTACCGCTACCAATATTGGGACCGCTTGGAAACACCGCTTCAAAACCCAGAACCTCGTTGGCGGTGGCTACCGCTTC

SEQ ID 1754

VQADLAYAERIETHDYPEPTGARKGKISTVSDYPRNIRTHSIHPRVSVGYDFGWRILADYARYRKWNNSKYSVNTKKNENKGEKINVTQYLKAENQENGTFHVVSSLGLSAVYDFKLND
KFKFYIGMRVYGVHVRHQVRSVEQETTTVTYLSGKPSPIVRGSLKLPHEHSRSLRLLFGFAMAGVGDVAPGLTLDAGYRYHYWGRLENTRFKTHEASLVGRYR

SEQ ID 1755

GTGTTTCAACACATAGCACCGCGCTGCTGCGCTTTTGTGCGTTTGGCGGCTTCGCGCGCGGAAATTTGCTACTTTTCCCGCTCGGCGGGCGGAAACGGCGGCACACTGTCTATA
AACCGCAATACCGTTTACAA

SEQ ID 1756

VFQHLAPRLLRVFLARSAAGNLPTFPASGGGRNGRHTVYKPYRLQ

SEQ ID 1757

TTGTGCGTTTGGCGGCTTCGGCGCGGGAATTTGCCCTACTTTTCCCGCGTGGGCGGGCGGAAACGGCGGCACACTGTCTATAAACCGCAATACCGTTTACAATGACCGCTGTTTCAAC
ACACTCCCGAACCAACATGTTTCAACACACCGGACGGCAGATCAAGCACCGCCCTATGTGTCTGTC

SEQ ID 1758

LCVMVRVRREICLLFPFRAGGTGGLSINRNTVYNDRLFHHTPERMNVSTHGTAHQAPPVVS

SEQ ID 1759

ATGTCCGAGTGGCGGGTTTCAACCGAAAGGAAATACAATGAAATCAGGCCGGGCGGCACAAACCGCGCCGACTTTCGCAACGGGCGCGGTAACCATAGGCAATTTTCGACGGCGTAC
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AACCCCGCCCTGCCGTATCAGCCCGCTGCGTACCAACTGGAATTTGCTGGAAGGACGGGTTCGCTCGATGCCGCTGGGTTTTCGCTTCGATCGGAATTTTCCGAAATATCCGCGCAA
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AACCGTTGAACGTCGCTTCTCTCAACAACTGCGCGACGAGGAAAGTTTACCGGTATGGAAGAACTGAAAGCGGATGGAAGCGCAATGGAAGCGCAAGTGTG

SEQ ID 1760

MSEWRGNRKNWTKIRPGRHNPDPFHGAATVIGNFDGVHLGHKHLQLKLEADARGLPVAVVFPQKEFFALRTGKTPPCRI SPLRTKLELLEBGTCDVAWVLRFRDNFSEISAQ
AFIDRLRLQPLNRYLLWGDFFRFGAGREGCFELLAQQPDMQFERTPSVIVEDIRTSSTAVRQALSDGNLAYAKKLLGHYDVLGGVVHGRKLRGLNAPTANIRLPGHRYALGGVVFVEA
DGAFCGTRRGVASFNFPTVDGCSQKLEVLHFDQGLDYQLNVRFLHKLREDEKFDGMEBLKRIEADMEAAKCM

SEQ ID 1761

ATGTCGCGAGAAATACACACAAATCGGCTGGGTAGGCTTAGGGCAATGGGTCTGCCTATGGTAACGGCGCTCTTGGACGGCGCATCGAAGTCGGCGTATACAAACCGCTCGCCCGACA
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CGGAGTTCGGCGAGCGATTGAGCGCGCAAAATCATCGTCAACATGAGCACCACTCCCGGACGAAAACCTCGCCGTCAAAGCAGCTTGTGCAAGCGCGAGCGGACAGTTTGGCGAAGCACC
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ACCTGAAATGGCAGAACAC

SEQ ID 1762

MSAETTTQIGWVLGQMLPMVTRLIDGGIEVGVYNNRSPDKTAPISAKGARVYGSTAELVRACPVIFIMVSDYAAVCDILNGVRDLGAKIIVNMSTISPTENLAVKALVEAAGGQPAEAP
VSGSVGPNATNGTLLILPGGSEAVLNPLQKIPSLVGKKTFFHGDVKGSGAKLVNLSLIGIFGEATSEAMLMARQFIDTDTIVEATGGSAMDSMFPQTKSLMANREFPPAFALKHASKDL
NLAVKELDQAGNPLPAVETVAASYRKAVEAGYGEQDVSVYLKLAH

SEQ ID 1763

GGCTTACGCTTGAAGAACAGCCTGTCCAGCGACCATGCTCCGCGCGCGCTGCCGCGATATAGAGAAATACGAAGCAGAACAGCACTCGCGACTCGCGCGCTTGGCAATCGGGAACAAA
GCAATTCGGGAAGCGTGGCCATAAAATAGGCAACCGCCATCTGCCCGGACAAAAACACGGCGAGGCGCGCAACACAGGCCAAATGCCCGCGCAATTTCTAAATAAC
CGCAAGCAGCAACACAGCCCGCGGCGAACCCTGTCATGATGGGGAAGCGAAGATTTTCGACGTACCGTGCAACAAAAACAGGTAGGCGGTTACGATACGCAAAACAGAAAGCAA
AACAGGTTGGATACGTTGACGCAATCGGACAT

SEQ ID 1764

GFTLEKQVQRPSCAARCRDIEKYAEQHCGLAAGVNRQSSISGSVRHKIGNRHLAGQNKRRARKQAQHQQAADNF*WTKQQQPAGRTAAHFNGEGEDFRRTVQKQVGGYDTQNRQ
NRLDTVAIGH

SEQ ID 1765

TTGGCTACAAATCAGCCTTTTAACTGTTTCAGACGGCATAGGGGTTCCCGTGTGAAATACTGTTTGGGGGCAATGCCGCTGAAACCGAAATATTGTAACAAATAGAGAT

SEQ ID 1766

LGYNQPFNCSDGIGVSRCEILFEGQCRLLPKYCNRD

SEQ ID 1767

TTGATACACCAGTCCGCGCGCGCAGACACGGCTGGCTCGCAGCGAGATCCAAAGCGTGGTCTGCTCAAAATGACGGCAAAACGCTTTGCCTTCGATACCTGCCAAGCGGAATCGCGCGCA
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GAAACCGCTATGCCGTC

SEQ ID 1768

LHHVRAGRHGLARRQSPRRGRPNDRKRFADTQAECCGKRDGVFKRIGNVRRRYFVVFHFRFRQRRRAIQAKLNRFRAPVZLAGFVDFAEHTHGIGFPEIHQVRIVPVQAHAQAD
KVFFLPGNLFPGIIPAAQFAETGRFHIIFAVQFPHHFDFGQAVAVPTRYLRVKTGLGFADNNVFKNFIDGMDMDVAVGIRRAVVFVNEPFAFDFQAFVLVTLVPAFQPRRLALGKIAA
HRKRAFEQVDGFTTVIGHFLISIVTIFRFQIALPLKQYFTTGNPYAV

SEQ ID 1769

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CAAAACCAAGCGGTTTTCGACGCGCTTATGTACCGGTTGGGACTGCCACGGCTGCCCATCGAAGTATGTTGGAAACTGCACGGCAAGATATGCCATAAGCCGCTTTCGCGGAA
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SEQ ID 1770

MDYSRTVNILLESPPHMRGNLAKREPAWLKSWYEQKRYQKLREIAKGRPKFILLHDGPPYANGDIHGHAVNKLKDIIRSKTQAGFDAPPYVPGNDCHGLPIEVNVEKLHGKDMFKARFRE
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SEQ ID 1771

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SEQ ID 1772

MNHFFLERDIPMLNGEHVTTDAGTGLVHTAPARGLEDYAVCNKYGIETYLPNVNABGKYISETPRVAGMSVWEANPVLQWPEETGNLLASSKIEHSYAHCHRHKTPLIYRATQWVFGMDK
AGSDGKTLRDKAIKAVDDTEFPFPNGRARLESMLBGRPDWVSRQYWGTPMTFTFVHKETGELHPNSABLLKVAQRIEKGIEAWFSLDKSELLSAEDCEHYDKLPDMDVWFDSGSTRY
SVVKQREKLEWPAADLYLEGSQHRGWQSSMLTGCASSMGRAPYQQLTHGFFVDQNGRKMKSIGNVVAPOEYVNEFGADILRLMAASTDYSGELAISKEILKRVTESYRRIRNTLSFLP
ANLSDPNPIEDAVQADMVEIDRYALVLARRIQRERLAGGYIPRYAFHPVKDIVSFCSIDLGAFFYLDILKRLYTTKADSRARRSAQTYLHYITRSLWLLIAPILCTFGEEAWDIIIGGEE
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SEQ ID 1773

GTGGGAATGACGGTTCGGTTGTCTACGGCCCGCTGATTCCCGACACCGGATCGCGTCTGAACCTTCTCAGACGGCATTTTTCATGCGCTCCGCCTTTACAGGCGCGGGCGGGCGGCAGTAAAT
ACCGGAACCGTCATCCCGACAACACCGTAACTCTCGAAACCGTCATTTCGCGCAGGCGGGAATCTAGATCTGTGATCGCAGGAACCTTATCGGCAAAAACGGTTCTCTGAGATTT

SEQ ID 1774

.VGMTVRLLRPADSPTTTPMPSEPSDGI FDALAVYRRGAGAVKYPNRHPRQHRNLETRHSRAGGNLDLSVQELIGQNGFLRF

SEQ ID 1775

ATGCGCTGTGAACCTTCAGACGGCATTTTGTATGCACCTGCCGTTTACAGCGCGGGCGGGCGCGGGGAATAACCCGAACGTCATTCCCGACAATACCGCAATCTCGAAACCGTCATT
CCCGCGCAGGCGGAAATCCGGACCTGTCCGACGGGAAACTTATCGGA

SEQ ID 1776

MPSEPSDGIFDAPAVYRRGAGAGKYPNRHSRQYRNLETRHSRAGGNPDL SARKLIG

SEQ ID 1777

[illegible]

SEQ ID 1778

MNPARKKPSILLFSSILLFSSILLFSSAAQAASEGNGRGPYVQADLAYAAERITHDYPEPTAPGKNKLISTVSDYFNRLRTHSIHPRVSVGYDPFGWRILAADYARYRKWNKNKYSVDIKLELNKN
 QNKRLDKTENQENGSTHFAVSSLGLSAVDYFKLNDKFKPYIGARVAYGHVREHSDSTKKITGTLTAYPSDADAAVTVYPDGHQPKNYQKSNSSRRLPGFAMAGVGIDVAPGLTLDAGYRTH
 NMGRLENTRFKTHASLGMRYRF

SEQ ID 1779

ATGAATCGTCATTCCCGCGCAGGCGGGAATCCGGTCCGTTCCGGTTTCAGTTATTTCCGATAAAATTCCTGCTGCTTTTTTATTTCTAGATTCCCACTTCCGTGGGAA

SEQ ID 1780

MNRHSRAGGNPVRSVSVISDKFLLFISRFPPLWE

SEQ ID 1781

TTGATGGAATGGCGGGCCGAAGCACACCCCTACGGCCGCCGCGGATTTCCGCTCGCGGGGAATGACGGGGTTTCAGGTGCTGTTCAGGTTTCGTGTTTAAAGTTTCTGTTTCGGTTGC
TATTTTATAGAAATGACGAAATTTTAGATTGCAAGAACTTATCCCTCCGCGCTATTCCACGGAAGTGGGAANTCAGAAATAAAAGCAGCAGGAATTTATCGGAAATAAC

SEQ ID 1782

LMEMAGRSTPYGPPDFRLRGNDGVSGCCFRFLFLSFCFGLLFYRNDEILDCKNLSPPPSFPRKWESRNKKQQEFIGNN

SEQ ID 1783

ATGAAACGCCAAGCATTAGCCGCAATGATTGCTTCTTATTGCGATTGGCGCGCTGCGGCGCGGAACCTGCGCGCGCAAGCCCTGCGGAAACCCCTGCGCCTTTCGCGAAGCGCGAAGTT
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GCTCTCAAAGCGTCAACCCGGGCGCTGTACATCTACCACCTGCGCGCTGCGCGCGTTCGATGACACATGCCAACGGTATGTACGGTCTGATTTTGGTCGAGCCTAAAGAAGGCGCTCGCGAA
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SEQ ID 1784

MKRQALAAMTASLPAALACGGEPAAQAPAEFPAAASAAASSAAQATAETFPAGELPVIDAVTTHAPEVPPAIDROYPAKVVRVKMETVEKTMKMDGVEYRWTFDGDVPGRMIRVREGDTVE
 VEPSNNPSSTVPHNVDFHAATQGGGAAATFPAGRTSTFSFKALQPLGYTHCAVAPVGMHANGMYGLILVEPKGLPKVDKEFYIVQGDFFYTKGKGGAQGLQFPMDKAVAEQPEYV
 FNGHVGALAGDNALKAKAGETVRMYVGNNGGNLVSSFHVGIEIFDKVYVEGGKLINEVQSTIVPAGGSAIVEFKVDIPGNYTLVDHSIFRAPNKGALGQLKVEGANPEIMTQKLSDTAY
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SEQ ID 1785

ATGCTTGACATCTTCAATTAACTTCCGGCACCGGGCAGGCGTTACACCTTACAGTCCACTTTCGTGTGGCAAGAGTGCTCGTGTTTTTAATAAACAAGTCGACGCCACCTATTCCTC
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ATCCTGCCACCCTGTGTCGGTTTGGCGTACGGTTCGATTCAAACTGAAGCTTAGTGGCTTTTCTGGAAGCGTGGTATCGGTTGCTTCGTGTCGTAACAACCTCGTCATCACTCTCTCGGT
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SEQ ID 1786

MLAHLQLFFRHRAGVFTYTSFVFLARVLWFLINKRSQPPILCDPGLTEQVLNLRGHTFSPRSYGINLPSSFSRVLSSALEFSSCPPVSVCGTVRFKLLKSGFSWKRGIGCFVSVNTRHHFFG
VKKTRICLSLPPITGLNKLFOOLANLTFSVPTSHLNOVOEY

SEQ ID 1787

ATGTCGGGTTTGACGAAACTCGAAGCCCCGCATACGGTCGATCGCGGTCAAACCGCGCCGGGGCGGCGGACAGCTGTTCCTCGTTGTGCGGCAAGACGCGGAAGGCAGAACTCTGGGCT
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GCGTTACCGGTTGTCGGACCTTGCCGCCACGGCGAAACAGGCGCGCGCGAGGCGTAATGATTGGGGCTTCGTGAAAAATTGGAAGCCCGCTGCTTATTTGTCGCAATCGCGTCTTC
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CGTGGCGAACTCAACCGCGCGTTGACGACGGCGGTTAAGCGCGCGCGATTGGTGGCGCCCTGCCGAACTGCCGACCTTGAAGGGAACACGGCGCGGACGTGCTGCCGTGGGC
CCTGAAGCGCGCGGTATGTATAACGACTCAGGCGCGCGCACGGCGCGCTGGTACGGCGGTGGGCGCGGATTGAGTTGTCAA

SEQ ID 1788

MSGLTKLEAPAYGCIAPKRRGGHVFVVGKDAEGRILGLGNQNMVSIIPDPADIDGYFWPSKLIIGKAVSPSPABGRYRLSDVAATAKQAGAGA*MIGALLKNWKPILLISAIAPF
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SEQ ID 1789

ATGCTACCGTTTTCATCGAATCCATCGAATCCGCTTTTCGACACCCCGCCCTACGCAACCGAACCGTCATCCACGGAAGTGGGAATCTAGGACGCGGGTTTGGCAACCGTTTTC
TCCGA

SEQ ID 1790

MSVFIIESIESAPSTPRPYATEPSPFRKNESKTRGLGNRFIR

SEQ ID 1791

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TCCGTGCGGTGCGGTGTTGGCGGTGCTGACAATATCTCCATCGCAAGATAGCAAAAAACG

SEQ ID 1792

VLRPAISINPTCLPFSNPNPPFRPPGTQPNRHSHGSGNLGRGVWATVLSDFKPCGRVRIACAGHTGFKITAFVSGTGKGGFRVEMHSFIRLLKNMSSSVSSKTRYWVLALAAIVLD
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CVGAVLAVLDNIVHRKDSKRT

SEQ ID 1793

ATGAACGGAACCAACATCATCTTCCCAATCCGCGCGGCTTTCGCGCGGTGTGGATCGGGCAATCAGTATTGTCGAACGTGCTTTGGAAGAATTCGCGCGCGCGTTTATGTCGCCACG
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SEQ ID 1794

MNGKTIILANPRGFCAGVDRAISIVERALEEFAPVYVRHEVVHNFVVDNLRKGAVFIEDLAEPVPGATLVYSAHGVSKAVQQAERGRFVDFATCLVTKVHKEVARLDAQDCKEIH
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SEQ ID 1795

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ACGTGCGTTCAGTAGGACGCGTTGTCACCATATACGATGATTCGCGCGATGCCGCCACTTCGCGCAGCGGTTGCTGTTGGACGAATTTGGCGGAACCGCGGTTACGCGCGGATGATGCTTTG
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SEQ ID 1796

VLPKHPMALTASTFAQIGFALAAQLGQDEHDAFFRPPFAHGFMPSPAYGQVFPHQHPRGRACRYADFAFAFKPRALQVGRVHHIRIDSARCRHFAQAVAVGRIGRTDHNHDV
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SEQ ID 1797

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CATCACCGCATCGTTTCAACCTGTTTTCGCTTTTGCAGAACCGGCAATCCCGGTTGACGACCTTATGCGCTACCGTAAATTCGCTATGCGCGGCGAGCCTATTTCGGGTGCTC
AAAGTGGTTCGCGAAAGCCACCTGAAGCGGATGTTGTAACCTGTTGAAAGCGCGCAACAGGCTAAGTGCGCCCGCTGCGCGC

SEQ ID 1798

MSVFRQTAQAMAKHIGRFLSELQVIDWQPIBQYLIHQKTRYLRDRGRPAHPLSSMFAVLPGQWHSLSDFEHSILITRIGFNLFCRFDEPGIPGCTFLCRYRKFYARAAYFGLL
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SEQ ID 1799

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CAACAACCGCAATATGACACTCTTTCCCGATGCCCGCCCTGTCTGGAAGAAGCTCAAAAGCGCAAGGCTTCCGCTTTCGCGTTCGCGCAACCGGCAAGGCGCGGCTTGGCAACCGCATC
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SEQ ID 1800

MTTPKLIIFDWDGTLADTTQPIIDTMRRSFACGFPFPEAERVSLIGYSLPEIRALLLEMPSEAAVADIARTYSAHYLNPNRNMFLFPDAPPCLDKLKAQGFRLAVATGKGRAGLDNAI
SQATAGGYWLAACAGGYPSKPSPEMVFLCGBGLDPKRALVVGDTAHDLHMAANAAGAAVGVATGAHSREQLLGAPHLAVLDGLSELPGFLARHYA

SEQ ID 1801

ATGAACCGACTCGACCAACTTGGAAATCCGTATCAACCTGATTGCAATGTCTTTGCAAAATGGATCGGGCAGCAGGATTGGAATTACAACCTCTTTACCGTACTTTATACCTCGGCAACCG
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CAGCGCGCAACGGTTGCTGCTGCTGACGCAAAAGGCAAGTCCATGCCGCACCTTTAAACAGAAAACCGCGAGGAATTCAGCGCAAGAGTATTTCCACATTCGCGCAGCAAGCGCACAAAC
CGGCTGTTTCCGATTGGAATGCACTGGCGGAAGTATGGAATAAATCTCGGAAAAATAAAAA

SEQ ID 1802

MNRLDQLGRINLINCNVFDKNWIGQDNLNLTFTVLYTLATEGSRFTQKHIGBWSLKPQTIVSGVCKTLAQGLIEWQEBQDRRERLLSLTEKGVHAAPITENAQEFSDKVPSTFGDKRTT
RLFADLDAEAEVMEKTTISENKK

SEQ ID 1803

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SEQ ID 1804

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EYQFAGLLRGSRTLEVKICIGSLQVPAARIEIVLEGVHPNETALEGPGDHTGYNEQGHFPVPTVERITMRENF IYHSTYTGKFPDEPAVLGVALNEVFVPLLQKQFSEITDFYLFPEGC
SYRMVAVSMKKQYAGHAKRVTGCSFLRQFMYTKFIIVDDDDVNRDWNKEVINAVTTRMDPVRDVTVLVENTPIDYLDPASPVSGLGKMGDLATSKWPGETDREWGRVIXKDPFVTVKID
GIWGLGL

SEQ ID 1805

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SEQ ID 1806

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SEQ ID 1807

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SEQ ID 1808

LCFIKIEPLSFQMGQFMSVFRINMTAATVLAALSPFVAQADTLETVHIKQRSYNALATEKNDYSSLKAAIIMTASIPASPPAA

SEQ ID 1809

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SEQ ID 1810

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SEQ ID 1811

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SEQ ID 1812

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SEQ ID 1813

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SEQ ID 1814

MRSQPEYGLAKENRPNRQADRFAAGSVLPLAASLTHKPNIMKPIPTDTQPAILPOAFETELKSTCGRIYRIQTATLGEHQSEGYFVLFLVDGEAFFPRCTTSCSR

SEQ ID 1815

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SEQ ID 1816

MQSLNNPVTNRSNAPCLIVGIGYTTGSRVRLDAQRAADYTPPLGDNATADERRQFGQADRFAFIDSELTAFLESRYTTLNRNETAVFGHSFGALFGLYSLLSHRCFRHRWLVSPTSIIWHNRRLDMPMPSENRLDGIDACLNLGALERSGCKRREERDMAGQABQMAELDRRGTAVFVREYPNADHGNVFPFYSUDCVETLEAWQR

SEQ ID 1817

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SEQ ID 1818

WASHKSHLEHNVQAKLLHHNSRNLSTTEAGEEYRYQCSYALDTLDDAAQKAAGSTEKPGQLLRVTETPLNPAQSQCINWLAERYRERYPEVALELILDNHREVDLILABGVDLALRVSTLSPS
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SEQ ID 1819

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SEQ ID 1820

MTEPYIPLRLRTEFSITDGMVRIKLLIAQAQYGLPALGISDLNNEFGLVKFYKACRGAGIKPVGAADVWIGNPNAPDKPFRAMLVIRNDAGYLRLESELLTEAYVQGDNRNTHHAILNPEH
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 PGRSGAGSLVAYSLKITDLDPLKYALLPERFLNPERVSMDFPDVDFCQANRGVILEYVREKYGAQAVSQIVTPTGTMSSKAVIRDVGRVLELPPMLCDKLSKLIPLANKPLSLDDAMKAQ
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 QGISREKSDIEFNMEKFAGYGPNKSHAAAYALISYQTAWLKAHPAEFMAATHSSDLOTDQLKHFTYDCRANGIEPLPDINDINESDYRFTTPYQNKIRIYALGKFGGEAAVESLIIAARQ
 SGGKPTGLLDFCERVGKEHNNRRLTALIRGGAFDSTIEPNRAMILLANDLMDNQAANANWGGGLFVDMEDAIEXPVRLIDAPMWSSEKLEAKERTYVIGFYLSGHPFGFYAQEVRQIAPT
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SEQ ID 1821

GTGGCAATAAAAGGCGTATTGTAGCAGGGTTGTCTTTAGATGGCGGTGCAGGTAATGCCGTTTCGGATTTCAGACGGCATGACCTGCAAAATGTTTTTTGAGCTTTTACGACGGCAAAAAA
TGCCCTCTGCGGTGTGGCGAGGCTTCCCAAGGAGTAT

SEQ ID 1822

VDNKRRIVAGLSLDGGAGNAVSDSDGMTCKCFLSFYDGKKMPPAVWRRLPKEY

SEQ ID 1823

ATGTTTGTGAGCTTTTACGACGGCAAAAAATGCCTCCTGCCGTGTGGCGGAGGCTTCCCAAGGAGTATTGATAGATATAAAGGACTATCAAACTAGTTATAAGGAATATATACCTTAT
TCGGACGGACGGCAAGCAGT

SEQ ID 1824

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SEQ ID 1825

TTGACGCTGATGCACATCTCTCAAACGCGGACTGCCGATACACCGGCAATCGGCATCAAAACGAAATCAAAAACCTGTGTAACGTAAAATCTATT

SEQ ID 1826

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SEQ ID 1827

ATGCCGCCATCCGTCCAAAGAAATCCTGCCCAACGGCAGGCTGCAAAATCCTGTTCGCCGACGAATCCGCAITGACGCTGATGCACATCTCTCAAACGCGGACTGCCGATACACCGGCAAT
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SEQ ID 1828

MPSPVQRNPQRQAANPVRIRIDADHPQTRTRYTGNNRQNEIKNLFERKIYLTACRPSE

SEQ ID 1829

TTGAGGATGTGATCAGCGTCAATGCGGATTGCTCGGGGAACAGGATTTCAGCCTGCCGTGGGCGAGATTCTTTGGACGGATGGCGGCATACGGGGTTTCAGACGGCATTTTACGGA
ACAGGCAGTCCGGACACATCGCCGGTTTTCGGCAATTTTGGGTGCGCGCGGCGAGGTCTACAATAACGCCCTCTTTC

SEQ ID 1830

LRMCISVNADSSGNRCSLPLGRISLDGWRHTGFQTAFLRNRQCGHIAGFAAILGAAAAGATTTPSF

SEQ ID 1831

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SEQ ID 1832

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SEQ ID 1833

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SEQ ID 1834

MDTFLKHKARALLGEPLLDREPVRPESWECGSDCGEACIQTYYWADKARYDAQRKLLKAGWPDADV

SEQ ID 1835

AATATATACTGCTTTTATTGATACAATTTTCCACACAAGAAATATGGACACCTGTTCAGCCTCAAAGTTTTCGCCCAAGTCGTCCAA

SEQ ID 1836

NIYCFY*YNFSTQENMDTLFSLKVFQVQ

SEQ ID 1837

ATGCACACTTGCCTTCTCGCGGCAAAACATGAAGATATGCCCGCAACCGGCTTTACGCCCCCTATCCCTATAATCAACTCAGTGAAGAAGACGCATTGCTTATCAAGCGGAATGCG
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SEQ ID 1838

MHTCTSCGKHEMDPATGTPAPYPYNQLSEERIAYQABCDSDFCILIRYSQDTRFIRALPIPIIGHQETLEYGVWVSVSEKSFNDYQSRFYDNPENAVYFGMTCNRLPPYETDTFGLHC
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SEQ ID 1839

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GCGCGCGCGCTCAAATCGATGACTTCTCGCGCGCTATTTTGGCCGTTTTCGGATTTCGGTTCCGCGCTGCGCAACACGACCGCTTCGGCGATAAATGCTTTTTCCTGTCGCCCGCTT
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SEQ ID 1840

VVLSSPTVFRHRPANPLPSVFSVAHRSVPCPPSKSSECTPRRSRCSIPTTRGGRVRPKAARPKGLRLYASGSYPSAISKRAPSNSMTSPPRILAVLRISVPLENTSPSAINAFACPL
SASPANFKRSHKAMYSLSR

SEQ ID 1841

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SEQ ID 1842

MQRKSRVAVIPAQARIQTLYWKCLRLTAISNFRIPAFEGMAI

SEQ ID 1843

ATGGGGTGTATTGTGGTGAATGAAGACCGGATGTTTCAATGTTGTCGGACAGTGTGGCGGCGCGGTCAATTTAAAAAACAGGTGTATGGCAATGCAAGGAAAAGCCGCTATGCC
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TAATCTACTA

SEQ ID 1844

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SEQ ID 1845

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SEQ ID 1846

VEVAARACQSEAVCQKRVVEAVPVAVAADFARAEEVFKFFKQVALGGCRQIITHRMGNHRAARAVIDGGDAVCQRRPFAVYRAGFAVAQVFGERLLLVFDVSFDEELGDVGAADHF
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SEQ ID 1847

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SEQ ID 1848

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SEQ ID 1849

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SEQ ID 1850

HPSESDGIPIKPICLTHTEFDMQPSAFGEKPTQHSGLQLMDDLGDALKSKDPVNLGGGNPARIPEIDRAFADIPSKLAAEHAVENIGNYSNPQDAALIDALTAPFNREYGNLTVGN
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SEQ ID 1851

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SEQ ID 1852

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SEQ ID 1853

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GCACAACCGCTTGTGCAGCAATTTGACAAAC

SEQ ID 1854

CAVAEGSPVIGIWDIAETNPRAAPYRQSAELAQGLARRGIPLYTAASPAGLVRLAVRLNTRAVLADESHTPADKLADNALHHELDKH

SEQ ID 1855

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SEQ ID 1856

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SVTGRMVLRLGLSDHQKRTDHPVIYAGRSGRQLLEAVKQMRYSAAAFVDNPKLHVTVYDYLAVYQDAFLIERYGVKILLAIPTAQEQRRRIISKLKAYPCEVLTIPGMKDL

MDGKISIGTLKKISVSDLLGRDSVAPDDRLMADTEGKTVMTGAGSGISELCROIIRRRPERILLFELSEFALYVEKELCEYCARNGIAARILPFLGSVQNRLLIHLMTAFSVATVY
HAAAYKHVPVMEFNTVEGIRNNIFGLTECALAATASGVETFLVISTDKAVRPANTMGAGKRMALCLOALAAEPQKTRFSMVRFNVLGSSGSVPLFEKQIAEAGGPITLTHEDITRYFM
TIPEAAQLVLIQAGANGRGDVFVLDMGESVKITDLARQMITLSGLPKPTPEQPDGDIETILTLGRPEKLYBELLIGDNVRKTGHPRIMTADETMLPHEL SALLDRITACORYDQQAIR
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SEQ ID 1857

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SEQ ID 1858

MPSEGLSCGFGDGFVFAERDFVVGQRRVHQRGGAAQDFGVQPLFGPPRRVVEGFPQIHFGAALLAGDVAVRVQFADDAVARPVVQVQVDEGVELVLRVSDVAGDFNQADAFEF
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SEQ ID 1859

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SEQ ID 1860

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HESPGTNWRMMQAVIGRIQLKHLPEWTARRQJENAAKLAESLRKPKSIRLIEVAGYIGHAQYKFAVPKPEHLKDDWTRDRIVSEIARNVFCYQGGCSEVYLEKAFDNTPWRKERLKN
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SEQ ID 1861

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SEQ ID 1862

LKDWQMSKAVKRLFDIIASAGLIVLSPVFLVLIYLIRKNLGSPVPIRIRPKGDKPKPMVKFRSMRDLSDGILPLDSERLITDFGKKLRATSLDELPELNVNKGMSLVGPRPLMQ
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SEQ ID 1863

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SEQ ID 1864

MNITIAAPYCSLSEPHFNRPWYLAELLSQSHDVLLITSNFKHYDKSFRPPEKAAASQRLKVMLEESGYSKNVSLGRVTSHHRFVKHFEKMLENCRPGEQDVVYSAYPLIATNLLIGK
HKARLGYKLVQDVQWPEFSVVPFLKIPHNLLPFASRANRAYRYADALVAVSQTYLDRAKEANPNVPGEVVYIGADFAAIAPPFRFSKTRVFFLTGLTSYNDVEVCKGRVRLID

DGENVELHIMGGGPDRLRKQYACDGKIFYGYTPYAEEMSVAKGCDIAVNAHSHYAMQSITNKLSDYMAIQKPIILNSQVHDEVAEVLTLPLPHENTYRSGDVGFPQAARDILKRKNDPQSD
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SEQ ID 1865

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SEQ ID 1866

MGGISGRLLHPAPPEKPAQTVSLFEKTRFPINKILLTSMGLGGTETATVRLGRLLKRRHGHDIILASDDGPVFGVEAQASGIRWQVDFYRGGGLAGLYKSTFAYARMLRREQPDIIDCQAR
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GIGEMDNLKAQAKRLGIEDKVFLLGGVRDLTGYPKEVDILVNTPHCVGDHAGVGNLLEAGLYDTPVWTYNMAGISEMVTGQTGYCIPFGDDEAFIEAVDTLKHPELRSQMKALHK
HVETLCSDDEIYRTTHAAYEH

SEQ ID 1867

TTGCTATATAATAACGCCGATAAAAAACGCCCGTTTCAGACCGCCGCCCGCCGGAAAAGCGCAACCCGGACTGCCGCACCCCGCCCGGCAGCCCGGACGGCC

SEQ ID 1868

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SEQ ID 1869

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SEQ ID 1870

MMKMLKHIAKTRHRKLIGTSPVGLLENLMLGYPPGGWAINAVIAGRVQALLYLVFVLMVLVGAARRIADTRTFTRIYTYEIAVPVVEQORQRPVPSAVTARVALSREFVSPFEEHLP
IAATSVVSI FGACIMLLVLEFWGVGSVAGILALFVLLPRPAAISENLYFRLNNSLERDNEFIRKGDREQLRYRHYGLVSLRLVLSINREAFGYLCVGAAMGILFGFAFVMMTLKGYGSAGH
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SEQ ID 1871

TTGCGTGTTCGGGCGCGGTGATTCAAATGTAATTGATATCCTGTCTCGTTAAATTGATGATGTTGGCGGTGTTCCGCAGCAGCCTGTTTGGCGGGCAGACGGTGATTGAAAAAATTCGCGGGC
TGCAACAGCCCCGACCTGCCTGAAAAAGCCGTGCCTATACCCGCCGGTAACGCAGGTTTGGTGCCTATTCCTTTATTGCGCAACGGGACGCTTGCCGCTTTGTTGGCCCGGTGTTGGGGCGATA
TGATTGGTGGGCGGTTTATACAGCGGTGATTGCCTATGTATTGATGGGGATGCTGTTTGGCGGGCAATGGCTTTACCGCAAACTTGTTGTGAAAAGTC

SEQ ID 1872

LVPGRRDSMYWYPVLVNLMLAVFGSSLPAGQTVIEKLARLQOPDLPEKAVRYTRRVTVQVHCVFFIANGTLAALLARLGRYDHWAVYTGVIAYVLHGMFLPAGEWLYRKLVLKV

SEQ ID 1873

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SEQ ID 1874

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SPLPFRFILLVLRMEGRALAFSSAQVLKLAITALLPLTVGLHFPANTSVLFAVYALANLAAAFFLPQNRCLKAVRRAPFSPAVLH~~R~~GLRYGPIALSSLAYWGLASADRLFKKYAG
LEQLGVYSMGI~~SP~~GGAALLQSIFSTVWTPYIFRAEENATPARLSATAESAAALLASALCLTGIFSPLASILLPENYA~~AV~~RVRTVVSCHLPPFLFYTUTEISGILGVVRKTRPIALATLGA
L~~AN~~ILLGLAVPSGGTGR~~AV~~CAASFWLFFVFKTSS~~CR~~LLHPLKRLPLYMHTFLCLASSAAYTCGTPNANYPLFAGWAA~~Y~~LAGCILHRK~~KN~~LHKLPHYLKQGGFPL

SEQ ID 1875

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AAAAACGGCAACGCTTT

SEQ ID 1876

MFSDWIMSMENALRIALGRFSTSPNPRVGCIVAHGSOIVGQGHVHKAEPHAEVHALRQAGEMA KGAFAVYLEPCSHYGRTPPCAEALLRSGVTRVVAAMRDPNPPVAGKGLVLLKAA
GIKTECGLEENKARILNRGLSRIERRRPFVRLKCAVSLDGKTAISDSSFWITGEBEARADVQVLAESCAVLITGIGTVLADNPRINVRAPPTLRQPARIVLDSRLRLPNSHLVFDGQSP
TYIATLEDEDKLRPYREHAHRIIMPSETADGKIDLHILMRLLADEGPGELINVEAGSELTSALFAENLADEIVLYRSPKILGGGKDLPSLPENRAALSAPPLMTPVSSKILGHDIKTVFR
KNGMAP

SEQ ID 1877

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CGCGCTCCGTTTCGCCCGCTGCACAAACGCTTCGACACCGCGGAACATTTCCGCTCGTGGCTGGCGCAAGCGCGCAAAACCTGATTCCCGCAACCATACTGATACGCTATCCCTATGTT
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SEQ ID 1878

MFVLRPRPHRCRFPAPDGRTRRPPFMPRLRQTLRHARNRRITQNNARRHRSQETALQCTTTPQRPDRRRPKIRPDTTRDRNRPPDGTQALHFGSARHILIRTCRNRAGGAVRAKHGS
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SEQ ID 1879

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SEQ ID 1880

VPKAWKSPAPPAYRFDVQTASGRWTKMCPFCAHPDTRVDSRLMEERNAVRRRRQCPGCGKRPOTLEAELKMPAVIGPKKRSFPNAQRLRNDLTAARKSALTPEQIDETVRLFEHRL
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SEQ ID 1881

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SEQ ID 1882

LRPSESFGQTMQLLGMNCTPTDINFSPFEGFRRRGGITDHDGFGIGFFEGKVRLFHDDKPSANSVPADLVRAQYIKSENVAHIRKASQGTSLANTHPPFREMGGYWLFAHNGHL
VDFFPBQGEFFHPVGTDTDSERAFCHILNRLRTRFAARPDDDTLFDIAIGLTHEIRKPLFNFLSDGISLFAHASTLLHYIVRQAPFGKARLDDDDVMVDFAEVITPDDRVAISTLPLTR
DESWSQLAVNELVMFREGNIVRHRDPENPVYMSAEEGLEIARAAGVSV

SEQ ID 1883

FTGAAATTCAGATTCCCGCTGCGCGGAATGACGGCTCAAAAGTTACGGAAAGAAAACAACCGAAACCGGACAAGTCGGATTCCCGCTGCGCGGAATGACGGAATCTTAAGTTTC
GCTTTGTTTTCTGTTTTTCGCGGAA

SEQ ID 1884

LKFIIPACAGMTAQKLRNEQPKPKDSRLRNDGILSPRLCFLPSRE

SEQ ID 1885

TGTTCCTCCATATTCCCGCGAAGCAAGAAACAAAGACGAACTTAAGATTCCGTCATTCGCGCGAGCGGGAATCCGACTTGTCCGCTTCGCTGTTTTTCGTTCCGTAACCTTTG
AGCGGTCAATTCGCGCGAGCGGGAATCTGGAATTTCAATGCTCAAGAATTTATCGGAAAAACCAAAACCTTCGCGCTAATTCGCGGAAGTGGGAATC

SEQ ID 1886

LFPIIPAKTENKGNLFRHRSRAGNPTCPVSVVFRSVTFEPSFPRRRESGLSMPQEFIGKNQNSAVIPAKVGI

SEQ ID 1887

GTGCTTCAGCACTTAGGGAATCGTTCCTTTGAGCGGGCGGGCAACGCGGTACCGGTTTTGTGTAATCCGCAACAGCAACCTGTGCGCGTATTACCGGAAAGCGGGAATCCAGT
CGGTTCAGTTTCGCTCATTTCCGATAAATCTGCTGCTTTTCATTTCTAGATTCCCACTTTCGCGGGAATACGGCGGAAGGTTTTGTTTTTTCGATAAATCTTTAGGCAAT

SEQ ID 1888

VLQHLRESFPLSRGATPYRFLIRNSNPAVITAKAGIQSVQFRSFPINSCCFSLDSHFGRNYGGRVLFVSDKFLRH

SEQ ID 1889

ATGCCGCTCGAAACCGCGCTCCCTTTATGCGGACACGCGCGCGCACACGCTGCTGTTCCGCCAAAACCTCCGATCCGCGACAACGCGCGCTTATGCGCGCGCTTGCAGGAG
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CGCGCAAAACCGCGCGCAAGCGCGCTTTCGCGCACTGCGCGCGGTTTTCTCGAAGCAGCGCGCTTCTACTCCGTTTTAAAGGATTTCCTTCGCGCAAAACACTTCGCTGATGGCGCG
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SEQ ID 1890

MFSETALPLYADTRAHTLVWFRQNLIRIDNAALCAAVAGSPVIGIWDIAETDNPRRAAFYRQSAEALQGLARRGIPLYTAASPAVLVRLAVRLNIRAVIADESHTPADKLADNALMH
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SEQ ID 1891

ATGAAACCCGGTTTTTTCGGACATATTTTTTACCGTATTAAGCATTCCTATCCCGCTTTGCGGTATAGTGGATTAAATTTAAACCGGTACGGCGTTGCCCTCGCCTTGGCGTACTATTT
GTACTGTCTCGCGCTTCCCGCCTTGTCC

SEQ ID 1892

KKPGFFGHIFLTVLSIATPALHYSGLNLNRYGVASPCRTICTVCGFAALS

SEQ ID 1893

TTGCAGGGATTATTCGGAATAACGACAACTGTCCCGCGTCATTTCCGCGCAGATGAAATTTGGAAATTCAAATACAGGAATTTATCCGGAATATAGCGGATTAAACAAAAATCAGGA
CAAGCGCGGAGCGCAGGCGAGTACAAATGGTACGGAACCGGTTCGCTTGGTCTTACGACCT

SEQ ID 1894

LQGLIRNDNLASVISAQMEIKFKITGIYPEYSGLTIRRRRRRQYKHYGTGSPGASAP

SEQ ID 1895

ATGTGTTGCCCGCGGGTTGACGCACGATGATGACTTCCATCATCATCTCCCGGAAAGCGGGCATCCGGTTATCCATATTCAGGGATTATATCCGGAA

SEQ ID 1896

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SEQ ID 1897

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GCAAAACCTCCGCGCAGATACCGCGCGCTCGCGCGCTGCTCGAAGCGCGGAGTCCGCTCCGCGACCGCGCGTGTTCCTTTGAAAAATGGCTGGCACATATGAGCCACGACAAAAA
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SEQ ID 1898

MKTLFVHTPSHSYPIFIGNLLPQAGSLLKPHLGKRAIITNETVAPLYLGLTQALDAAGVSHPSIILPDGEAHKNWTLNLIPDGLMQRNRAERTLLIALGGGVIQDMVFAAATYQRG
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LNLGHTFGHVAEMGYVWMLHGEAVALAARLSQLGKTSAADTARLAALLEAAGLPSAPPVFAFEKWLHNSHDKKVSQGGIMRPIGLNRLGEAVITKTIOTDILRLTLQPYL

SEQ ID 1899

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CACC CGCGCGCGCGCTGTTAAAGAAGAAAAACCGCGCTTATCCGCAAAAGCGGACGCTGCTTATCTGCAACGCGCGCGCAAAACCTGCTCGAAGCGCAGCGCTCGGACAAACAGC
CGCGCTTCTGCTGCAAGTTGCGGATCTTTGGCGAAATGCGGCAACTCTACGCGCGCAACCGCGCTTACCGCAAAACCGCGACTTTACCGTAGAATCGGCAAACTGCGCGGAAACCG
TGCAAAACCTGCTCAAACCTTATCCCGA

SEQ ID 1900

VKNPFGKLLILGLMAGKTTLGRQMAQRLDYRFYDSHDEIAAAAGVPIPTIFEMEGEQFRSRETAILKLLIVLPHIVLSTGGGAVLKEENRALIRKSGTVVYLHAPPETLLERTRCDNS
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SEQ ID 1901

ATGTTTGAACCGCGCGCTTTCGGGGCGGAGGTTCCGGCTTGTGGGTTACGGCGGATTTTATACGAAATCGGCGGCGGCTAGCTTTGGAAAAATACCGCAACATCCCGAAT
TTTCTGATTTTAAAGAAAA

SEQ ID 1902

MFDPAPFRGGRVRACRVTAGFYTKSAGRRYVWKNPPTIPNPSDFKEK

SEQ ID 1903

TTGTTAATCCGCTATAGTATTGATAAATATTTATCTCAATATATTCAATTTGGATAATTGTTTACCTAAGCAAGATAATTGCCCTTTCTGACAAAT

SEQ ID 1904

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SEQ ID 1905

ATGAGGCAAGAAATTTATCGGAAAAAACCGAAGTTTAAAGACCTAGATTCCCGCTGCTCGGGAATGACGGGTGTTTGGGTTGCTTTTGTGGAAATGACGAGGCTTTGGATTGCG
AGGATTATCCCTTCCCGCTCATTTCCCAAAAGTGGGAATCTAGAAATGAAAGCAACAGGAATTTATCGGAAATGACCGAAAC

SEQ ID 1906

MRQEFIGKPKFKLDLSRLGNDGVFRVAVPCGNDALDCRDLSPSPFPQKWSRNEKQEFIGNDRN

SEQ ID 1907

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CTGCCGATATCGCGCATTTCCCGCACAGGCGGAATC

SEQ ID 1908

VRTCSDFLRGNDSGITDSSGRRVGFSPILISPHQGFVIGVTRFRFLAKLVIGIGLKHITLQSTLQPLIRIRLTHLSFACRYAVIPAQAGI

SEQ ID 1909

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SEQ ID 1910

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SEQ ID 1911

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SEQ ID 1912

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SEQ ID 1913

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SEQ ID 1914

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SEQ ID 1915

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SEQ ID 1916

MTFKLTKLII SGLFVATAAQTASAGNITDIKVSLSNPKQIKVVSFDEIVNPTGFTVSSPARIALDFBQGTISMDQVLEYADPLLSKISAAQNSSRRLVLNLNPKGQYNTFVRGNKVM
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SEQ ID 1917

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SEQ ID 1918

MKHYALLISFLASACQNSSEDLNEWMAQTRREAKAEIIPFQAPTLPAVPVYSPQLTGPNAFDPRMETAKKGENAPDTKRIKETLEKPSLENMRYVGLKSKQKVSQFIEABGYVYTVG
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SEQ ID 1919

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SEQ ID 1920

MASKSKTNLDLNLHLNLPLRFLIALLVAAVLGLYAGLFKQSMESLBEYAKETELKNTYKQKSIDAASLNLRLDELASIRSTPDNLKQLPTDARIPLNVLQELHQAGSSNGLRLDS
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SEQ ID 1921

ATGGTTTGGCAGCCCGCAAGCTGCAGGCTGAAGATTTCGCAATGTCGCGACCGTCAACGACGCTGATACAGGCGGTATTGAAGATTACGCGCGC

SEQ ID 1922

MVVAARKLQADFRNVRTVNDVVQAVLKIQAG

SEQ ID 1923

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SEQ ID 1924

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SEQ ID 1925

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SEQ ID 1926

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SEQ ID 1927

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SEQ ID 1928

VSNRFGIRNGFLVLCITLKPCTFVIGCYFTLFNTNNGKLLPSYD

SEQ ID 1929

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SEQ ID 1930

MVNYISAMIKLITTCFGLFFGFCVFGVLVAIALIVTYPKPLSLDSLQHYQPKMPLTIYSADGEVIGMYGEBQREFTKIGDFFEVLRNAVIAAEDKRFYRHWGVDVWVARAAVGNVVS
SVQSGASTITQVAKNFYLSSEKTPTRKPNVLLAYKIEQSLSKDKILELYPNQIYLQRAYGFASAAQIYFNKNVRDLTLAFAALAGLPKAPSAYNPVNPRAKLRQKYLINMLLEK
MTTVQQRDQALNEELHYERFVRKIDQSLYVAEMVRRELYEKYGEDATYQGFVYTTVTRTDHQKAATEALRKALRNFRDGSYSYRGAENYIDLSKSEDEETVSQVLSGLYITVDKMPVAVL
DPTKKNNVVIQLPGRRVALDRRALGFAARAVDNEKMGEDRIRRAVIRVKNNGRNWAVQEPPLQALVSLDAKTGAVRALVGGYDFHSKTFNRAVQAMRQPGSTPKFPVYSAALSKGMT
ASTVVNDAPISLPGKPNGSVWTPKNSDGRYSYITLRLQALASKNNVSIIRILMSIGVGYAQYIRRFGRPSSELPAISLMAIGTETPLKVAEAYSVPFANGGYRVSISHVLDKIYDRDGR
LRAQMPPLVAGQNAQPAIDPRNAYIMYKIMQDVVRVGTARGAAALGRDILAGTGTNDNKNDAWVGFNPDVVVAVYIGFDPKPSMRAGYGGTIAVPVWVDMRFALKQKQKGMKMPFG
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SEQ ID 1931

ATGAACCTTTTTCAAAACGCCAAATTCCTACGACGGTAAACCATCTCAAGACCTGCCGGACACACCGCTCGAAATGCCCTTCGTGCGCAGGAGCAATCCCGAAAAATCCAGTGCCATCA
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TGCTCAAACTTATTTCCGACAGGCAAAACATCAGCTACAGCTGTTTTCAGCTGAAAAACAAGGTATTGACGAGGCCAACCGAATGTCGGAAGCTGGTTGACCGCAGCAGATGCGCG
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SEQ ID 1932

MNLFQNAKFTTTHNLKDLPTDPLEIAFVGRSNAGKSSAINWLTNHLVLAAYSKTPGRTQHINFFELQNGNFMVDLPGYGYAQPVEAVRAHWNLLGDYLRHRQLIGLVLINDARHPLKE
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SEQ ID 1933

TTGAAAAGGTTTCATGGCAGATATCTTGTGTTTCGCGCGCGGTTTGTCCGACAGCAAAAATATCGGTTGGTTTATGTGAAACACAGTGG

SEQ ID 1934

LKKVHGHLVFRRLSDSKNMLVLCETQH

SEQ ID 1935

ATGCCCGAACACCGTCCGACACGATACCGTACCGCATCCGCGCAATGTTAAAAATGACCCCAATCATCCGCCACCGATACTATGCTCACCGATTAGAAAAAACGCCATCCGCGACC
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AGCAGCGCGCAGGTTGCTTTCAGAGCAGTGTGTAGACCGCGACCTGCCGTTTCTGGTTCGAAAAAGCGGTTTGGAACTGACCTTCGCACTTGCCAAAGGGCGCGCGCTATCTCTGCC
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CGTCTTAAAGTATGGGGCTGTCTGAAAACGACAGACGAACCAACAGCGAACCAGCTTGGCTGTGGGAAGACGGCAAAATCCCCGAAGGCTCGAAACCACCGTTTCCAATACGGCCATG
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SEQ ID 1936

MPPEPSNDIVPVRPNVKMTPNHPPTD/TMLTDLEKNAIRIDHYQNIQKLPGRFPASQREMIAAVANAFSRT/ITREEGGEPKREGESIAVIEBPTGVGKSLAYLLAGGIDMAQTRGKRLIV
SSATVALQEQLVDRDLPLVEKSGLELTFALAKRGYRYPYKLYQLTQSNQNLGFEAPAVLWDSKPKPEELKLELDIADEFSAARRFNGDRDAMPEKIDDAIWLKVTNRHGLKAAAC
PNRPECPPYLIARDMLTVDVVVANHDLILLADISMGGVILPAPENSFYCIDAEHLHPKALSRFAEHSWNIAVWLEKLPQITGKIAALTDKAELANLADEAAASLDSLHEWQFHLAE
PSLSMGLSENDRTINSEPTWLEWDGKIPEGLEPTVSNATAARSLLKHVGLNDALSAARREKEQDGLIDRLTGFGLFIARIEQISAVWDLSTVSI8GEEPLAKWIARRADKNDYIF
NASPISSASHLANSLWRAAGAVLT/SATLQSLGSPNLLRQTLWLPEPTTLALKSPFDFEKQELIYPSIYASFKDPEAHTAAVIEWLPKLLISPTAIGTLVLFSSRQMDVAHLPG
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QRYGQQLLAGLPPFKRI8

SEQ ID 1937

ATCGCGATATGCGCCATGGAGGAGTGGCGGAATGTCCGATTTTGGCCAGCGTTTGGCCGATGTAGCGCGGAATGCCGTTCCTGCCCGCTATCGCGCGCGCGCTTTGAGTAAGG
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GAAATCGCATACCGTGTCCGCGACTTCGTTCCGTTTGTCCGTCACAATCGACGCGCGGCAATGGTCGATATTGAGCGGGATATGAGCGAGCAGACGGCATTTGCCGCTGTGTCCGAC
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ACGACGTGGTACAGCGGTAT

SEQ ID 1938

MRDMAQWRQWAECPDFADGLPDVRELPFLPAMRRRLSKAARLVCDAAWDIASAHPGSPVVYASHDGEARSFDLWLELLKSHTVSPTSGLSVHNATAGQWSILRRDMSBQALAVCAD
GVETALAEASLLIEGCGSVLVLAAADPLPEGYAVSATRAPFAYALANVLTKGTRYSLTASDMPSEAGMLPEAYWGLEWVRFLINGRSRECRVYRNRWMLQPASCRKISAMSAPS
TIWYREY

SEQ ID 1939

GTGTTTCACATAAAACCAACCGCATATTTTGTCTGTCGGAACAAACGGCGGCGGAAAAACAGGATATGCCATGAACCTTTTCAAACGCCAAATCTTTCACGACGTAACCATCTCAA
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GGACACAGATATCAACTTCTTCGAGCTCGAAGCGCAATTTATGGTGCATTTCGCCGCTACGGTTATGCCAAGTCCCGAAGCGGTACCGGCACATTTGGGTCAATCTGCTCGCGA
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GCCTGAAAAACAGGTAT

SEQ ID 1940

VFHKPAYFCRTTGGGKQGYAHEPFSKRQILHDGKPSQRPAGHTARNCLRRQEQCRKIQCHQYDQPCPSCLRFKNTGTDTAYQLLRAAERQFYGRFARLRLCPSPRSQTRTLGQSARR
LPPPSSETAYRAGFDYGCPPSPFKRTRHPYAGLPFHDRQTGSHPAVKSRQIIQKRTDKNPVPSQKTAQTLFRQAKHQRTAVFQPEKTRY

SEQ ID 1941

ATGCTCTTTTATATTCAAATATGGGATTTTGAACCGATTAAACCGGATGTTCTGTAAACGTTTATTCTATACTAAATTTACATTAATTAACACTGTGTTTCACATAAAACCAAC
GCATATTTTGTCTGTCGGAACAAACGGCGCGGAAAAACAGGATATGCCCA

SEQ ID 1942

MLFFIFKGFIDPIKTDSDVNVLFYTKFTLNYHCVSHKTNRIPLSDKRRRTTRICP

SEQ ID 1943

ATGAGACGATGACTTTATTTGGCTTTGTTTGGCTGCCGCTGCGGTTTCCGCATCTCCCAAGCAGAGCTGGAAGGCAACAGGTTGCCGCAACGTTTGTGCGGCTTGCCTGACG
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GAAACCGGTGTTAATGAATTTGAGCGATCAGGATATTTGAATGTATCCGCATCTATGCCAAGCAGCGCCAAATCCGCGAAGCCAACTCTAAGGAAATCCCGAATTTGGCGCGGAA
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TATCCAGGTTTGGT

SEQ ID 1944

MRRLTLAPVLAAGAVSASPKADVEKGKQVAATVCAACHAADNSGIAMYPRLAAQHTAYIYHQITIGIRDGRTHGSAAVMKPVMNLSQDILNVSIFYAKQPKSGEANPKENPELGAK
LYRGLSDKVPACHSCHGPSGAGMPGGSEIQAYPRLGQHQAYIVBQMNAYSQGRKNTIMEDIANRMSSEDLKAVANFIQGLR

SEQ ID 1945

ATGGAGCTGAAAAAGCAACACGAGCGGAAAGAAAGTGTGGAGATATACGGGATTTACTCATTTGTGTGTTTATTCGCCCATCAGGAATATGGGAAGCAGAATTTGGCGACAGAAAA
CAACGCTCCGATCTACTGTCTTGATGCTTTTATTTTCAAGACAATGAAGACAGCTGCATCGATTCACCGGTTGCGAT

SEQ ID 1946

MELKXANHRERSVGDIRDLLIVCLFRHQYKAELEGRQKTSRPFYCLDAFYFKMTACIDSNCCD

SEQ ID 1947

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SEQ ID 1948

MRFAVALLSLGLASVIGTVLQNPQDYLVKFPFWTRIFDFLGLDYVYASAWFVIMFLVSTSLCLIRNVPPFHEMKSFREKVKESLAAMRHSSLLDVKLAPEVAKRYLEVRGF
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RAVTOGKKNYTNIPSVYRIRDAAGQAVEYKNYMLPILQKDYFWLGTGRSLQOQYRWLRILPDKQKADTFMALREFLDGEGKRRLVADATKDAPATREBQFHLAENTLNIIPAQK
YLGLDFTSNIPKQDQKMGYPYEMLYGVMAALDETRRYGLPEWQDEARNRPLHSHMDAYTGITEYPAFMLQLDGFSEVRSSGLQMTSPGALLVYLGSVLLVLGTVMFYVREK
RANVLFSDGKIRFAMSSARSERDLQKEFPKHVESLQRLGKDLNHD

SEQ ID 1949

ATGACTGAACACTATAAAACCTTCCGGAACACGAGCTGCTGATTAGCAAACTTTGATCCGCAATCTGAATCTTTGGGATTGGGTATTTGCGCTGCTGGTTTTCGCGCTACGGTTTCG
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TTCCTGCGCTGTTTCGCTATATTTCCGCGCGGTTTTCGCAAGCGTGAATAATGTCGCCACCAACACGCTGTTGGGTATGGGAACCGTGTTCATCGGTGTCTGCGCTAGCAGCTTTA
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SEQ ID 1950

MTERHYKLEPEHLLIQSLIRNLNLDWVFAVLVFAATVVFQTRSGMHMDIYETVMLWASAGIAVLFGLWFFKPMRWFVPLSVLLAYAAVGLYGNKISAKIFLLRYPLSSQSAIMWQCAPV
FPALFAYISGAVLASVKNVPTNLLGMCTVFAWVAVAGTGLLVWHESTLLRPDAGHIIPVSNLYEVILFLVITALMYLYEKGFAVQKLGSGVFGMAVVGFWLWVSVSREHPTQP
LIPALQSWMMKIHVPANFITYGAFCSAMLGIAELVSLRAEERGGKLLWPPSALIDEMVKALIAVGLFPFTIATILGALMAADAWGRYWSWDPKETWAFIVMLNYAVWLHLRLVAGWRCKV
LAWMAIGLFTVAFPIGVNMFSLSHSYGL

SEQ ID 1951

ATGTTGGTATTAGGAATCGAATCTTCTTGCAGCAAAACCGCGCTGCGCTGACGACACCGAAGCAGGATTGCGGTGCGACTGCTGCACACTCAATGCGAATGACAGCGGAATACCGCG
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GCCCGCTTTGGCGGTGCGCTGCTGCGCGGTTCGAGCTACGCCAACGCGCTGCTTTCAGCGTTGGAATAGCCCGCTCATCCCGCTCATATTGGAAGGACATCTGCTGTCGCGCTGTTG
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SEQ ID 1952

MLVIGIESSCDETVGLYDTERGLRSHCLHTQAMHAHYGGVPELASRDHIRRLVPLTEGCLAQAGASYGIDDAVAFQPGPLGALLAGSSYANALALADKPVI PVHLEHGLLSPLL
AEEKPDPFPVALLVSGEHTQINAVRIGIDYELLGESVDDAAGEAFDKTAKLLGLPYGGAKLSLEAESGRPEAFVFPMPHISDDLQMSFSLKTAFLTAVEKVRANGSETIPEQTRNNT
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SEQ ID 1953

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AGGGATT

SEQ ID 1954

MNFRLLNQVLSVQKGNITSGSPLNSFGGALVAGVASHLLNGKNRKTITKIGSTAAALGYLAYRGYQMWQONKGRATVTSDFQPAKTEETYSRTVLRTHIAAASDGMIDEAERTI
BQESGDPETAANLAAEYRLPASIGDIAAAGVNDALAAETYLARLVCADLSRKETVFLARLSQALKLDDNLVESLERQLGI

SEQ ID 1955

TTGCCGCCGAAACCGCTCAGTCGCGGATGTCGAAGTGGAAACCGGCAATAATCGCGCGCATAGTTCTTTCAAAAAATTACACTGTCCGCGATTTC

SEQ ID 1956

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SEQ ID 1957

TTGGATTCTCTCTGTTTCAGGCAATGAACATATCAATATTGTCATCCCATCCGACAGATAAAAAATAACCGCTTGGAGCGGCAATGTCATTTTCAGCTTGGTGGCGGAGCGGCAATCG
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SEQ ID 1958

LDLFLPRHEHINIVPHPTDKKITAWSGIVIFSLVPGAGIEPANDV

SEQ ID 1959

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SEQ ID 1960

LPQYFFSDGMFRLQFRLFPPLRTAMHILLTALIKCLSLLSLCLHTLGNLGLHAFYLLKEDRARIVANMRQAGLNPDTQYTKAVFAETAACGLLELAPAFKKPEDIETMFKAHVHWEHV
QQALDKBGLLFTPHIGSYDLGGYISQQLPFHLTAMYKPKIKAKIDKIMQAGRVRGKGTAPTIGQVKQIIKALRAGEATILPDHVPSPQEGGGVWADFFGKPATYTTTAAKLAHV
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SEQ ID 1961

TTGCCGCAATATGCTTTTCTGCTACGATGCGCGCTGCATTAAGAGTTGGGAATTCATGCCAACCTGCTTTTCAAACGGAAAGGTAAGGTGGACGGTTGAAAAACCGATGTGGCTCGCG
GAGCAATCAAACCCGCTGTATGCGGGAATTTTTCGCTGTACGAAACGTACGCGACAGAGATTCCAAAGCGCCGTT

SEQ ID 1962

LRQYAFSATMRAALRVGNSMPTCFSGKVRMTVEKPMWLAGAIQTRLMREFFCLYETYGQRFSV

SEQ ID 1963

ATGTGCACAGCGGGAAATATAGCAAAATTTCCCTATTCGTCGCATTCACTGAGAAATATTCCTATTAAACGGCGCTTTGGAATCTCTGTCCTGACGTTTCGTACAGGCAAAAAATTC
CGCATCAAGCGGGTTTGGATTGCTCCGGCGAGCCACATCGGTTTTCACCGTCCACCTTACCTTTCCGTT

SEQ ID 1964

MTAGNIAKFPYPSCHSVEKYSYLALESLSVRVQAKFPHQAGLDCSGEPHFRFFNRPYLSV

SEQ ID 1965

ATGGTTTGTTTTCAAAGGAAATTTCAATGACGAATATCTGTTTACTTCCGAATCGGTTTTCGGAAGCCATCCGACAAAGTAGCCGCAAGTATCCGATGCGATTTTGGATGCCATCT
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CATCAACGCATCGGCTACAACTCTCCGAGCTGGGCTTTGACGCCAACGGCTGCGCGGTGCTGCTACGACCAACATCCCGCATCGCCCAAGCGGTGAACGAAGCGGAAGC
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AATTCGCGCAAGACGCGCCCTGCTTGGCTGCGCTGACGCAAAAGCCCAATGACCGTGGTTTACGACAGCGAAACCGGCAAGGTGAACGCAATGATACCGTCTGCTCCACCCA
GCACGATCTGCCATCAGCCAGGAAGAACTGAGTAAAGCGGTGATTGACGAGATTATCAAGCCGTTTTCGCGCCGAACTGCTGACCGACGAAACAAATACCTGATCAACCGACCGC
CGCTTCGTCATCGCGCGCGCGAAGCGCATGCGGTTTACCGCGCGCAAAATCATGTCGATACCTACGCGCGCGCGGCTCCGACCGCGCGCGGCGCATCTCCGCGCAAGACCGCTCCA
AAGTGGACCGTTCCGCGCGCTTACGCGTCCGCTTATGTCGCGGAAACATGTCGCGCGAGGCTTGGCAACCAATGCCAAATCCAAGTTTCTACGCCATCGCGCTGCGGCAAGCGATTC
GATTTCCATCGATATCTTCGCTACGGGTAAATCAGCGAGGAAACATGATTCGCTGCTTTGCGAACATTCGACCTCGCTCCAAAGCATGCTCCAAATGCTCGACCTCTTTCGCGCGC
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SEQ ID 1966

MVCFSRKISMSSEYLFTESEVSEGHPIKVDQVSDAILDAILAQDPKARVAETLVNFTGLCLVAGEITTTAQVDYIKVARETIKRIYGNSELGFDANGCAVGVYTDQSPDIAQGVNEGEG
IDLHQAGDQGLMFGYACDPTPLMPFAIYYSHRIMQRQSELKDKRLPMLRPDAKQALTVVYDSBTGKVRIDTVLSTQHPAISQELSKAVTEQIIPVLPPELLTDETKYLINPTG
RFVITGGPQDGLTGRIKIVDTYGAAPHGGGAFSGKDPKSVDRSAAYACRYVAKNIVAAGLATQCQIQVSYAIGVAREPISIDTPTGTGKISEKILALVCEHFDLRPKGIQVMDLRLR
IYKSAAYGHPGREPEFTWERTDKAASLKAAAGL

SEQ ID 1967

GTGCGTTTCAATCATTTTCAATGGAACGATTATTATATATGATGATTTCCTCGCAAAACAGCGGTCGCGCGCCCGCGCTTCCCACTTATCCGCTTTGCTTATAATTCCTTTT
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CGGCTGTTGCGCTTAAACACCGGACGCTCAACAATGTCGCGCGCTTGCAGGTTTATGGCTGGGCGCAACCGATGCGGCTGGTCTCATCATCAACAGCGCGCGCGCTTTCCTG
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SEQ ID 1968

VRFNHFINVITIIYVISPANKPVRPGVPTYPALPYNCFFVYVDSMNFPTAASLLLLASLAHALDTGRI PQNEIAVYVQELDSKVIIDHRAGIPVNPASTMKLVTAFAAFKTPGNS
YRWATEFKSNGTVNDGTLGDLNLYWAGSGDPVFNQENLLAVQRQLRDKIRNITGRMLDHSILNGEVSPDHPEADSGSPFMTTPNPHLSAGVMVRAERNAAGSTDILITDPLPHIFAQ
NLKITASQAACPSVKLMRASFGNFTLKRNI PESCILKPVGVRMFALDELIRQSFTNRLWLLGGIRISDGTIGIADTPEGAQTFLVAHESKPMKEIITDMNKRSDNLIARSVFLKGGDGKL
PAVSEQAASAVRRELAVSGIDVADLVLENGSLSRKERTVARMMAQMLETAYFSPPAQDFIDTFLIAGTGTGLRNRFPQSGGLRLKGTGLNNVRALAGYWLGDKPMVAVVLIINSRAVSL
LPDLNPFVAKNIISGGDGLDAKLMCKERRA

SEQ ID 1969

GTGGAACCGCAAAATATCGCGCGCATAGTTTCTTTCAAATAATTACACTGTGCGCATTTCAACCAAGCCCATCCCGCTGCAATGCCGAAATTCAAACGCAATCCACGCCATTTTTC
GACAACCGCGCCCTCGGCAACCGCGCGAAT

SEQ ID 1970

VEPANNRHSHFFQKFTLCRILTKAHFPDNRBIQTHPRHFRQRRPSANRPN

SEQ ID 1971

ATGTGGAAGAAATTTTACTGAATTACGCTATTTTCTGCTCGAATGCTTACCGTGTTCGCGCAATTTGCGTGATTGTTGTTGCTACAGATGAAGAAACAGTCGGAAGCGGCA
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TTGGCTCATGAGATTACGGCGGTGCTTTTATTGCCAAGCCTGAAGATGAGGTTCTGCTCAGATTTGAAAGTCCGGGCGGCGTGGTTACGGTTACGGTTTGGCGGCTTCGACGCTTAGGC
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TCGGCGCGCAGCGGTGGCGTTGAACCTGATGACGAGATTTCGACCACTGATGATTGTTGTTGTAAGCGTTTGAACCAACAGGTTATCGAAGTGAAATATCAGGAGAACGCAAGCCT
GATCCAGCGCATTTGGTTTTCGAGCGGAAGCTTCCGTTGAAAGTTGTTGCGCAACTTGTCAACCGCGGAGCGGATGTGATG

SEQ ID 1972

MWKEILLNYGIFLLELLFVFGAIALIVLAI VQSKQSESGSVVLTDFSENYYKQRFSTFFFLSEETKHQEKKEKKKAKAKAEKKRLKEGKSAETQKSRFLVLPDGDLYAHAVES
LEHETFAVLLIAKPEDEVLLRLESPGVVHGYGLAASQLRLRLERNIPLTAVDKVASGSGYMAACVADKIVSAPFAVIGSVGVVAEVPNIHRLKKHIDVDVHTAGEFKRTVTFHGEHT
EKGKQKFRQLEETHQLFKQFVSENRPLDIEKIATGHEWFRQALALNLIDEISTDDLLKAFENKQVIEVKYQEKRSLIQRIGLQAEASVEKLFKLVNRRADVM

SEQ ID 1973

GTGGCATTGAATCGCGCGAGATGTTCCCGAAGGCTGGCAGCGGGAATCTCGAATCGGACATCTGCGCCTTTACAATTTGATATGACGACCGCTGAGGTGGAAGATGTGCGCTGC
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ACCGAATCGCGACGTGGCTTGGAAAAACAACCGCGCGCATCATCAGCCATTCCGTCGCGAAGATGGCGGTTACAGTTCCCAAAAAACCTCGCGCTTCCCTGTGCTGATTTTGTATATG
CCCGTAACCGGACAGCCGGAAGTATTTTGGCAATTTCGCGACGCTGTTGATGAAACCGTAAGTTGATGACTCGCAAGGGATTTTGTTCAGTCATATATCAATCAGTTTGTGCGTT
TGATTGAAAGAAATGCCAA

SEQ ID 1974

VALNAEMFPEGWQAEIVEIGHLPLYNFDYDDPEVEDVPLPESTYAFRETIKASDGLFVTSENNRTIPACLKNAVDIGSKPNADVAVKKNPAGIISHSVGKMGYSQKNLRLALSFTDI
PVTGQPEVFLGNSPTFLDENGLIDSARDVQSYINQFVGLIERNAK

SEQ ID 1975

ATGTCGCGCAGCGTGAATGGAATGCAAGGCTTATCCCGCATATGTTGGCGGTTTGGCTGCACGGCGGTTTATGTTTCAAAATAAAATAAGAGAAATAATGCTGACGTTTATCGGATTG
CTGATTATCGGGTTCATGATGGCTGTGCTGACGGAAGGTCGCGCCATCATCGCATTAATCTTGGTGGCGCTGATTGGGGCGTGTGCTGGCGGGGT

SEQ ID 1976

MSAGVNGMQLSRICWRPCLHGRFVYQNKIKNNADVYRLADYRGHRNAVADGKSVAHHRINLGAADWGVAGGV

SEQ ID 1977

TTGCTGGCGGGGTTTGATGATATCCCAATTAAGAATTTTATTCGGCGGCGACGAATCGGTGACGAGATTGTGATTATGTTTATGTTTCCATTTTGTGTTTGGAAATCATGAACGATG
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GACGTTTATTCGCTGCTCCCGCCCTTTTGCCTCTTACAAGCGCTGCAATPATGAATCTTACCTGCTGTTTTCGCTGCTGACTTCCAGCGCGGGCTAATCAACCTTTTCCGCGGGG
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SEQ ID 1978

LLAGFDVSQLKEFVSGTKSVTQIVIMFMSILFFGIMNDVGLFRPMIGLLIKLTRGNIVAVSVGTVLVSVAQLDAGATTFLSVVPALLPLYKRLHNPYLLFLLI/SSAGLINLLPRG
GPGRVASVLGADVGLYKPLLVQIIGVVFILVLSLFLGVREKRRIVRELGAAPADLLKAPLSREEQLKARPLFWNVLLFLAAMSLFSGIFPPGYVFLAATAALLNYSRQPE
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SEQ ID 1979

TTGGGCGCGATTGCAACACACGACAGCGAGGCAAGCCTGCGACAGATCACAGGAACGATTCCGGCTTCAGCGCGCTTCGCCGTTTACGGCAGAGGACAGATTCTGCCCTATCGAAC
TGACCAATATCGCCAGCGACAAACCCACGCCAGAAAAACGAA

SEQ ID 1980

LGRDCWRTGRQSLRQITGTTIRASGFAVYGRGTIPAAIELTNIASDKPHAQKNE

SEQ ID 1981

GTGTCGCAAGTTTGAAGACGGCGGCTATGCGGTGATTTGGTCAAAAACGGCGCGCAGGTTCGGCGGCTGCGCGCTGCCAGCCTTATGACTTGATGCTGCTGGAATTGGGTTTGCTG
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SEQ ID 1982

VSASLDGGYAVDVKNGAQVAAAAAQPYDMLLDLGLPGRDGLDVLSEIRAAGCTVPVLIIVTARDLISRLNGLDGGADDTYKVPFDMAEFKARMRAVLRRSGQAQCLSNGLSLNP
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SEQ ID 1983

ATGCCGAAATCAAAAGCATCCACGCCATTTTTCGACAACCGCCCGCTCGGCAACCGCCGGAATTAGCCTGAATTTACATTTATCATTTGATATGCCGATTAACGACACCGCTCC
CTGCTGCCGACAGCGGGCTATGTTCTGATAGACCGCATTAACCGATACGCGCA

SEQ ID 1984

MPKFKRIHAIFSDNAAPRTARI SLNLHLSLIMPYRHRPLPAAQRAYGSDRPHYPIRR

SEQ ID 1985

CTGCAATGCGCGGCTCGGGAATGCTTGACGAGCGGCTGCTGTTTGTGAAATTCGCCGCCATATAAATAAGAACGAAATAGGTACAGTGGTCTTGGTGGCGGTAAAGATAGCGTCCGCTG
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GCCGAGGATTGTTTATAGCAATCTTTCAATTTTCTCCCTCAAGGAGAACGCGCTGATGATGATTTGTTGCAAAAAACATATACAGTTTACGCGCGGCTATCTCTTGACGCT
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AAGAGATTTTGGCCGACAAATACGATGGGGCTTGGCCGACAGGATGCGGGTGGAAAGTGTCCGATTTGCATATCCCGGATAAGCAGCGCCGTCAGCAGGACGGAAGGAGCAGGTTATTCC
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SEQ ID 1986

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RDKRIVFVDHEQADKQCAETE**KQLPFSIFCLPSAVLRFPVNRQORTHQQLGKPKRRVISIGLVEDVGIKPGRQR*CGQNKQDADITQHP**FGPFTVEYQKRIQEVILFLYRQR
PDMQYGLVGTQIEPQSEPIINIGQKNRRKLYGPHLVEIFVKEDLRNHSRQGHCRNKSRINPLNPAIGIKI PERKRTVLYFRKNDVGNESRDKENVPQESSGPVAVIQVENNDG*H
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SEQ ID 1987

TTGCGAGGGGAGGGGTGGCATTGAGCAACCAGGAGTTTTCGGTATTGCAGGCTTTGCTGGCGAGGCGGGGTGTGATTTTGTGCGCGCTCGGATTTCGAGGACAAGGTTTACGGTTTGGGGCG
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SEQ ID 1988

LPRGGVALSNQEFVLIQALLARPVILSRSDSEDKVYWGGEVESNAVDFLIHGLCKLKGKESIQNVRGVGMLMPQDAV

SEQ ID 1989

ATGCCGGACCGTTTAAAAATTTAAACATTCGCTTCAGGTCAGAAATCAGCTTGCCTTGATTGGATGTTTGTTCGCTGGCAATGCTTGCAGGTATGTTTCTCTACTAGCAAACTT
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SEQ ID 1990

MPDRFPKILKHSIQVRI SLALIMFVPLAMLAGMSYETFHETALQDILLRQAALYVGPDSKPETLPEGDITRILVQMPQEDPVVSLPAHLADGLHTLQADGDDOYRYVIRTEPG
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SEQ ID 1991

TTGACCCGCTCTGCGCGCGGGCGGAAACGGATGCAAAAATATTTTATTACATTTTCAGGAAAAACCATGTTGTGTCAGGACTCCCATCCCAAGACATGCGCGCCCGCCGAAACGA
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SEQ ID 1992

LHPICAAGRNGCKNIFITPSGKTMLSGLPIPKDIARPPETILVNIPTQETRVAVLENNICELHIERNSGHSLVGNILYGVVRRVLPQMGSFIDIGLERAFLHIVDVLEQRNPEETQR
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RELRLNLGGIIIDFIDMAQESHREAVLQELAKALAFDRTRVTLHDFTSLGLVELTRKRSRENLNQVLECEPCSCQGRGLKTFQTVCYEIQREIVREARRYDAESFRILAAPNVIDLFL
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SEQ ID 1993

ATGCAAAAATATTTTATTACATTTTCAGGAAAAACCATGTTGTGTCAGGACTCCCATCCCCAAAGACATCGCGCGCGCGCGGAAACGATATTGGTCAACATCAGCGCGGAGAAACCGCG
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CGTTTATCGACATCGGCTTGGAAACGCGCGCGCTTTTACACATCGTCGATGCTTCGAACACCGCGCAACCCGAGAAACCCAGCGCATCGAACATATGCTGTT

SEQ ID 1994

MQKYFYIIFRKNHVVRTPHQHRAPARNDIGQHAAGNARGVGKQYLRAAHRAQRAQPRQYLSGRGAPRTARDAERYVRHRLTRGVFTHRRCPRTTPQPRNPAPHTYAV

SEQ ID 1995

ATGATAATCAATATAGGGCAATCGCTCCGTTTGGCAAGTCCGGAACAGATGCACGTTTCAGACGGCATGTGCGGAGTGTCTCAAAGTTTCTTTTAAAGTA

SEQ ID 1996

MTIHGAIAPFGKCGTARSDGHCVCQSFYFV

SEQ ID 1997

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SEQ ID 1998

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SEQ ID 1999

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SEQ ID 2000

SEQ ID 2000
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SEQ ID 2001

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SEQ ID 2002

SEQ ID 2002
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SEQ ID 2003

SEQ ID NO: 203

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SEQ ID 2004

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SEQ ID 2005

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SEQ ID 2006

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SEQ ID 2007

SEQ ID 2007

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SEQ ID 2024

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SEQ ID 2025

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SEQ ID 2026

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SEQ ID 2027

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SEQ ID 2028

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SEQ ID 2029

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SEQ ID 2030

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SEQ ID 2031

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SEQ ID 2032

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SEQ ID 2033

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SEQ ID 2034

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SEQ ID 2035

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SEQ ID 2036

MDFAHYLKHWKA AVL IYLA I SILTDILCYFLNFDGVFYKGRFPSVTVAGPVGALSFLAYLLYLKREENRSH

SEQ ID 2037

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SEQ ID 2038

UTNCLQLYITLRTLCRLKPVFQRIKNDVFVVVRYGEORSGPPGNFTARQKRLVYVPLRQARPKRLSNQNDRTRRHFARLHQGDQFKQVQVRPEAARHHDICLGIAEKHCLAPGKTGKPGQGV
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SEQ ID 2039

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GAACTTCGTCGCGGAACACTCTTTTACAGCGCATTTTGGCACGCGCTCACTCAACGTGTACAGCCCGGAACACCATGACGGAAACAACTGACGCGCTGTGAACAGGCACACATACGGAGA
ACAACTGACTGAAACCGTCTGATTACCGGCTCAACAGAGGCATAGGCAAGCCGCCCACTCGGTTTTGGCGGACGAGGCTT

SEQ ID 2040

MLPYTAFIELMAQAVGAYAGIQARKNRPVRLGFLPGTRKLEIFAQSVFVGLHPATAHMSIQDAGVMACPTANCVGRMRRLRPEHSFQAFWHAPHSTCTAPNTMTBQLTPSEQAHIRR
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SEQ ID 2041

ATGAAATATCACCGCTTGGCATTGTTGCCGCCATAAGCTGCCGTGTTGTTCGCGGTTTTTATTCACCTTACCTGACGGCATTTCACGAACAAGAAAAATATTGAAATATGCGGATT
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CATCAGGCGCGGCAAGGTTAAGATTGTTTAAAGCGAAACCGTCGGCAAGGTTTTTAAACGGCGTTCGTGTTGGAATACCGCAACAGTGGCAGTGTCTATAGCAATAAAGATTTTCCCGC
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SEQ ID 2042

MKYHRLALFAISCLLSAVFIAPYLTAPEHEKIFAYADLTPTAPNRSRAIKLEADGRQYRLSCYGFDSLCTGNNIGRAIRARQKIVLSETVKGFLNGVILLEYRNSGSVYSNKDFSR
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SEQ ID 2043

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CGCAATTTGAGTGCATGTGTCAGGACGACGATGTTTTA

SEQ ID 2044

MDYLQNLISLGLTKLPLVILQTEVAECGLACLAAGVGYFYTDLRALRSKYCLSLKGENLADIVRFADDMGLTGRALRLDLDELGLSLRPLCILHWDNLHFVVLSESVSDGAAMVDPASGR
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SEQ ID 2045

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AACCGTGAATCAGCAGATAGGAAATGCTTTAGGA

SEQ ID 2046

MIREESAMPMEYETFLIGDMGSALSGGQKQRIVLARALYCEPKILFLDEASHLDIANEKAVNANLGLSIIKIMAAHRKETVESADRKMSLG

SEQ ID 2047

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SEQ ID 2048

MTFLQRWQGLADNKICAPANFVIRFSEERVPAQAASMTPTLLALVPLTVMVAVASIPVDFRWSDFSVFVNQTVIPQGDMMVFDYIDAPRDQANRLTAIGSVMLVVTSLMLRTIIN
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FVYRPLPVERDHVQAVDAVMTPLQTLNMTLAEFDAQAKQQQS

SEQ ID 2049

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CCGCTTACCAAAAC

SEQ ID 2050

MNPPLKILVLYSQNGSTRNPARRITRGIDSVEGCEAVLRTVPKVSACEAVKKDIPDSGSRPDRRKQYRLRTRQTLGGTRQVQIRRVFRRHGVQMPSEVCLYNPRLYCPTSRFANL
PRYQN

SEQ ID 2051

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CTTCGACAGCGCGGACACTTTGGGACGGTGCAGCAATACGCGTTCGCAACCTTCAACGCTGTGATGCGCGGAGTGATTGCGCGTTCGCGGATTCGCGGCTGCTCCGTTTTGGGAATAGTA
GAGGACGAGGATTTTGGGGGATTGGGTTTCATGGCGGATTCGTTAA

SEQ ID 2052

LTYYRLVLVTVREYCEPRSWTVKTRIIQANAFRRHLNAMPSEHAAYADLTASSAKRLPKAKILFSSAVRTGAAGVNIFFDGFADGGHFGDGAQYGFATFNAVDAASDSACGIAAGVILGT
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SEQ ID 2070

NPNRVIPAQAGIQTLIYQYKLKIAAIPNLWIPACAGMTVNSVLI

SEQ ID 2071

ATGAATTCCTCCCTCCACCTCTTAGTCTCTCTCGTCGCCGCCGAACATTTTCATATCGCCTGGCTTGAAATGACACAGATTCCCGCGGAAAAAGCGCGGAAATGTTCAAGCTGCCTTACG
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SEQ ID 2072

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SEQ ID 2073

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SEQ ID 2074

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SEQ ID 2075

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SEQ ID 2076

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SEQ ID 2077

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SEQ ID 2078

VYPTAASYSRLRFPDWAEMSAVSRGSGTLSPYVKHRQNGTPAL

SEQ ID 2079

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SEQ ID 2080

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SEQ ID 2081

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SEQ ID 2082

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SEQ ID 2083

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SEQ ID 2084

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SEQ ID 2085

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GAGGCTTT

SEQ ID 2086

LEYTAMTVPHIPRGFVNMADIAAPRLTEEEKQRLDPAIGGIILFRPNFQNTBQLKTLTAEIKALRTPELIJAVDHEGGGRVQRTIEGFTRLPAMNVLGQVNDKDGASAAETAAGQVGRVLAT
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EAF

SEQ ID 2087

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SEQ ID 2088

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SEQ ID 2089

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SEQ ID 2090

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SEQ ID 2091

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SEQ ID 2092

MFKDWEKHTALVKKSPGELGKAHPKILQAYGALEQAAAAEALDAKTRELIALAVAITPRCESCISVHAAAAAKAGATDSEIAGALATAIALNAGAAITYALRALEAVETQK

SEQ ID 2093

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TAAAAATGCCCGGTTAATCGGTTATGACGGGCAATTTATCATTT

SEQ ID 2094

VLSVRMGGYLSASGLGVGKMGGNI PCRKKYLFKINQLIFVKCPLIGIDGHFII

SEQ ID 2095

[illegible]

SEQ ID 2096

VFKKYQYPAALCAALLAGCEKAGSPFGADKKKASFVERIEHTTKDDGSVMLLPDPFAQLVQSEGPVAVNIQAAPAPRTQNGSNAETSDPLADSDPFYEFYFKRLVFMFPEIQEEADGG
 GLNFGSGFIISKNGYILTNTHVAGMSGIKVLLNDKREYTAKLIGSDVQSDVALLKIDATEELPVVKGIGNPKNLKPGHEVAAIGAPPGFTNSVTAGIVSAGKRSLPNESYTPPIQTDVAIH
 PGNSSGPLENLKGVGVINSQISYRSRGGFMGISFAIPIDVAMNVAEOLKNYKGVKORGOLVITOEVSYGLAOSFGLDKASGALIAKTLPGSPAERAGLOAGDIVLSLDCGEIRSSGDLPMV

VGAITPGKEVSLGVWRKGEETIKAKLGNAEHTGASSKTDEAPYTEQQSGTFSVESAGITLQTHDSSGKHLVVVRVSDAAERAGLRGXXXXXXVFNDEAGFRKAMDKAGKNVPLL
VMRRGNLFIALNLQ

SEQ ID 2097

GTGCGAATATCCCGCAAAATCCTGACCGCCGCCCTTCAAAATGAAACGCTTGAAAATTCGGACGGACGTTGTAGAATTTCAACCTATGCCGTC

SEQ ID 2098

VRISQILTAALQNETLENSDGRISTYAV

SEQ ID 2099

GTGCCGGAAGACCGCAGGCTTTGGAATCGTTGCTGGCTGGGGCGCAAAACGSCAAACGTTGTAACACAGCGTTCCGACACCCCGTTATGGCGGTGATACGCATATTTCCGGG
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CTACACCTGCAAGGCTTTAAAGCGCAATGCGCAAACTGCATCATCAACGATTTGTGCGAATATCCCGCAAAATCC

SEQ ID 2100

VPEDREALSLPGVGRKTANVVLNIAFGHPVMAVDTHIFRVSNRTKIAPGKDVREVEDKLMRFIPKEFLMDAHHMLIHLGRYTKALKPQCQCTCIINDLCYPAKS

SEQ ID 2101

ATGCGTATCGACCCCAATAACGGGGTTCGGAACGCTGTGTTCAATACCACTGTTGCGCTTTTGGCGCCACGCGACGCAACGATTCCAAAGCCTCGCGGTCTCCGGCACTTAGCCGTTG
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TATCGCAACCGGAACAGCTTCGCCCTCGCCTGTGTACGCGCATCGGTCGCTCGCCGAAAGCAGAACGGCGAT

SEQ ID 2102

MRIDRHNGVSERCVQYHVCRFAPHARQRFQSLAVFRHLAVVFFQHDAAGLHNVFLGLFIQPDGFRVFFHVAQAIQHRLRRIGNRKQLRRRLVYADIGRLRRKQNGD

SEQ ID 2103

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CGCGGTGATGGAATACAGAAACCATCGGCTGTATAAAACCAAGTCCAAACACATTTATGCAAACTCCCGCATCGTGTGAAAAATACAAACGGC

SEQ ID 2104

MPTAQTDCTKKNRQIQEIRFERFRAANPHPTTELNFNSPFELLIIVLLSAQATDVGVNKATAKLFVADTFQAMLDLGLDGVMEYTKTIGLYTKSKHMQTCRIVLEKYNQ

SEQ ID 2105

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GACGGATTATACGCTATTTTACGCCCCCGCGAAGGCGGAGGACGCTGCAAAATACGCGCACGCGCTATGCCCTTTTGTGCGGGCATACGACATCTTTTCGCTCCGCTT

SEQ ID 2106

VQSVCAVGIIITHSGGVILHSPQNEGVTRRFADNQHPACPRIQPQAGGKQCVADDGQPRKRKQPNTEPTPYQIQCFRRHFRSGRQQTSHPIGNHTAQSVGKAGAAQRAVCFVGEVADEQ
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SEQ ID 2107

ATGCCGACAAAAAGGGGCATACGCTGTGCCGTATTTTGCACCGTCTCCGCCCTTCGCGGGGGCGTGAAAAATACCGTATAATCCGTCGCGGATTTTACCTGTTTGGGACTGTTG
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ATACGCGCGCTTCTGTGCGCGCGCGCTTGCACCGGATTGGCGAGTATGGTTTCTTATGGATGGGACGTTTGTGCTTCCCGAAAAATCGCTGTGAAAAACACTGAATCTGTATACGG
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SEQ ID 2108

MPDKGAYGCAVFLHRPPPGGGVKIPYNPSIPTCLGLFAMI PSYTYAALAFSAFTSATLLPGTSEAFALFVRNPKHAYGALLCAGLANGLGSNVSYWMGRLLPSRRMPSEKTLNLIR
RFGIWLAFANLFPVGDALPLTAGWLRNLNPTSLGLMLVIGKTARYAFILWGMQYIAA

SEQ ID 2109

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SEQ ID 2110

MQVAQQVDGCLSGFLLDVLPHGIADTFLRRAGIAHFVQFDDVPAELGADRADLSGFERVDGFFKGGNHVAVGKPAQVAALARACVLGISACQTCIRAVARLVVDFADGTFRADGGVFA
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SEQ ID 2111

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SEQ ID 2113

SEQ ID 2114

SEQ ID 2115

SEQ ID 2116

SEQ ID 2117.

SEQ ID 2118

SEQ ID 2119

SEQ ID 2120

SEQ ID 2121

SEQ ID 2122

SEQ ID 2123

SEQ ID 2124

SEQ ID 2125

ATGCCGCGCGGTGAGGCACCTTGCCTGCTGCTGCTGATTGCCGCAATGGGCTATACCATCATTTTCAATTGGAGTGGCTGCCGCATATGTCCATTATTGCCGCCATCTGCTGCTCGAATTT
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CTGGAGCGTGTGCGCGTATTATCAGCCACGCCCTTGGCGTACCGCTTGGGAATATCGCTTATGCCTTTTCTGCTATTGAGTTTGGCTTAAACCTGTATTTCGGCTGGACGG
GCTGACTTTGAGCAAAAAA

SEQ ID 2126

MPRGEALAVVVALIAAMGYTTISLEWLPHMSIIAAIVVLILYGLARGLKYNDMAGNIGALNQMGSAVYLFFPFIGLMVSAIMMSGAIPTLMYYGFLISPTYYFSAFALCSVIGVSIGSS
LTACATVGVAFMGMAAFQADMAITAGIVSGVFFGDKMSPLSDTTGISASIVGIDLFPHIKNMYYTIPAWLISAALMLWLLPSVAAQDLNSVESFRSLEATGLVHGYSILPFPALLVVL
ALMRVNAVVMFLFTVIAAIVTYLHSTPDLRQLGAWFYGGYKLEGEAFKDIARLISRGLESMTPTQITVILGMSLGLLFPALGVIPSLLEAVRTPLTNAGRATPSVAMTSVGVNFLIGEQ
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SEQ ID 2127

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GCTTTGGGACGGCGCAAGACGACCCGACCTGCGCCCATTAACCTGACCGGCGCAGCGCTGGGAAACCGGAAACCAATTCGCGCCAGCTCGTCTGTTCGCTTCGGGGGAAGCAACTCGCTC
TTAATCATCGA

SEQ ID 2128

LQHAGLAPEDIGRINLHGTGTHHDSMESRAVAAVFGNTPCTSAKPTQHTLGAAGAIEAFAWGIADRSNPEKLPRLWDGQNDPDLPAINLTDGHWETEKRIASSSFAGGSNCV
LTIIG

SEQ ID 2129

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CGGCAACGGGCTGGATATGAGCTGTTTTCGCCCGCTTCCGCTACGACACCCAGCGGATTTGATGAACGGGCTGCCGGAACCGCTTTTCTGAACATTGCCCATCCAAGTTTCAGTAT
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SEQ ID 2130

MCSAFWADNDETQREGLVHIVTAGSYLCTDGETSPRPVGTGDIIVFPRLGLHVLHSDGKYGESLQPDIRQNGTFMVKQCNGLDMSLFCARFYDTHADLMNGLPETVPLNIAHPSLQY
VVSMLQLESEKPLTGTVSVNALPSVLILWILRAYLEQDKDELGVLRGWQDKRLGHLIQKVIDKPEDWNIDKMVAANMSRAQLNRRFKSQVGLSFHAFVNHIRLQKGLLKKTPDS
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SEQ ID 2131

TTGTATCGACTTAATCTGAAACACAAAAGCAGGATTAAGACACAAACAGCAGTAAGCTTTATCAAAGTAGGGATTTCAAGTTTGCTTACT

SEQ ID 2132

LYRLNPETQKAGLRHNAKVSFIKVGISLLT

SEQ ID 2133

GCCAAAGCAGGCGAAGTACCGCGGGCTTCGGTACCTTGTGCCAAGGCAGGCGAAGTACCGCACTTTGCGGGCGAAGCCGCAACAGCCGAGAAAGCGGGGGGATTCGCGATAAGCGCG
AGGGGGTGTCGCCACAGCGCTGCCGCGCGCAATTCGCGAGCAA

SEQ ID 2134

AKGRSTAGRLYLVRQAKYRTLRAKPQTAEKRGIGDKREGVSPQRCAANAQ

SEQ ID 2135

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TTGCGAAATTTGTCGATAATTCGAATTTTGATGATGTATTCTGT

SEQ ID 2136

LALYKQPSSEYFGQSMVIAQSEFVFAKINKSENVDCFSFFWNRRIKHDIWLSFFDNSENVIKESLNDGHKTYKFEFCEIWDNCFDQV

SEQ ID 2137

TTGCCCGTTTGTAGGATTTCGCAATGGGAGATAAGCAAGGATGACAAAGCGGTTCGCCGCTGATGACGGACGCGCGGCGGACGGCAGGAAGCCGGCAACCCCTTCGAATCTTCCCC
CCCCTTATCTAACAGGGGGGTACAGAAACCGAAACGGCGGCGAGGTTTCAGAAAGTCTTCGAATGTTACGAAACGTACA

SEQ ID 2138

LPVFEDSQMGDKQMTKAVAGVMTDAPDGRKPATASNLPPPYLTGGVQKPKRRAGFRKSSNVTKRT

SEQ ID 2139

ATGGACGGCGCACAAACGAAACAAATTTTGAACGCTGATTGCCGACTCGCCCGGAACCCGATTCGCCGAAGACGTATTAAACCTGCTTCGGCAGGCGCACGAACAGGAAGTTT
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CAGTTCACCTGAAATCCGCTTTCGCCCTGCCGTTTTCGTGCCGGAAGCAAAATCTTTGACCGCCCTTTTAAAGAGTTCCGCGAAGCAGCGCAACCATATGGCAATCGTCATCGACGAAT
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SEQ ID 2140

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QFHLKSVLRPAVFPBGSLTALLKEFREQRNMAIVIDEYGTSLVTFEDIEIQVIGDIEDEDEDESADNIHSVSAERWRIHAATEIEDINAFGTETGSEEDTIGGLVQLGHLPL
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SEQ ID 2141

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SEQ ID 2142

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SEQ ID 2143

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SEQ ID 2144

LNALNMPKFLVIASRESILANWQAKHIQGRILKALYPDCEVELLGMTTRGDRILDRTLKVGKGLFVKELEQSLQDGRADLAVHSIKVPMDLPEGFALAAISERANPFDAFVSNRYARL
RMPFEGAVVGTSSLRREAQLRARYPHLVIKPLRGNVOTRLSKLDNGEYDAIILAAGLQRLLEDERIRMLSESDSLPAAGQALGIEIATHREDLYEVLKPLNHDTTHACVPAERALARL
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SEQ ID 2145

TTGTTTTTAATTAATTTATTAATAAGTTTACTACCTTATTTGTCATTCCCGCGCAGGCGGGAATCCAGTTTGTCTGGTTTCAGTTGTTTTTAATCAATCTTTCGACGATTGGGTTTC
CAGATTCGCCCTCGCGCGGAATGACGCGGAAAGGTTTTTGTGCTTCGGATAATCTGTCGCGTTCAAATTT

SEQ ID 2146

LFLNLNFKPSPYFVIPAQAGIQFARFQLFLINSCSIGPDSRLRGNDGKVFVASDNTVAFKF

SEQ ID 2147

TTGGTTTTCAGATTCCCGCTGCGCGGGAATGACGCGGAAAGGTTTTTGTGGCTTCGGATAATCTGTGGCGTTCAAATTTGAATTTGAGAATGATGATATTCGATTTTTTTATTTG
GCTGTACTAGATTATCCCTAAATTCACACCAATCCCGCAGGATTTT

SEQ ID 2148

LGFIIPACAGMTAERFLMLRIILWRSNFEFENDDIRIFYCGCTRLSLNSTPIQDF

SEQ ID 2149

TTGCTCCCTGCGCTCAAAAGAAAAATCATGCGCGAGGTATTGTTTTATGCCGATAGCCCGGCGAGCGCGCAAGTTGGACGCGCGCGGTTTTTACCGTTGCCGATCAACCGTTTCAAGG
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CGAATTTGCACTTAACCTCCGCGACACCGTCCCGCGCAGCTAAAAATCTGCGGGATTGGTGTGGAAT

SEQ ID 2150

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SEQ ID 2151

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CGCAATCATCAGGCTTTGATTTTCATCAT

SEQ ID 2152

ADVDIRAGMQVQVQDGLSGFLEEDVLPHGIADTFLRRAGIAHFVQFDDVPAELGADRRADLSGFERVDPFGKGNHYAVGKPAQVAAIARACVLGISACQTCETRAVARLVDFADGTF
RADGGVFAVGFQNDVLGAVLAQRCAFGQDALFLRLLEEGINFSFAHAAVLHCLLADDFGNDVVGKLAALGGAEVFEGGILCDDGIDFRFTCLNVAAPARLYNQGLVDKLHQLHSLQLGF
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SEQ ID 2153

TTGATTATAATGGCGGGTATGAAAAATACCTTATCCCTCTTCCATTGCGCGAGTCTTTCGCGGTGCGAGTCTATTATGTGCCACATTGACGGAATCCCGGTGAATCCCATCAATA
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CAAGGTTACGCGCGCAATATCTGAACAACTTCAGAAAACGCTGCTGCGACGCAATGCCCTCGATGACAGTATGATGAATCTACCTGCGTTGCGCGGTAGACAGCCAGCGCGCGGAA
ATCAATACGGAACAGTCCAGCTGTATATCGAGAATGCTTTCGCGGCTGCGACGAGCTTGGAAAAATATGGATGCCAAACCCGATAATCCCGCATTTACCACTTTTGTATGGAAGTGA
TGAAGATGCAAGCTTTGAAA

SEQ ID 2154

LIIMGMKYLIPISIAVLSGCCQSIYVPTL/TEIPVNPINTVTEAPAKGFRLAPSHWADVAKISDEATRLGYQVGIGKMTKVQAAQYLLNFRKRLVGRNAVDDSHYEIYLSAVDSQRGE
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SEQ ID 2155

TTGTTTTTAAACAAAAACAGATGCCGTCTGAACCTGGTTAAGGTTACAGCGGCATTTTCATATGGCTGCGCTTTTACAGTATATTCAAT

SEQ ID 2156

LFFNKRQMPSELVKVQAIFYGCAFYISIFN

SEQ ID 2157

TTGTTTGAATTTGTTATAGTTTATTTGTTTTTAAACAAAAACAGATGCCGTCTGAACCTGGTTAAGGTTACAGCGGCATTTTCATATGGCTGCGCTTTTACAGTATATTCAATTAACAA
AATAGTACAACTCGAGCTTGAAGGT

SEQ ID 2158

LFEIVIVYCFLEKNRCLNWLFRRHFMMAALFTVYSIRKNIVQHSFLKV

SEQ ID 2159

ATGGCATACTCTCGGACTTAAGAAACAAAGCTTTAAACCATAGCGGATTAACAAAAATCAGGACAAGGCGCGGCGGACCGCAGGAGTACGAATGGTACGGAACCGGTTCCGCCGCGCTCC
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SEQ ID 2160

MAYSADLRNKALNHSGLTKIRTRRRTAGSTNGTEPVRPALHHLRESFPLGRGGATPYRFLIRYITDNAKTPAKPQORLTQETRTFCGALKNKQAA

SEQ ID 2161

ATGCCGCCAAATCGGATAGGCAAAAACCGCTCGATATGTGCGGGCGCATCCGGATGCTGTCTGCATGAAATCGCCAAACATTTGATTGTACGGCAGCCGCGGTTGCCATGCGCCCAA
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AACCGCGGATGCTCCGATGTTTGTCAAATACGTTGCCCGGGCTCTTTTGTAGCGCGGTTTCAGCAATGCTTACTGCCCGCATTTGGCTCAAAAATCGGTGATTATTTTCAGATAATG
CGCGATTTCCCGGATGAGTGTGCTTACGGGGAACCGCGGAAAAATTTGGGACATAAGGTATTTGCCCTCCCGCACCTTATTCGCTGAGCCCAACCGGATTGAGAAAGTGTGGGCGAATATTAA
CGGTATCTGCGAACCGTTTGTCTGATTACGCCCGATTTCAGATGCACTACTGTCTTATTTGATTTTAAAT

SEQ ID 2162

MPPNRIGKNRLDMSGGIRMFVCMKSPNLIIVRQPPFAMRPNRCGRWAKKTAAYKQDPAKVTHYLTPAGFSDCQVCPDETGFDRRLFRPYARSLKQMAKARIRVKRYRRLSLVSAQVG
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SEQ ID 2163

TTGCTGCTGTACAAATATCATTTCCCTTTTCCACTCAACCATCAGGATTTCCCAATGCCACCAATTCGATGTCCGCGTAATCGGCGCAGGTCGGCAGGTCGGCGCATCCGCCCTGC
TCCGCAAAAAGGTTATCAAGCTCGCGTGTGGAACAGCACTTTCCGCGCTTCGTATCGCGAAAGCCGTGCTGCCGACTGTATGGAANTGCTGGAAGAGCGGTTTTCGCGATGCC
GTTCCGACCCGGCGCGCTTTCAGT

SEQ ID 2164

LLPVQYHFLFHSNHQDFPMPTQFDVAVIGAGPAGSAASALLRKKGYQVCVLENSTFRASSAKACCTVWKCWKFPVLPMPFAPGPAFS

SEQ ID 2165

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SEQ ID 2166

LKNGAAF SWGSRYTEFDTDFKPSDGPVTYQVRRRAVDFKILIEAAKQGVFVGHGVTAFTNSGDFARLNIETDTGESYELTAKFVLDSAGYGRVLPRLINLETFPSHLPPTQTHFTIID
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SEQ ID 2167

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AAAAAGACATTTTACGATCGGGCTGGATGCTGTGCGCGCGGCTGCTTACCCTTATGAACGATTGAT

SEQ ID 2168

LFGKKNKISASEAGKNTPFKRKYVNPVLIATTVYGYRKRHRFIRGLDAGGGELLHRYERID

SEQ ID 2169

GGGCGGTTTGTTCGCTCCGCGGAAAGAGAGTGGCGGGGATGAGCGGGAACCGCGACATCCTCTGCTGCGGGGTTTCTGCGCAGCGTCTGAGGCTCTTCAACTGAAGTGA AAAA
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SEQ ID 2170

GPVVASGGKRVGGDVAGNDIHPACGVSAADAEVFLK*KKDGVFVGVFAGNVALGVHARAPAAATFVFCGKHFYRFPFKTVVVDGRQVQRPLCGQVELAEFVVKIGTIVRLQVD
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EKLPAVEAARFRTEIGQVWLRFRGNITVEQARLDGLHDSAAEQARIAFEGCAAVDIDNQAPDAAGCPAETVEAVISGVQPEFGADVAPAVAEIIPFDGIHQSAVLAIVVAEAGKLC
GHADLRPAVFMPIGRKAGHDGVRFFVVAALVQRLVFLNRKAGIQASRRPAIILQPTAAVEVDVAGDFFAAVKVAVVAAGDLVEIDTRLKRVGNVVPVLPCLIAVVPAAFLIVRQPG
QVGLSAVIGTQVTDLSVKRRRAAFADNAGGESGIEVGGKVEIIGDGKNAVTRGTYRDEQSAFAVAVKREVRPRRIKGNAAEHGGVFNAYAFSPIGFDRGGLDIPAGISGGTGVELGF
RQVFTPPAQHFGGAADALQPPSALFGFHTDVVRFAGLLIEIVGQGFAPNQRVTLLGEPEVAVYGNVAVRLVVRIGIEDCAVFPFDNASFRAHLNRLSLPHVGNNAIRIVFGDGFPAALD
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SEQ ID 2171

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SEQ ID 2172

MSNFFSSLGLTFLVSALTQAQYENPTPIQAAAIKALAGHDLAAQTGTGKTAAPMLPSLERLRYTASTSPAMHPVRLVLTPTRELADQIDQVQGYIKNPLRIHTVLPFGVNHDK
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LIVDLHMNQVIVFCKTKQSDRVTRRELVRNLQAQIHGDRSQSRLETLNAPKDGSLRVLVATDIAARGLDIAELFFVINYEMPAQPEDYIHRIGRTGRAGDVAISLMDSEBQKHFEA
IRELTGNKLLIERIEGFEPRWWEQEGSKPEKTETSEPRQRNRYESARAQREKNTREPETANDAGAACKIAGRSRRSRRGHRTCALLQPRYGVK

SEQ ID 2173

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SEQ ID 2174

LGRAPPYGI IRTQIPVPAVHRAVYFFVLSVSRFRHRHV

SEQ ID 2175

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GGG

SEQ ID 2176

VPAPIAGASADWKSCLKNVQWRTFLKRGPIIMHIGYFIDNPIALAPWAGIADKPFRLCRAPGAGWAVCEMLASDPTLRNTGKTLHRSDFADEGGIVAVQIAGSDPEQMADAARYNVGLGA
QVIDINMGCPARKVCNVQAGSALMQDEPLVAAILLAVVKAAGVPTFLKTRLGHWDHQLPALAKIAEDCGI AALAVHGRARTQMYKGEARYELIAETKSRLNI PAWVNGDITSPOKAAAV
LQQTAAADGIMIGRAQGRPWFRLDKHYAEHGLVLPALSLAECRAAILNHRAMHAFYGETGVRIARKHIGWYI GEMPDEQARRRINRLDAAAQYDTLAGYLERLAGKTRDRACGYRE
G

SEQ ID 2177

ATGCGCGGTTTCGGGTTCCGACGGCATCTGCTGTCATGGTTCCGAGGTCGGCGGAATCCCGCGCGGCAATGTCGAAACAAATAATGCCGCTCGAAACAGGATGGAACGGGTTTCGCCA
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SEQ ID 2178

MPPFGFGRHLSANFGRAESRPANVENNKRLKTSGTGFAKRLSDGIPS

SEQ ID 2179

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SEQ ID 2180

MNPATADIAQCTEQNLNQYFKDLNGTEPCGVYDMVLHQVEKPLLVCVMEQCGNQSKASVMLGLNRNTLRKLLIQHGLL

SEQ ID 2181

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SEQ ID 2182

VNMSATVRIIGIDPGRVTFGFIIDVRGRDFYVAGCIKTPADEPLADRIAVIRHIGEVVAIVYKPPQAAVEQVFNVPASTLALGARGAALALVSHKLFVSEYALQVKQAVVGGK
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SEQ ID 2183

TTGAGTGAAAATTAACGAGCAAAATTCGCCCTCAAGTCGGTTTACCGGTTAGAAATAGTGTTTATGTAACCCGAAATGCCCGGATCTGTTATGCAACGGCAAAACCGAAC

SEQ ID 2184

LSENKRAIAPQVGLFVRIVFIVTRNARILLNGKPN

SEQ ID 2185

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AAAGA

SEQ ID 2186

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GNIRPMRRGEAKTPRCRFRFDGIDGIDHDFRQCGHINRLAPGKDCRNKGRDVPFPHRYHNQVLEKTWCSARKIKFRHQKQAKTHSTSLAARFTIRPSLSQRPFMDTAKKDIILGSGMMLV
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SEQ ID 2187

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SEQ ID 2188

LVSQGGKKAQTVVRWELVGPVGFPTTKGL

SEQ ID 2189

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SEQ ID 2190

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SEQ ID 2191

TTGAAACCCGGGTTGTACAAACAGGATTTCGCGGACGGTTTAAACGGTTTCAGTTGTTTGTAAAAACAATGCTTTTAAAAATTGACAAAAACGAAATCGGTTTAAAGGCTTATTCGAG
AACAAAGGGGAGTGGATGCCGAAAACCGGTTAATATATTA

SEQ ID 2192

LKPGLYKQDLPDFNGSVVCKNNAFLKLTKEIGFKGLFREQRGVDAENPVNLL

SEQ ID 2193

TTGTTAATCCACTAATATATTAACCGGGTTTCGGCATCCACTCCCTTTGTTCTCGGAATAAGCCTTTAAACCGGATTTCGTTTTCGTAATTTTAAAAAGCATTTGTTTTCACAA
CAACTGAACCGTTAAACCGTCCGCAATCTGTTTGTACAACCCGGGTTTCAAAATTCGCAAAACAAATCGGGGTTTGTATCTGAACCGCTGATTGTTTTCGTAATTTTATGTAGTCA
G

SEQ ID 2194

LLIHYNILTGFSASTPLCSRNLKPIISFFVNFKALFLQTEFLKPSGKSLYNPGFKPKTIGVFDLKRILCFVILCSQ

SEQ ID 2195

GTGAAAAAGGCGTACATTCGCTACACAGAAATACAGATACAGCGGAGCAATCCCGCTGAAAGGATTTCGCGTCAGTCTTGGGTTGGTTCGGGTTTCATCGGATACGGTGAAACGAA
AGTTTCCCGCGCAGGGTTGAGCTACGCGGTAAGCCGCGAGGCGAAAGCCGTGATTGTTTG

SEQ ID 2196

VKKGVHSATQNYRYSAMPSEIRFSVLRLVGVSSDVTVRKFPAGAGLSYAGKAAGESLYCL

SEQ ID 2197

ATGCAAGGTACTGCCATGAATACGATTTCGGCTTCGATATTGAAACCGTACCGGATGTGCAAGGTATCCGTCAGTTGATGACTTGGCGTCTTCCCTGCCGATGACGAAGTGGTCTGT
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SEQ ID 2198

MQGTAMNFTLAFDITVPDVQGIPTLYLDLPSLLPDEVVFLAQQKRAQTGGDFMQHLLHQVAVSSCMRWGQDKVHVGTIGEMDDGEEVVIKFPFELVEKHTPQLVSWNGGDFLVLHY
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EIKRIRNYLSAQTEDKPHWAEFVQANK

SEQ ID 2199

TTGGACAAATTCGCCAATCGGTTTGTCTCTGTTTGGCGGAGAGATAGTTTCTGATCCGCTTGATTTCATTTTCGTTATTCGTCGCGCTCGAATCTGCCGCTGACACAGAGAAAGCG
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SEQ ID 2200

LDKFCPMRFVFLGGETVSDPLDPHFVVRVESAADQETQTHQIRIRINGIGFAIIADFLQPARVEKLPHLAAVHTQLARKAAQPRHIVQRHIRPRLVKREQIHQIAVALVITADVVPVLEI
AAVAETAVARIPIARGVDVAVYQGAVMQYQGVETAAPADQLRRMFNQFEKLGNDHFFATVHLADGADNMLVLPAAHTAGNRHNLMEVVLHKIAAGLCAAFLLRBOHHFVIRQGRRQVIQR
TDTLHIGYGFNIESQNRHIGSTLHSTDLRLCH

SEQ ID 2201

TTGTCCAAGCGTGGAAAATAGAAACCTGCTGTCGGAAGGCGGTACGCTTGTGCCGCGGTTTCGGTTTCAGACGGCGTATGGTGGATTAAATTCAAACCGGTACAGGCTTGCGCTCTCCTGGC
TTACTATCTGTACTGTCTGGGCTTCGTCGCCCTGTGTC

SEQ ID 2202

LSKRGNRNLLSEGGTLVPPFRFQTAYGGLNSNRYSLASPCLTICTVCGFVALS

SEQ ID 2203

ATGCAACCGGCAAAACCGAACTGAAAAATTGGCTTCAGACCGTTTATCCCGAACGGGACTTCGATCTGTCTTCGCGCGGGGGGATGCTGATTTCGCGCGCTATTTCGCTGCGCGGTTTTCAG
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SEQ ID 2204

MQRQTELKNWLTQVYPERDFDLSFAAADADFRYFRAAFSDGGSVVCMDAPPKMSVAPYLKVQKLFDMVNVPOVLHADTLGLFVVLNDLGNHTFLTAMLEQEQGEAAHKALLLEAIGELVG
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SEQ ID 2205

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TATATCTCGATTAGCAATCCGCGCGGAAAAATTT

SEQ ID 2206

MKKVSVLIVAKNEANHIRECIESCRFDKEVIVIDDHSDANTASTAEGLAKAVFRRLHNGDFGAQKTFATIEQAGGEWVFLIDADERCTPELSDEISKIVRTGDUYAYFVERENLFFNHPATH
 GAMRPDSVCRMLMPKKGSGVQKGHEVTQTFYPERRLKHFMHYHTYDNEQYFNKFMKYTSISAEKYREQGGKPVSFVRDILLRPIWGFFKIYILNKGFLDGKMGWIMSVNHSYTYTHIKYVKL
 YYLYKSGGKF

SEQ ID 2207

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SEQ ID 2208

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SYEEMNFTYTHYVYKGAEEVVRMYHTLLGEBGFQKGMKLYPQRHGDQAVTCDDFRAAMADANGINLDQFALWYSQAGTPVLEAEGRLKNNVFELTIKQTPVPTPMADKQPMIIPVKVGLL
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SEQ ID 2209

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CCTGTTGAGGGTGTGCTGCGCGCGCT

SEQ ID 2210

LFHQVFAVRLLELVAEVERLHQAGDLRVEAVDFDDFVGDEAVAAVLCVKMRDVAAEAADERTGFVGVFETFRMLQGGNLNLQGVAAAA

SEQ ID 2211

ATGAAGATACACACTGCAAAATTAAGAAAGAAAGTACAAAAAGAACCGCTCCGTTCTTTGTACCGGAAGTACCGCCCGTCTGCCGCCGATATTTGGGTATCCATCCCGATTGCGCG
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SEQ ID 2212

MKITHCKLKKVQKEPLRSFVPEVTARSAADILGHPDAAALFYRKIRTVNHLALAADEVFEGPAGPASCFGRRRKRGRGAVGKAVVFGIPKRNGRAYTVAEDNAEPETLLPAVKK
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SEQ ID 2213

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SEQ ID 2214

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SEQ ID 2215

TTGGGTGAATTTTGAATTTGAAGAAACGGTACAAAGATTACTCGGAAATCGGAGTGCATGCGATTTTTGGCGCGCGCTTGTCCGATTCAATAAATGGAAGTATTATCGGGTA
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SEQ ID 2216

IGEYLEPEENGTKITARIGSAMHFLGAACRISINGKYVAGHRIVWFKAERS

SEQ ID 2217

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SEQ ID 2218

MHFLYSLFNQIINISVGMALAAHAFCKFIIG

SEQ ID 2219

TTGGAAGAGATAATAAATCTAAGGTAAAGGAGACTAATTTAATCAGGATGGCGTGTATACCGCCATGCAATAAATAATATATCTGATGAACAGGTTATGATTGTCAAATGTCTT
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SEQ ID 2220

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SEQ ID 2221

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AATACCGTTGAATCGGCAGCGCGTGGCATTTAATGAAATATAAGAAATATTAATACACATTTAAGAGGTACGAACTTCCAGGTTCTAAGTGGAGGTTCAAGATAAGGGCATTTT
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SEQ ID 2222

MQLICADWTGIGNFMKTPEKTWSAQYRIMEISVRNFWNLKRTGAEVYINGRRVYHNEAGMASASLSLNGEYLEFESGTRITVEIGSAMHFNFTIRNINHLRGTLPKSNWVRVQKGF
HLNER

SEQ ID 2223

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SEQ ID 2224

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SEQ ID 2225

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TA

SEQ ID 2226

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SEQ ID 2242

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SEQ ID 2243

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GGCGGTATCGGTA

SEQ ID 2244

LPTSLSKLQIMTFSLLSGLTFRFLALIAVLINGVILMAVS

SEQ ID 2245

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TGTGCGCTCA

SEQ ID 2246

LGIGMSIIVENLTVSRRPVAHVHDITFEHSMWAVFGPNAGKSTFLKSLMGLQPIDTGSIRLDGLTRQNIAYLPQSDIDRSQPMPTVFLAAMGLWYIEGPFKINTAQKQVHEAL
ERVGMQRFARRQIAHLSNGQFQRLVFAMLVQNAKFLLLDEPFNAVDARTTYELLDVLQKCHCGHAI IAVLHDVEQVRAYFPNTLLAREKIAAGATETLLTBSYLAQASAKMQQESPD
WCAS

SEQ ID 2247

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SEQ ID 2248

MNLIQLEQEEIARLNKEIPEFAPGDTVVVSVRVVGTSRLQAYEGVVIARRNRGLNSNFIVRKISSEGEVERTFQLYSPTVEKIEVKRRGDVRRAKLYLIRGLTGKAARIKEKLPARKG

SEQ ID 2249

ATCGCGTCTGAAACCAAGTTTCAGACGGCATTTCCTAAACGGGCTACTGCGCGCTTTTGTCTTCACGTACTTTGTCCGCCAAAAGTCTGATGCTGTCATACCGGACTCCAGTGG
GCAAAATTCGACTTTATATTTGCGCGCGAGATAACCGTGGCGTACCGTCTGATTTGGAAGGTTCGGTCAGCTCCTGCAATTTGCGCGCGCGCGCTGACTTTTCGGGGGATTCGATAGCGG
CAAGGACTTTTTCGCGCTCAAAGGCGGTGTGTTGCGCCAGCCATTTCCTGAGGACTTCGGGCTCTGACGCTGATTTTGTGTTGACCATCGCATCGAAATATGCTGTTGCCACATC
TTTGCTTTGCGCGCGACCATATCGAGCGCGCGCGGAGCGTCCAGCGCGCAGCTTTCTTCTGCCAGACGAGTGTTCGGTACGCAAGTACATATGCTTTTAAAGACTTGGCGGT
TTGCTCAAAACAGGTTTCAGGCGCGCGCAGTGCAGCAAAATAGCCGAAAACTCAAGCACTTCAACCTTGCTGCTGCTGTTGGGGGAATCGGCTTGGCAAGGACGCTGTAGTTTGGC
CTTGACAGCTCTGCCGGGCGCGGCTGCCGAAGCGGCGAGCGCGCTGTCGGCGGGGACGCTGGTTTGGACTTTGCTGTGCGACCGCGCAAGGCGCAACAGGCGCGCAACCGCGAGGCG
GAGGCGGAGGTGTCGATTTTCATACGCTCTCCGTGATGTTGGAATAAATCGGATATTGATTTTATTTGCTGTTTTCGCGGTGTGATACAGTTTTCGCGCGGAAAAAGGACGTTTTCGTT
TCGGGAAACCGCTTCAGACGGCATCAAACCGGATGCCATCGAGCGGTTCCTGCTGTACATAACCGCGCGCGCCGACGGATACGCTGTGTTGGGAACAA

SEQ ID 2250

HPSENOVSDGIPQTGLRGLFTTYFVRQKVDGVHTGLPVGKDFIPADNRGRTVDELFGFQLHFGARLTFGGFVGGKDFFAVKGGLFAQPFDFRLLQLDLVDHRIENMAVRHI
FAGGSHIDGGGACQCHFFLPDDVFGTVHIVFKRLGFAQNRFEAGAVRTKIAEKLKHFNLACLLGNRVKGDGVVLPFDQSCRGGGCRSGRRVAGGDAGLDAVARGKGEQGNABG
EGEVSGFHTALRDVGNKSDIGLILLYFRVLIQFAAEKGRFRPGKPLQTASNMPSEAVSVVQYAPPRTDVAGEQ

SEQ ID 2251

ATGCAATATAAGCCGCTTTCAGACGGCTATGCGCTCTGAAAGCCTTTGATGCAACAAACCGCCAAATATATTCGTTCAATGGAAAAACACCCCGAATTCATCTTCAAA

SEQ ID 2252

MOYKPLSDGLCRLKAPDATNRQIIFVHKRTPRIHPKX

SEQ ID 2253

ATGCAAGGAATGATAATGGTCAAAACATCTGCCACTCGCCGCTCTGACTGCTTTGCTGCTTGCAGCGTGGCGGTTTCGGACAAACCGCTGCCGAAAAACCGGACCGCGGAAAAACCAA
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CCGGCGGCAATTGAAGTTTATGCTGCCAGTGGCAGGATGTAAGGCGGGGAAA

SEQ ID 2254

HQGMIMVHLPLAVLTALLAACGSDKPPAEKPAEENQNLKIYNWSEYVDPETVADFEKKNGIKVTVYDYSDEYLESKVLTKSGYDIVAPSNFVGRQIKAGAYQKIDKSMIPNYK
HLNPEMRLMDGVDDEHYAVFPYWGNTNFAINTERVKKALGTDLKLPDQWDLVFNPEYTFKLKQCGISYLSAAEYIPVNLNLYGKNPNSSNTEDIREATALLKKNRPNIKRFTSSGID
DLARGDCTVTIGFGDLNLAKRRAEBAGGKEKIRVMMKPEGVGIWDSFVIPKADKNVANAKHYINDFLDPEVSAKNENFVYAPSSKPARDLMEDEPKNDNTLFPSEGLDKNSFMVPIR
PAALKFMVRQNDVKAGK

SEQ ID 2255

ATGCTTATCCAGGAGTACCAATTTTCCCGAAATGTTTCGACAGCATTACCGCTACCGGTAACGGGACGCGCAACAGACAGGGAATCTGGCAGTTTGAAGCAGTCAATCCCGAAAGT
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CGCAAAAGTCATCTACCTCAGCCCCAAGGAAACCGCTGACACACCAAAAGCGGCAGAACTGGCAGAACTTACGCATCTGATTCTGCTGTGCGGACGCTATGAGGGAATAGACGAAAGA
CTGCTGCAAAAGCAGCGTCGATGAAGAAATCAGCATCGGAGACTTCGCTGTTCCCGCGGAGAGCTTCCCGCATGATGCTGATGCGGATTCGAGGCTCGTACCCGCGATATTTGGGCG
ACATTGAGTCTGCGCGAAGCAGGATTCGTTCTCAAGCGGTATTTTGGACTGCCCCACTTACACCAAAACCCCTAGAAATTTCAAGGCATGGCTGTTCGCGAAGTATTTGGCGCTCCGGAATCATGG
CTTGATAGCGGAATGGCGGTGGAACAATCGCTGCGCGCACCTTGGAGCGCAGACCCGATCTTTTGGAAAAGCGGTTTAAATCCCAAGGAATCCCGCTCTTGAATAAAATCTACAA
GAGCAACGGGAATCAATCA

SEQ ID 2256

MLIQAVTIFPEFDSITRYGVTRGRNRQIWFQVAVNPRKPADNRLGYIDRRPFGGPGMIMAPPLHAAIKHAKAQSSQTAQVITLSPQKPLTHQKAAELAEHLILLCGRYEGIDER
LLQSSVDERISIGDFVVSGGELPAMMLMDAVLRVLPFGILGDIQSAEQDSFSSGILDCPHYTKPLEFQMAVPEVLASGHGLIAEWRLBQSLRRTLERRPDLEKRVLIIPKESRLINKLIQ
BQREIQS

SEQ ID 2257

ATGACAGACACTCAAAACCGGCTAGCCATGGCTACATCAAAAGCGGTATTCGGCATAAAAGGCTGGCTGAAAATTCGCGCCAAACACCGAATATTCGACAGCCTTTTGGACTACCCGAGT
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CGGTTACACCATCGAAATACCCCGTGAAGCATTCGCCCGCAGAGAAGACGAATACTACTGGGAGACTTTGGTCGGCATGACCGCTCGTCAACAAAGACGATACCGTTTATAGGCAAGGTA
AGCAACCTGATGGAACCGGCGCAAAACGACGATTTGATGATTGACGGAGAACAACGGGAGATTTCTGATTCGCTTCGTTTCCCAATATATCGAAACCGTCGATACCGGACGAGACCAATTA
CTGCGGACTGGGTTTGGACTAC

SEQ ID 2258

MTDQNRVAMGYIKGVFIGKWLKLAANTEYSDSLDDYPEWHLAKDGKTVSVTLKAGKVVNGELQVKFEGIDRRDSAPSLRGYTIIPREAFAPTEDEYTWADLVGHTVVNKDDTVLGRV
SNLMEGTANDVIMDGEHQIILIPFVSQYLETVDVTSKTTTADWGLDY

SEQ ID 2259

ATGGTAGTTATCCGTTTGGCAGCGCGCGCTCGAAACACCGCCCTTCTACAACGTCATCGTTACTGACTCAGCAGCGCGCGCGAGCGCGCTTCATCGAACCGGTAGGCTTCTACAAC
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C

SEQ ID 2260

MVVIRLARGGSKHRPFYINVIVDSRSDRGRIERVGFYFVANEKQERVLNADRLNHLIAQGAQVSDSVAKLIKEQKAV

SEQ ID 2261

ATGATGGAATCATCATCAAAACCGCCGACAGCAAGGCTACCTGAGCATGAGTGGCGACATTTCTCAAAACCAATACCCCATGATCAAACTTGTGAAAAATCAGGATTTACCTCAAGG
AATCGGACACCGGAAAAACCTGTACCGCGCATATCTGAACCTTGGCGCAGACAAAACAACAGGAAAAACAATAAAACTTGGCGACCGCGCCACAAAATAACC

SEQ ID 2262

NMELIQTAAQGYLSMSADIILKTNTPMIKLAESGFTLKESDTEKNLYRAYLNLAADKTTGKTNKNLETGHEKIT

SEQ ID 2263

TTGGATGATGAGTTCATCATTTTCTGTGCGAGCCGCTGCGCGCATATGTTCCGCCAGTGATGCCAAATTCGCATTCGTTGCGGTTACGGCGCTGTGGGGAGCAGCGCGACGATG
TTGCTGTGCGCATCCCTTGGCGTCCATGCGGTTTACAGTGG

SEQ ID 2264

LDDEFHFLCQPAAAHMFRCDAKFAFVAVQAAVADGDDVAVGIPCRPGSGJH

SEQ ID 2265

TTGCAGCGGCAAAATCCCGCCCTGCTGCGCGAAGCCCTGCACCTCCCCCTACCGGCACACCAACCCATAACCGCGTCCAATTCGAATTCGGCAGCCACCCCTCTATGGCGACATCCTGACCG
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AACACAGGCAAGCGCCGCAAAACCTCGAACATGCGCCGCAAAATGCAGAGTGGCGCGCATACCTCGGAACACAAAACCGGACCGCGCAATTTCTCGCCACACAGCGAAGCGG
CGCGAGAACTGCTCGGCGCAAAACCGAAGCGGAGCGGTAACCAACGTAAGTACTTGTCCCTTATCCCGAGCACACCCCAAAACACTGTCCCTTAAAAACAACACGACCGTTACCATTA
CCCCCTTTTACCGAAGACGCAAGCGCAAAACAGCATTTCTGCGCAGCTCGCGCCGCAAGCAGCGGTACACAGCTTCATGACCCACACCAAGCACTGCCCGCAGCCAGCTTGGCAGCG
CTGTCAACCCCGATACCACTGTGAACCGCATGAGCGGCAAGGATGCGCAGCAACATCTGTCGCGCTGCTCGCGCACAGCGCC

SEQ ID 2266

LQRQIPCSFKPCTSPYRHTHNAVQFPQGSHPLYGDIILFARNGQTAVLPPPTLDSRLHARFAELDGTQFLDQFLHTLTVIPEYRQIHFGITLNLNGQYSSDFILKTPGHTDPKRE
NTGKAQTLLEHAAKMQSAAAYLEHKNPTAAEFLRHTSEAAABLLGSKTETGAAVFNVLAPYPAHPEKTLISKNNITVTIIIPLLPEDAEAKQFVRSIGPEARYTRFMTHNLPAATLAR
LCNPVYHCRPHRGQMPATSSPSSATAA

SEQ ID 2267

TTGCAGCGCTTCCCGGCTGTGCGCGCGCGTCAAGTGCCTTGTACAATGCATACCTTCACATTTCTTAATAAATTTTATGAGTAACATACCTTCTTGTCGTCCAAAATCGGTTTCG
TACTTGTGCGCGCAGTTCGGCATCGGTTTGGGCGCGATTGGAATTTCTTATACCGCGCGCACCAACCGCGCGCGGTGTTTTCCTGCTGTTTGTGATPTTACCGTCTTGTGTCG
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GCTGCTTATTTTGTGCTGCTTTTACAGCGTGTGCGCGGATGGTATTGAATATGCTTCCACAGTTTACAGGAGCAATCCATGCGGGAGCGGACTTTGAAGCCCTGTTGCGCACAA
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TCTTGTGTTCCCTGCTTGC CGCGCTGCTGATTTTCCCGCGGTATTCGCTTCGTTTGAACCGAAGCAGGCGCGGATTTGATTTTATCGTATTTCCCGCAGTGTTCATGAAAATGCC
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AGTGCTGCTGCTGCTGCTGAATACCTTGCCTTACCTTGCCTCGATTCGCTTATTTATGTTTTCGTCATTTCTTAGGCACTCTT

SEQ ID 2268

LQRLRLVPPRQVLCYNALPSHFLINFMNSHTSWSSKIGFVLAAGSAIGLAINKFPYTTAGTNGGAVFFLLFLIPTVLVLPVQLAEFYIGRTGKNAVDSFVRLRPGTQHLVHVRGVA
ACFILLSFYSVGGVNLVNVVHSPFGAIIHAGADFEALFGTTISNPAGSLSQALPMLITVWVVGKGISDGIKANRYLMPGLFILFIALAVRSLTLPDAMEGVSLFKPNHSGYFKADTHTT
ALGOAFPALSGVAMITYASVGLKQDMFRSGHTIMMNLVSLLAGLVIPAVFAFGFEPNQGGLIFTVLPAVPMKHPFGTFLPAVPMHLLVVPATLSPASHLETVIASITRQDERKR
KKHTWLIGTAIPVIGPSALSFGANGFKVFGRTIFDLWDYVISAVIMPVIGALSVSIPITAWIQDKSVLKDAGAGSTVPRVLLMLNLRLYLAIPALIIIVFVNSLGLL

SEQ ID 2269

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TGCTCGAAGCGCGGTAGGTAACGAAATGCGCGTTTTCGCGCACACTCCCGATCGAGGAAGTCTGTATGATTTTGTGCGCGTTGGCGAGCTTTTGGCATTTCCGGAATCAGGAAGA

ATCCACCCAAATCCCCAGCCCTCTTCGGCATCATCAGCGGATTTTTTCCTTGCGGCCGCTCTCTCGGCACGGCGTTGGCGATGTTCAAATCTCCGCGAAACCGATTGTTACGCAG
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ACCATTTACATTCTTGCATATCGGTTGGAGAAAGCGGCCATTATAGCCGATTTGGTATGGTAACAGGCTTCAGACGGCATTCAAAATCCCGCAATGCCGCTCTGAAGCCGCGCTTCATAG
C

SEQ ID 2270

SEQ ID 2270
LPSNSGCKPSSAKDKKCRPNILQTVAYRALFPRHLHILPLAHHKLQCRPRDRHDKAVQIFPARENIRIVVFKFVLHQIARRLARRRVGNELAVFRBHRFIEKEVVDFVRVGDVFRIFRNMHER
IHPNCPALPRHHADFPFLAARFPOTAFGVDILISAEOTCYAGIAARQIIDKAGRSKAFDIGAVBLEGGCCLPDVFRILAAVRVPAQIVQHGINFRRAVQIADAALPEFERVFGVEHQIFLVLV
IQLVRTQSLFHAFGIDGEGICPPIKRHGVFVVGIDPVHQPHFRVEMFIIGNHRLIDFLIRTCIALPAHKRIGRRDNNVTVGFSQHLAFQRFITVYHISNLDAVFLFKIGNGFRIDVFRP
VINQYVVLVFRRCRFPGRFRVRTAARCKQSSQDGENQMFDEHYHSLHIGLEKAAIADIGNRASDGIONPAMPSESRRFES

SEQ ID 2271

SEQ ID 2271

TTGCACAAACAGGTATCCCAAAACAAACACACAGCGGGTGCACTCTCCAAAATACGACACATACCGTTCGCGAAAGGAATATATCATGCCGGGCACAAACCGATCCGGGCTACTTCTTCATGC
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CACCATAGCGCGGGCTTCCGCGCTACACCAAGCTCAACAAAATCCCCGGCAGTCAGCACTGATTAATACCGTTACCCCGCCCGCAGGTATACGACACCCCTCTCAAAACCTGCCGTAAAGA
CAGCTCCGACACATCATCTCTCATACGAGACTGGGACAGCTGTCTGCCGCGAAGCTGCACACCGCGGAACCTGCACATCCGCAAAACACCACGGCAACGGACTCAACATCACCGCTTGCACCA
CCGAGGCAATCCAATGCCCCCTCACTCGGACTCAACATCAGTACCCAAAGACGGATATGCCGCGAGGCCATACCCGCCATCTGACCCGGCAATGCCCGCCGTACGCCGCCAAATCGACAACATCT
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CACCACACCCCTGAAGAGGACTCCGCGAGGCTGTGTACATCCCGCAATTTCCCGGCATACGCGCGCTGATTTCCACATCACTCTGCCACGACAGAAACCGACCGCTGCCGTACTGC
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CACCAACCA

SEQ ID 2272

LHKQLPQNKHTAGASPKITHIPSAKEYIMPAQTPDGPYFMPNMHILIGASEQPYSLGERVLSNLLSTPFQGIKTPVMPRHHTIAGLPAYTSLNKGPSADLIITVTPPDSDYDTLLKFCRKK
QLRHIIILIQDWDSLSAAELHFAETAIRKHHGNGWINTACTTAGIQLPSLGLNISTQDGYAAGHTAILTGNAAVSRQIDNILNKLQRQTSRHSILHGPISITSDWLNRPFGSHLTKTAVI
HHNPEEDQRRILFSAIRQFTRHTPLILHITCLTETTRAVLHCLARHCNPLISFNADDLEAALSQAQLSDLPLPSRLDLITDTPAEWLHAHAPKNLPLHGFPHILPHIRHGLHTGTPFSI
IASRQLARPDTQAVLITLPGSGHEDYKKTARALIRLSEGTAKPLLVSSPSDGIHTFDTPAQAIRTLSTYRNTAAALKQAQLDIAPPQPCRLKTPQPQNIKKALAAANPALLAEALHLEPLPA
HHP

SEQ ID 2273

SEQ ID 2273

ATGGAACGTGTTCCAACGCAATTTTCGCCACATTTTCGCCGTTATCGTCTGCGCAATCTTTGTGGCGAATTTTCTTTTGGCTGGTGCAGAACACCCCTTGCCGAAAACCAATTCAACCAAC
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TCTTCATAGCGCTTTTCTACCGTCGACATCCGATCCGACAAACCCGGAACAGGACTGGGGCTTGGATTTGACCCAACATATTATTGAACAGCACTGCGGCAAAATCATGCGCGAAAAATCAAA
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SEQ ID 2274

SEQ ID 2274

SEQ. ID 2275

ATGAGCCGCGTATTACTCGTAGATGACGATGCCCTGCTGACCGGAACCTGCTGACCGAATACCTGAGCGCGCGAAGGTCTGAACGTCGCGCAGCGTTCGCCGACGGGGAAGCAGGCGTACAGGAAA
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 TGTCTGAAGTCTCTGATGCGGCATGCGCGGACAGTATCGTCAGCAAAAGAAACCTGTCCCTGCGCAGACCATCGACGCGGATATCGACGCTACACATCTCCAGCAT
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SEQ ID 2276

SEQ ID 2276

MSRVLLVDDALLTELLTEYLAEGLNVRSPVDFCEAGVQEILSGQYDVVVLLDSMPKMKGLDVLKNVRASVPIIMLFAKGDDIDRIIGLEMGADDYVPKPCPTPRELLARINAILRRAGE
SCQONNAENSTSVSDVILYPAKROASVKIMPLELSTEPNLELLEVMRRHGAOVVSKETLSVEALDRKLAKFDRSDIVHISSTIRHKLGDASLIQTQVRLGYLFVK

SEQ ID 2277

SEQ ID 2277
ATGCAAGACATTGCAAAAAACAGCAAAACGGTAGGGAAATACGCTATCAAAAAACATTGCAGCCGTGTTAAGATAAACTGTCAAAACAATCTTTTCACGCCACGCCCGAAACAGGGTCGGG
CATACCCCTTACGAAAAAGGAACACCA

SEQ ID 2278

MODIAKNSKPVGKYA I K K H C S R V K I N C Q T I F S R H A R N R V G A Y P Y E K E T P

SEQ ID 2280

SEQ ID 2281

SEQ ID 2282

SEQ ID 2283

SEQ ID 2284

SEQ ID 2285

SEQ ID 2286

SEQ ID 2287

GTGTCGGAACACAAAACGAAACAAACCGTCCAACCGCTGTGCGAACACCTCATCGAGCTACGCGCGCGCTGATGTGGATGGTGTGTCGGCATTCTCGTCTGCTTTTTCGGCATGATGCGGT
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CGCGCGCTTTGTGCTGTGCGCATCATCGCGCGCGGACATATTATTTCTCAGACCTGCTTGCATTCCGCTGAFTCTTTATACGAGGCGGCGCATTTGGTTTCGGAACGCTTCTTCATCCA
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SEQ ID 2288

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PFIHAFAYFLVFPVIFKFLAGVTPVGVNMTDIDKXLSFLGMFVAFGTAPEVPIVVILLTKIGAVTTBQLKHARPVYIVGAFVVAIVTPPDIIISQTLIAIPLILLYEAGINWGRFPFP
RSEQDGDIOPPAKT

SEQ ID 2289

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SEQ ID 2290

MFDFGLGELIFVGLIALIVLGPRLPEAARTAGRLIGRLQRFVGSVKQELDTQIELELRKVKQAFEAQAQVRDSLKETDTDMQNSLHDSIDGLKPKWKLEPQRTPADFGVDENGNIPLD
TANTVSDGIDSVMPSERSDTSAETLGDRTGTSTAEPAETDKDRAWEYLTASAAAQVQAVEVSYIDTAVETPPVHTTSLRQALNRRKDRPRKRAKPKLRKRS

SEQ ID 2291

ATGGGCACTTTTCTCTGACGCACTGGATTATCTGACTGATTATCTGCTGTTTGTATTTGCGCACAAAAAATTGCGCAACGTCGGCAAGACCTCGCGGTGCGGTTTCATGACTTCAAC
AGGGGCTGAACGAAGCACAGCGCAAGAACCCAAAAAGCAGATGTAACTGAACACAAAAAGACGAAGACAAAGCA

SEQ ID 2292

MGSFSLTHNIIIVLIVLIFGKILRNVDLGGAVHDFKQLNEGTDGKEAQKDDVIEHKKDEKA

SEQ ID 2293

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SEQ ID 2294

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SEQ ID 2295

GTGCTTTTTCAGACGGCAACGGAGCCGTTATGGACAACGTATTTTCTGCAAAATCGCCGCCAAGAGATTCCGGCGCAACCGCTCTATGAAGACGGGAAATGGTTTGTTCAAAGACA
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CGCAAAAGCTTCGGACTGACCGACGGTTTCAAAACCTTATCAATACCGGCAAGGCGCGGACAGAGGCTTCCACCTGCATATACACATCATGGGACACCCGTA

SEQ ID 2296

VLFSDGNAGVNDNCIFCKIAAKEIPAQTVYEDGEMVCFKDLNPAAPLHLLIIPKVHFDLSLAHAPEHQFLILKMLKVPETAKASGLTDGFKTLINTGKGGQEVFHLHIHIMGTFV

SEQ ID 2297

TTGCCCGAGAGCAGCCGTTTACCTTATCTCCGAACAAACAGAAACAGAAAGAAATCATGGGAGATTCCGCTACTATCCGCCATCCAAACCAACATTATACAGCGCAAACTGCGG
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GGTTACGAAGTTCGCGACTTATGTTCCACACCATGATCTTCTGACACACCAAGCTGAAAGCGGAAGACGTATTTGAGCAAACTTTCCGCCCTCAGGGGCTGTGCGGGCTGCGCGAA
AAAGCGCGCGTACAGAATCC

SEQ ID 2298

LPSSRLAYHSEQTETNRRKIMGDSVLSAQQTIIQRKSADPSESYVAQLLHKGEKILKXVIEEAGEVLMASDKDKPSHLVYEADLWFTMILLTHHDLKAEDVLDLSRRQGLSLAE
KAARTES

SEQ ID 2299

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SEQ ID 2300

LLIHYIVRHGQPNFKPPAFGNRPYQRIHGHKRRRQIGNRRIIRHYAHAFITRRTHAGSRIBQMGKPARFVHRPIAARSCKRLVFRDICIQHAFVVRIDADADIPHPAVCIKPPDFAH
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SEQ ID 2301

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CAACGCCGTGATCTTTTAGCGGCAGTAACGAGGGTAAAGTCTCCCTGTGCGCGCGGTATCCAAAGCCCTGACCGGAAAGTCAAAGCAGGAGATCTGGTTAAATTTGACCGCGCAACAA
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SEQ ID 2302

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DISHPQAVTAEEIAEVERRVNEAILANVAVNAADMSMEDAQKTAMMLFGKGYGDEVRLVQMGGFSTELCGGTHVSRGTGDLGFKIIIEGGIAAGVRRIBAITGLNALKWAQBERLWKDI
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SEQ ID 2303

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GTTGCATCCCAATAATCAGTGAAGAGGATTTTACGGCGTTAAACAGCGCTGCCAAGGCATTCAACTGTAC

SEQ ID 2304

MMFYRSGQQPMFPHAGRLRLTKSGGIFIGRLFFATALHKAVFCVRTAIIACHRGRLMPLKQPPRERSVIMCDFRGYEPFEMVKRPFVVVIARNRHNGKLVTVVPLSSTEPVFLADCH
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SEQ ID 2305

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ACCGCTTACCTGAAGCATTTGGATGAAAAACGGCAGCGCAGCTATGCGCGGAGCGCGGCAATGAAACAGCGCGTTACCAATATTTCTCGTGTTCGCGGCAACCGCTTATGCGCGCA
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SEQ ID 2306

MKYVRLPFLGTAAGTAAAAEMVQIEGGSYRPLYLKIDTGLIKVKPFLDKYPVTNAEFAEFVNSHPQWKGRIGSKQAEPAYLKHHMKNRSRYAPKAGELKQPVNTNISWFAANAYCAA
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NLGPRCASR

SEQ ID 2307

TTGTGCTTAATCTGCCCTTTTGTGTTTCAGGATTAAGTCGATACAATCATCACCAATACTATGTTTGTGTTTCTTCTTCGAGAGGTTTATCTCTTGCAAGAATAAAAAATC
AAAACAACTCATGCTTTGTTGT

SEQ ID 2308

LCLNPAFCVSGLSRYNHPNMFVFFSLARGFYPLQRIKQNKLIIVFC

SEQ ID 2309

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AAGCC

SEQ ID 2310

LRFVGKRLSVSDGICAVANVICLQVMIHNNFNGFVVVDQTEAFGNQFVQLDALGDEGEVDFDAFFDQDFGRVVVAVGNRAHIQFPHDVAVDVGGGVAPDGYDNQVGGGFAGFDQS
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SEQ ID 2311

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SEQ ID 2313

SEQ ID 2314

SEQ ID 2315

SEQ ID 2316

SEQ ID 2317

SEQ ID 2318

SEQ ID 2319

SEQ ID 2320

SEQ ID 2321

SEQ ID 2322

SEQ ID 2323

SEC ID 3324

SEO ID 2325

SEQ ID 2325
TTGTGCAAAATGCGCTTATATTTTGGATTGTTAGAATGAATACTTAAACAGAGTTTACAAAAACTTTTAGAAGAGGATATATCAACTTTAAAAGAAACACTTAATCTGTAGATGCTCTTCCTC
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GTACCGGTT

SEQ ID 2326

LPKMLIPWIVRMATKTELQKLLEEDISTLKETLIRVDALPFRYVRSIATPIVRRLIDKQLANILAKEIGLTIELPILDTSLVPEKLSLENKVNPFYSRLTKIRTRRAADSTNSTARRGHA
VPV

SEQ ID 2327

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SEQ ID 2328

LMKLYADYFAARPDATPPENSVKETLKRVPFGKVSFDDREIRPAEKGMGLSLNGIAQGYITDKVALLKANGVPAALVIMGEIRGFDITNGRMNVGIRNPDDEGVLANITTKDKAFAT
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SEQ ID 2329

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SEQ ID 2330

LEPHFGGVGIXLPQKRQNPSPKPKTERQHPYALRVGTWSSRLLEFKTKRIRAFPMRLVGTNQSTFAAIALRSTSTSLFVPCPISTVKNCPTLVTLPLKPAKTTLSAPAKAASIA

SEQ ID 2331

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SEQ ID 2332

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GKRMAMVLIDQKSEVVTAIVRTAITGGRVEISGSMITABANDTSLLRAGSLAAMQIVERTIGPSLGKENIEKGFHSTLWGAIVAAFMVYVYRLMGFFSTIALSANILFLIGILSA
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VWKPEATAAGKE

SEQ ID 2333

ATGGAACCTCTTAAAAATCAAAACCGGATATTCGCTTATGAGCTACCGCAAACTGACAACCTTCATTTGTTGGTTACCTTTATTCGCCCGCTATCTTTTGTGTTGCCAGAGGCTGAAAT
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TATCTGCCATTATCGCAATATGACGACATCGTGAATTTCTCGGCTGCTTTCGCTTCTTCAATGGGAATTTTCGCTGACCGCTTTCGCGAGGTATCTTCCGCTATTTGGCTATTTCTGT
GAACGAATCCGCTGCTGCTGACCGTATCCGTGAAATTTCCGCAAGCGCGGATGCGCGGACATACCGTCCCGGAAGTCATTGACAACCGGATTACCCCAACGATGAGCCGACCATC
ATTACCCACGCTTCGACCGAGCGATGGTTGTTCTATGCTGCTGTCGCGGTCGAGCTTTCGACCGCTTTCATGCGCATGACCATCGGTATCGGTTCGCGCATCTACTCTTCGCTAT
TGGTTCGCGCGCGCTCTTGTGATGTTTCGCTTTCGAGCGCGCAATATCGCAAGGAAGCGAAACAGAAGGAAGAAATGTGCT

SEQ ID 2334

MELFKIKRDIIPFMSYGLITFISLVTFLAAVFLVARGLNFSVEFTGGTVMEVQYQOQADVNMKRRERDLTKMGDVQVQALGTNKHIMIRLPNKEGVTSAQLSNQVMDLLKIDSPDVTLEQ
VEFIGPQVGEELVNWGLMALGFVVIGIIYLSMRFEWRFVSAIIANMHDIVIIILGCPAFFQWEPFSLFVLGILAVLGYSVNESVVVFDRIENFRKPAHRGHTVPEVIDNAITATHSRTI
ITHGSTAMVVSXLPVFGAALHGFSMALTIGIVPGIYSSVLVASPLLLMPLSLRDNIAKRAKQKEIV

SEQ ID 2335

TTGCCGTTGTGAGGCTTGGCAAACTTGTCCGAATCCCAATTTGGGGTCTTTTATTTTTCGAGGTTTTTCCATTATGCGACTGACCGTAGAACAAAAAGCACAAATCGTTAAAGATTTCC
AACGTAAAGAGGCGACACCGGCTCTTCTGAAGTACAAGTTGCCGTGTGACTTTCCGATCAACGATCTGACCCCCCACTTCAAAGCCAAACCCAAAGCACCACAGCGGTGCGCGCT
GTTGAAATGGTCAGCAACGCGCGCGCTGTGCGCTTATTCGCGCTTACCCAGCCGATACGATTCGCGCGTTGATTACCGCTTGGGTCTGCGCTAA

SEQ ID 2336

LPLSRLKLVRIFFGVLFIFRSFSTHALTVEQKAQIVKDFQRKEGDTGSSEVQVALLTFRINDLTPHFKANPKDHSRRGLLMVSRRLLLAYLRRTPDTYRALITRLGLRK

SEQ ID 2337

ATGGCTGGTGGAGTTTATTTAGCGGAAAAATTTATAGCCCTATATATCATTCATCACAAGAAATTTTCGTTGAACCAATAATCTATGCTGAACAAATAATTTTATGCTGCTGAA
AATTTTTAACTTTAAACGAGTTTCCATAATGGAATATTTTAAATATGAATCAGATAATTACTTTTTATCCAATAAACAAGGGGAGTACGTTTGATAAAAAATACGATAAATATAA
AACTTGGCAAGTGTCTATAGAAAAGCAGCAAAATTTTAAACTCGGTAATCCATATAAT

SEQ ID 2338

MAGGVYLGKKIISPIYHSSQEFSGREPIIYAETNIIICPAEKFLTLKRVPHNGNIPNNQIITFLSNKQGGVRFDKNYDKYKTWQVAIEKAANFLKLGPNYH

SEQ ID 2340

SEQ ID 2341

SEQ ID 2342

SEQ ID 2343

SEQ ID 2344

SEQ ID 2345

SEQ ID 2346

SEQ ID 2347

SEQ ID 2348

SEQ ID 2349

SEQ ID 2350

SEQ ID 2351

SEQ ID 2352

SEQ ID 2353

ATGCAAGAAATCCAAATTATCTGTGGTCTTGAAACGATGTTGGCACAATCGCTGGCGTTTCTGTATATCCCGCTGGTGTGTTTTGGTCAATCTATTTCGTTCAACGAATCCAAACTTGTGTACCG
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TTGTCACTCCGTTGCGGGCTGTGCTGAGCACTGTGCTGTGAAAGAGCCGCAATGGACTTGGGCGCGCGTTCGCTGAAATCTTTTGTGTACATCACTTGGCTTGTGATGCGCCATGCGGCAAT
TGTCTCAGGCTTCTCACTACGCGCATTAACCTTGCTTTTGGATGATTGTGTAATTAACCTCACTTCCCTCCGCGCCGCGTTCATCCAACATTGCGCGCAGGTTATTTTCTCCAAGATCAAGTTGGGT

CTCGATCCTCAGATGAATGTCTTGGCAACCATCTGATCGGCATCATCGGAACATTGGTTCATCTGCAATTATTGGATGATGAGGAGGCAACCAAGCGCAACCGAGAAGCGGAGAG
CCTACCGCCCAAGAAAAATTGGCTGCCGAGAAAGCAAT

SEQ ID 2354

MQKSKLSWFLKMLALSLAFLYIPLVVLVIYSFNESKLVTVWGGFSTKHYGALLENDTILEAAWLSLRIAVVSSLAUVIAGTLAGYAMARIKFRGSTLFAGMISAPMVPDVTGLSHELL
LLIQVQIFLQGSSEWLQHLVYFDRGFTTIFLGHITLCMAYITVWIRSLVELDQSLREAAAMDLAGRLKIFVITLPLIAPATASGFLIGITLSDLDLVTISPLSGPSSTLPQVIFPSIKLG
LDPQMNVLATILIGITLVIIVNYMMRQATKRNREABAYRQELAAERAN

SEQ ID 2355

ATGAAGATAACACACTGCAAAATTAAGAAAGAGTACAGAAAGAACCGCTCGTCTTTTGTACCGGAAGTTACCGCCCGTCTCGCCGCGATATTTTGGGTATCCATCCCGATTCCGCGG
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ACGCGGTGCGCGCGCGGAGAAAGCGGTGTCTTCGGCATTCGAAACGCAACGGCGGCGCTATACCGTTGCGCGGACAAATGCGAGCGCTGAAACGTTGCTCCCTGCCGTCAAAAAG
AAAATCATGCCGCGAGGTATGTTTATGCCGATAGCCCGGCGAGCGCGGCAAGTTGGACGCGCGGCGTTTACCGGTTGCCGCAATCAACCGTTCCAAGGAATTTGCAGACCGTCCGAAAC
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CACACCGTCCCGGACGCTAAAAATCTCGCGGATTTGGTGTGAAT

SEQ ID 2356

MKI THCKLKEVQKEPLRSFVPEVTARSAADILGIHPDAAALFYRKIRTVNHRLLAALAEDEVFGGPGAGPGSGYFGRRRKRRRGAAGKAVVFGIPKRNGRAYTVADNAEPETLLPAVKR
KIMPDGIVYADSPGRSKLDAGGFTRCRINRSKEFADRRNHINGIGNFWQAKRALRKYNGIDRKPFPPLLRCEFRPNFPGTSPRQLKILRDHCGI

SEQ ID 2357

ATGCGCCACGCTCTCGACAAACGGTACGGAACAAATCAGACCGCACCGGTACGGGTACGGCTCCGATATCGGTTATCAGATGCGTTTGTACTTGGGCAAGGTTTTCGGCTGCTGACGACCA
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CGACTTGGGCGCGGTTTACGGCTACCAATGGCGCAGCTGGCGCGCGCCGACGCGGAGCATATCGCAAAATCGCCAATGTGTGGTGGGAACAAATTAAGAAAAACCCGCACTCGCGCGCGCTG
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GAAGGCTACGATCCGATCCGACATCAAGCGCGTAGTGTGCGTT

SEQ ID 2358

MKHVLDNGFDKSDRTGTGTSFVGYQMRFDLKGFPFLITKLLHLSRIHLLWFLKGDNTIKYLDKNNVSIWDEWADENGDLGFPVYGYQWRSWPAFDGRHIDQIANVVEQIKNPDSSRL
IVSAWNPALVDEMALPCHALPQFYVADGKLSQLYQRSADIFLGVFPNIALITMMNAQVCGLEAGFVHTFGDAHLVYRNHFQAAQLQLEREFPALPVNKINPEVKDLFAKFEDEFEL
BGYDPHPHIKAVVSV

SEQ ID 2359

ATGACTGGGTGAGCTGTTTTTTTCAACCGATTTTCTGTTTGGACGATATGGCCCGACAGCTCTGTATCACTCCGTCGGAATAATACCGGATAAAGCAACACAATGATTCGCTCGATT
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ACCGCATATTTCCGCGCTTTGGAAACGCAAGCGGATTCGCGTCAGCACCTTTATTTATGCCACCGAACCTTTGGCGCGCGCACAAAAGGCTTATCCGCAACAAATGGCAGTATGGCAAC
CGCGCATATTTGGATTTATACCGCTCAGCGCGGACGCGCGGCTTTTCGCGCGTGAAGGATAACGAATTTATCGCAATCTCGCGCATGACCGAGCTTTGCGCGCAAGATGATGCTT
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SEQ ID 2360

MTGSACFFSTDFPGRYPTVCIIPSENIIPDKATMIRPDPFQYELPSYFSSVNPHTVYPKLCRLKAETCIIGGSLGLCTALPLAEHGEAVVLEAARI GFAGSAGSGGQVVSIDYACGH
GEIEKQVGLBQAQWFWQSLQAVELVDERVRKHAIDCDWQRYATVAVRPQWHEELQWHEHAQRHYGASHYQLWDKAEKQQLDSMNYQGAQFPDPLSGHLHPLMYTLGASAAAEAGAQI
FBQSPMTRIEPYQNGMLVYTPGSEVCKNVVYVNTYVGLNPIPRPLERKALAVSTFIATEPLGARTKGLIRNNMAVCNDRHILDYRISADGRLLFGGCKNEFIDNPARMTLVRQDML
KVPQLADVRLISYWSGBCDITANLVPHFGRITSNVFTYQYSGHMAITAGLAVAEAILGDCRLKPFELQCPNIILOPPLRLKLSGLSKYQWQKDSR

SEQ ID 2361

ATGCGATATTTCCATATTCAAACAAGGGAATTTGTTTACGCAACAGGCGGACATCGGCAAAATCCCGCGCGCGTCCGCGAGGCTTGGCGCCATCCCGGACAAAGCCCGACCCCGCTT
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CGCGCTCAATTCGGGCGATACCGCTGGGTGATGACTGCGGCTGCCCTTGTACTGTTGATGACGCTTCCCGGCTGGCTTTATCTACCGCGGTATGGTGGGAAAAAAACCTGCTCTCG
ACGATGATGACACGCTTTTCCATCGGACATTTGGTGGCATCTTTGGGTCCGCGTCCGCTATCTTTGGCGTTCACGCGGGAATGCTTTATCGCGGTTTGGGCGCGCTATTTTAA
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GAACAGTGGAA

SEQ ID 2362

MRYHIQTRDLFHAQGGTSAKSPRRSGRACAHQAPPTPPFRKTGPTIKETLIKMKHIWAASLLPASLSAEPLNWMKPYSAVNSGDTAWVMTAAALVLMTLPLGLALFYGNVRKKNLS
TMHSFSAIATLVGLWVAVGYSLAFTPGNFIGGLGRVFLSGMIDAAARMLTVSPNATVPEVPMFPFQMTFAIISTAIITGAFERMKYSAMMLFSGINFLVYVPGHVVWGGGFNSK
GGVLDYAGGTVVHINAGIAGLVAALVLRRIGYGREAMPNHNMTLIGAAMLNFGWFGPNAGSALAADAAGMAMAVTVQSAVPGAAGWLACEKIAHGKPSALGLASGAVSGLVGTTPAA
GFTGPSGAAAGILTAACAFVSVTVVKHLRYDSDLDAFPIHGFGLVGGILTGIFPINRIFGGDAAVWQQLNIQVKGDFIMAAYSGLMSHAILKAVGKICGGLRVGKDVREGLDLNIBG
EHVE

SEQ ID 2363

EQ ID 2363
TTGAATATGGAATATCGCATCCTATCCCTTGGCCCCGTTGTCGCCGGGAGGATTATCTCTTAGCGGGCGCATATGCGGGCGTATGCAATTGTCAACAATTACTGTAGGAAATATACAG
AGGTTTGGGGCATAAGTCAAAAGATTGTTGACAAATATTTTATTTTA

SEQ ID 2364

LNMEISHPIPCPRCPAGGFILRRRICGRMDCQQFTVGKYTEVWALSQKIVDNIFIL

SEQ ID 2365

SEQ ID 2365
TTGCAAAACCGGCTCGAACGATCCCTACCGGCAATGAAAACCGATGCGGGAACTTGATTCAAGGTTCGCGCGAACCGCGCCATTTTTGTATAAATTTTATTTTTTATTTCCAATTAGAA
ATTTT

SEQ ID 2366

LQNRLEIPTGNENRCGNLIQGCAEPRPFYLYFYFLFPIRNF

SEQ ID 2367

SEQ ID 2367

TTGACACCCACGCGCCGATGCTTCAAAATCCCCCCTTCGCGAGCAACGGCAACAGTCAGCTTCTCTTTTCAGACGGCATCCACCGCTCTTTTCTTCTATTCATATATCAITGATTA
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GCAACGCGCGCGAAGAGCTGCTTGTGCGGACGACCATCTGCAACGTATGTGTTCTACTGCTTCTGCAACCGGATGGACGAAATCGAAGCTACCGAGTTCTTAAACGGAAAAATCAA
AGCATTCAAAAAATGATGATTTCTTTGAACCTGATGCGCGGAAAA

SEQ ID 2368

SEQ ID 2368
LPTTRRLPTTPPSPNRQQSASSFRRHPPVFSPLFYISLINHSELQTLHISKLLLEAEHGIENANFRKQDLVFAIVRQMMKKGEQGTCSOTLEILPDGFGFLRSADTSTYLAGPDDIYV
SPTQIRRFNLHGTDTIGSVRVPKDNERYPALVRLDSINGDHPVCHKILFENLTPLFPTQQLKLERDLKSEENLTGRAIDLSPIGKQRALLVAPPKIGKTVMLQNIABVTANYEV
ELIVLLIDERPEFVTEMRSVRGEEVSSSTFDEPAQRHVQVAEMVLEAKRMVEHKDVVILLDSITRIARAYNTVVPASGKILTGGVDANALHRPKRFPGAARNVEEGSGSLTIATALVET
GSRMDIIVYIEFKGTGMELHLDRMAEKRLFPAININKSCTREELFLVPNDQLQRNWLRLKFLHPMDEIATEFPLNGKIKASKNNDFFELMRGK

SEQ ID 2369

SEQ ID 2369
TTGTGTGGCAATTTTCAGCCCTTTTTCACAGCAAAAGCAGGCGTGAAAACAAATATATCTTGATTGGAATCAAAAATCTAGTTTAACACTACT

SEQ ID 2370

LLAISALFHKSRRNKIILIGIKKSSLTT

SEQ ID 2371

SEQ ID 2371
ACGGTGTGATGCTAATAATTCCTCCCTTTCCCCGGACAAATACGGAACACGACATGACCGACATCCTCAATAAAATCCTTCCACCAAGGCACAGGAAGTTGCCGCCCAA

SEQ ID 2372

TV*C*YSPFPRNTTEHDMTDILNKILATKAQEVAAQ

SEQ ID 2373

SEQ ID 2373
GTGGGAATCCAGGATGCAGGGGAACCGCTTTTATCCGATAAGTTTTTCGCACCGAAAGGCTCGGATCCCGCCTTATATGATCGCGCTCTACGCGGGAATGACGGGATTT

SEQ ID 2374

VGIODAGETVLSDKF SHRKVNTIPALYDALYAGMTGF

SEQ ID 2375

SEQ ID 2375

TTGGACACACAAATGGCCGACAACTACGTAACTCGTGTGTGAAAACCTGCGTATGACAGATGTTGAACCGGTGGCGGTAATAAACCGCTCGCTGGGGGAAATGATCAGTCAACTGACCGAA
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SEQ ID 2376

SEQ ID 2376
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FYVFKPTLKAGKPAILRLKTMGSKHKIMFTDKEAGKSVNVVEVPEEDNRNFSYDDEKIELAHYALTIEKHYGRPMDIEWGRDLGDKGLYLQARPETVKSQEESRNLRARYALNGKTV
LCBGRATQKVQVQKVRILKIDASEMDSVAGDVLVITDMPDWPWEVPMKRASAVTVNRGGRTCHAAI IARELGI PAVVCGGNATELLENGQEVTVSCABGTGFIYAGLLDQVITFDVALNM
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ENPMLGFRGAARYVAESFKDCFALECKALKRVRDEWGLTNVEIMIPFVRTLGEABAVKALKENGLERGNGLRLIMCELPSNAVLAEQFLQYDFGFSIGSNDHTQLTLGLDRDSGLVSE
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SEQ ID 2377

TGTGCGGCATTTGTGTGTCATCCAAAATATGTTAAAAAGAAACAAATCCGCTGCTTATTTTAAAGCGATTGTTCCGCCGTGTACAGCTTTTATCTGTCCGGACAAACCGCTGGCGC
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ATTTTCTGTTTCTTTTGTGAATTTTATTT

SEQ ID 2378

LSAICVSNPKYKETNPPLAYFKRFVPLSRFYLSCQPLRLKNSGFRICSLKPMAGILFFSGISFVKQVNLNRMFYAVFPLFLFFGILP

SEQ ID 2379

ATGAAGATAACACACTGCAAAATTAAGAAAGAAAGTACAAAAAGAACCGCTCCGTTCTTTGTACCGGAAGTTACCGCCGTTCTGCCGCCGATATTTGGGTATCCATCCCGATTCCGGCG
CACTGTTTATACCGTAAATCCGCACGGTGGCAACCATCGTTTGGCTTGGCTGCCGATGAGGTTTTCGAGGGCCCCCGCGGCCGCGCAAGCTGTTTCGGCGTACCGCGTAAAGGCAG
ACGCGGTCCGCGCGCGCAGGAAAGCGGTGCTTCGGCATTCGAAACGCAACGGCGGGCTTATACCGTTGCCCGGACGATGCCGAGCTGAACGTTACCCCTCCCGCTCAAAAAG
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ACATTACGGCATTTGGGAATTTTGAATCAGGCAAAACGCCCTTTCGGGAAATACACCGGAATCGATCGTAAACCTTTTCGCCGTTCTTGAGGGAATCGGAATTCGACTTAACTTCGG
CACACCGTCCCGGACGCTAAAAATCTGCGGGATCGGTGCGAATT

SEQ ID 2380

MKITHCKLKKEVQKEPLSFVPEVTSARSAADILGHPDAAALFYRKIRTVANHRLALAADEVPEGPAGPGASCVPVRRKGRGRGAAGKAVVFGIPKRNRAYTVAADAEPELPPAVKIK
KIMPDGIVVADSPGSRGKSDAGGPTCRKINRSKEPADRRNHINGIGNFWQAKRALRKYNGIDRKPPPLRECEFRNLNFTGTPSRQLKILRDRCGI

SEQ ID 2381

GTGGTGAGAAAGTCAATCGGAGCCGGCAGGAAACGGTCAGCGTCCGATTGCGTTTGTACGCGTGGTTGATGACGAAATCCGCCGATTATTAAGGGCGGATGCTTTTCAGATTAAAT
TCTTTGAGACTTTTGGGACTGTTGGAGAAGGAACCAATACCGAAGCAACGGTATCCGGCAGGGGATCAAGTATCGGCAATACGAAGCGTTACGATGCGCGTATGGAGCGGTCAA
TTTTCCTTTGAACCATGATGACGGGTGACGATAGAAACCTTCAGGAGCGGATGATGATTTCGATGGGCGTGTCCCGTTCCGGGCAAAACCGGACCTGCCTGTATCTGGCGTTGCAATAC
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SEQ ID 2382

VVEKVNRSQEQRPFIAPVSVVDDEIRRIKIGADAFQINFETFLGLLEKELNTEATVSGQGHSTGNTRYDARMEAVNFSLNHDDGVSDKMLQADVILMGVSRSGRTPTCLYLALQY
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SEQ ID 2383

ATGGCGTTTGAACGACAGATTGCCAACTGGTTCAGCAAGCCCTCGCCGATATCTCGGCAGTCAGACCGGTGCGGTGCGGAAATATAAAACACTTGGCGCGGACTGCTCATACCCCTCC
TTAAATACAGAAATAAAATATCATCA

SEQ ID 2384

MAFERQIAKLVQSLADILGSQTGAVGNIKHLARTAHPLKRYIKISS

SEQ ID 2385

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CTATACCGCATGGCGCACCGAATATCTGGAGGAATACGACAGCCGCTACGCCCAAGACACCACTCTCTTCGACGGCGTGAACGAACATCATCGCGCACTCGACAGACGCGGCATCAATGG
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AACCACATGCTGCAACCGCTCGGGAATAATGCACGCCGACCGCAACACACCTCTACGTCGGCGACGCGGAACGCGACATCCAAGCCGACGCGCGGTATGAAAACCGCTCTCGCCGCA
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SEQ ID 2386

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SEQ ID 2387

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GGGACAGCTGCGCATCGCAACCGGTGATCAACACCTCTGCCGCGAAGCGGTTTGGAACTGTGCCCTGTTCCGAGCTGATTGCGCGCTTACGATGTTTATCTTCCCGGCTAT
GTGAACATCGAAGCGCGGAAAAAGCGGCTTCAGCCCTCGAATTTGGATATGTGGAAGATTTTCGAGCAGGCTTGAACAAAAATAACATCGCGCTC

SEQ ID 2388

MNPDIYALPERALLSGDPDEKGRITDEFAAVQNAADGAENAPPADFPFRAGRPDTPVLVAPSQLTPRKMNTAEGYAAMLHAITHIEFNAVNLALDAAYRFTLPPQFVRDVKVAKKEVYH
FRLVDRDLRAFGFDYGSFEAHNHLMDMAYKTAVDPLLRMLVPRVLEARGLDVMPGIRAKVBQRGDSATCGVLDITYRDEVGHVAGNRWYQHLCRERGLEPVALFRSLIARYDMFIFRGY
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SEQ ID 2389

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TATTA

SEQ ID 2390

MFILFQTLLEIFQHIQFEAAEARFFPRFDVHIAEDKHIVTGNQTAEQGDRPQTAFAAEVLIPVADGDVSHFVAVNDVQHAAGCRIAALLHLRAVPRHNQVQARLQHARYQRHTQQRVVG
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SEQ ID 2391

SEQ ID 2391
TTGAAAGGGGACGCTGGCGCGCTGCTTTTCCGACCGGTCAAAAAATCAGCCCTCGGAAACGGGTTTGCAAAATGCAAAACGGCCCG

SEQ ID 2392

LKGORGAPAFSERSKKSALGKRGLQANRP

SEQ ID 2393

SEQ ID 2393

TTGTCGGTACTGCACCGAAGCCCTATTTCGAAGGTTGCGCCGAATACCTCAAACAGGCGCGGAAGCGTATTGCTGCCCGTGCTGCGCAAAAGACTTCATCATCGACGAATACCAAGGTTT
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TTGGGGCGGAAGTGGCGCAACTCTTC

SEQ ID 2394

SEQ ID 2394
LSVLTDEPTFQGSPEYLKQAREAVLLPVLKDFIIDFYQVYQARAMGADAVLLIAAALBQQLERFEALAHGLMTVLLLEHDETELEKCRNLITPLMGVNNRNRLTTFEVSIDQTLSLPA
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SEQ ID 2395

SEQ ID 2395
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SEQ ID 2396

MPSLILHKLTLFFPYFRYMMFIADNQPIIIN

SEQ ID 2397

SEQ ID 2397
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GTTTATCCGA

SEQ ID 2398

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SEQ ID 2399

SEQ ID 2399
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SEQ ID 2400

SEQ ID 2400
 MYTARNAARMIVLPRTYPAPHPSRQGIKIMKPHNLQFLAVCSLTVAASAQAQAVDALQPNNDADGISGSFTQTVQSKKKTQTAHCTPKILRPGLPKMEYTLPYRQTIVGDGQTVMLYD
 VDLAQVTKSSDQAIIGSSPAITLNNKTALESYTLKKGDSNGIDYVRATPKRNNAGYQYIRIGPKGKNLAAMQLKDSFGNQTSISFGGLNTNPQLSRGAFKFTPPKGVVDVLSN

SEQ ID 2401

SEQ ID 2401

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CAAAACGCGGAGGAATTGAACAGGTTGTCGCGTTTCATCATCTTTCTCTGTGCGGATGGCTTGACGCGCAAGATATCGGCGCGGCAAAAACATCATACGGCGCGGCTTACGGCGGTTT
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SEQ ID 2402

SEQ ID 2402
LVAAEAVFKLHGGEVAAFEADADVLVAGVVAFGRCPHIIDAVGRITVLFQRVITAFEGGFVVRQDGGAAADGLVLGRLGHLGCLQINIVEPNGLTVADNSLSVGSQVFPFEARAQDFFERAVRGLG
FLFALDGLGEAAADTVGIVVELLERVHRRLCGSDGCGQANGEBLEQVVRPHHYFSLSGWVNRKVSARQNNHETGGVTGGLHFANRVFRGLIFLTARKKQARHAALSTVCRVTD

SEQ ID 2403

SEQ ID 2403
TTGGCCCTTGGTGCAGCAAGGTTTGCATTAAACGGCAAAACAGCCGGGGCGCAACCCGTTAAATTTTCACGGATTTCGCGTTCCGTTGCCCGATCGGCCGATAATGCGGGACATGTTCCGC
CTGGC

SEQ ID 2404

SEQ ID 2404
LALGAARFALNGKNSRGATVNFHGFVPLDPRPIMRDIVPPA

SEQ ID 2405

SEQ ID 2405'

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TATCCGACCAAGAACATGATGAAAAAAGTTTCATCGTATCACCCAAATCCGCGAATCCGTCAAACCTGGGCGTGAAGCTGTGGCAAGGGCTCAAAGCGGCGCAA

SEQ ID 2406

SEQ ID 2406
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KAGAYQKIDKAQIPHVGNIDKDLLKMKRAVDPEGNEYAVPYWNGINTLAINTRQVQKALGTDKLPENENDLVFKPEYTAIKLSGSGISYFDSAIEQIPLAHLYLKGDPNSENPEDIKAAVMM
KAVRGDVKRFSSSGYIDMAAGNLCAAIGYGGDLNIAKTRAEEAANGVEIKVLTPKTVGVVWVDSFKPIPRDAQVNAHRYIDTYTLRPEVAKNGSFVITYAPASRPARELMDKYSTDAST
FPTKELMEKSFIVSPKSAESVKLGVLWGLKAGK

SEQ ID 2407

SEQ ID 2407
ATGAATTAAAGTATTGTCGTCCTATTTTATAATGTCGAAAGGTATTTPGGAAGCGTGTTTAAATCTATAGAACCTATATTAAAGTAATGAAATGTCGAACTTATTTCTGTGAATGACGGGT
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CAGGGGAATATT

SEQ ID 2408

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FLNAVYDKRGVSYPGEDYQPEKILNQSKVEVLKGLCRPKFPGSAWNKIIKRELIIREKLFFKGIYSEDIEMSNRLFNAAITTSYLDGCTYYRQRKDSITGTVSEKIKSLYLLEK
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SEQ ID 2409

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TATCGCGGAAGACGTTACCGTGGGCAAAAGTGATGCTGCACGGCTGCGCAATCGTAACCGCGTCTTGGTGGTATGGGACGACCGCTTTTGGACGATGCGGTTATTGAAGATGACGTG
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SEQ ID 2410

MNAIRTFQNRTEIHECTMIDEACVVI GEVSIAEDVSVWPCAVLRGDVNSITVGARSNIQDGSVLHVSHKTAAPGSSPLVIGEDVTVGHKVMLHGCRIGNRVLVGNGSTVLDVAIVEDOV
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SEQ ID 2411

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SEQ ID 2412

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SEQ ID 2413

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SEQ ID 2414

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YAAEKALQLGAKVLTIVSDSGFVLPDIDMTEAQLAALI ELKEVRRERVATYAKEGGLQYFENQKFWGVAARIALPCATCNELDEBAKFTLLANQCYVVBAGANMPSILGAVBQFIKAGIL
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SEQ ID 2415

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SEQ ID 2416

HPSEGLSISDGIIDFKRRREGFLPINNRKRNSNRVGFSPILIDKQK

SEQ ID 2417

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SEQ ID 2418

VRRRTFAIISHPDAGKTLTEKLLLFSGAIQSAGTVKGGTKKFPATSDMMDIEKQGISVASSVMQPDYKDFVNLIDTPGHQDFSEDYTVRLTAVDSALMVIDAAGVQAQTIKLLHVC
RLRDTPIVTFMKNYDREVRDSELELLEVEDILQIRCAPVTWPIGKKNFPGVYHILWDEIYLFZAGGERLPHEFDILKGINNPLEQRFPLEIQQLRDEIELVQAASNEFNLDEFILAGELP
PVFFGSAINNFGIQLILNSLIDWAPAPKPRDATMRVGPDEPKFSGFIKIQANMDPKHRDRIAPLRVCSGKFERGMKMLIRINREIAASSVVFTHSHRELAAREAYAGDIITGPNHNT

QIGD5FSEGEQLAFTGIPFPAPELFRSVRINPLKIQLOKGLQOLGEBGAVQVFKPMSGADLILGAVGVLPQFEVVT SRLANEYGVGEAVFDSASTWSARWVSCDDKTKLAEFEKANAGNLA
IDAGGNLAYLAPNRVNLGLTOERNPDIIVFHETREESVKL

SEQ ID 2419

ATGATGGCAAACGTCGGCGCGCGGCCTCTGGTCGAGGATTTCTTGGGACATGTTTCTTTGCAAAAAGGTTTCAGGCCGCTTTTCAGACGGCCCGGACAGTGTTTTGAGACGGCGAAATTTGACAAAAAATGCGCTGATAATTCATGTTGGAGGCGGTCAGTCGCTGTCGCCGTAAATCTCTTTTTCGCTTTTCAGGACGGCATCGCGGTTTCCACGCACCCGCGTTCCATTTTGTGTAAGCAGCTTTCGCGCCCGGTGCGCAGCGGATCGCCCGTTTGGCGGATGAGCATCAATGGTATCGCCGTGCGAGTCGAGGCGCAGTTCGCGGACTTTTTCGCTGTGTCGCGACTCTTCGCCCTTCATCCATGTGTTTGGCGCGAACCGCTGTAATAGTGGGCAAGCCGGTTTCGACGGTTTTCGACGGGCTTCGCGGTTTCATCCACGCCACCAT

SEQ ID 2420

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FALHPLFLARTAVTVGKAGDFGLOGFGVHPRHH

SEQ ID 2421

TTGGTTTTCGCCATCGCCCAAGATCGCGAAACCAACGTGTTTTAATGGTGGCGTGGATGAACGCCGAAGCCCTGCAAAAAACCGTGCAAACCGCGCTTTGCCACTATTACAGCGGTTCGC
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SEQ ID 2422

LVCAIAQDAETKRVLVAMNABALQKTVETGFAHYYSR SRQKQWKGESGHTQKVRELRLDCDGDITVMLIAQNGGLACHTGRESFYKKNWGGANETADAVLKDEKEIYGSTH

SEQ ID 2423

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CCTTCGCGCGTTG

SEQ ID 2424

MAQTKPFSNNLTASSRFLSTIPFRHRSGGQRRTPMPASRIVRLASRMASIPKWKMPAASTASALPSVMPISIRCTLTPTPPRAMTGMSTASATARVSGRIKPCFVPSLSLIPVSRISPA
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PSPL

SEQ ID 2425

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AAACGCACTATTCGCGAAGCCGCGGATCGGACGCTGCGGCTC

SEQ ID 2426

MALAKRIIPCLDVKDGKRVKGVNFIGLRDAGGPVEAAKRYNGEGADELFTLOITASSDNDRDTILHIIKEVAGQVFPPLFVGGGVRTVADIRRLNAGADKVSINTAAVTRPDLINAEAGFF
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 KRTMRAGIEVEL

SEQ ID 2427

TGTGTAATAATCGCAGCCATATTGCAAAAAAGAGGAGGAAGCCATGCAAAACGCCATTATCGATTACGGTATGGGCAACCTGCATTCCGTATTGAAATCGTCCGGACGGGGGGCAGCTTG
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SEQ ID 2428

LLKSPCYCKKEEAMQTAIDYGMGNLHSLVLSVTRTAGQLGKNTKIFLSGDPDRVSRADKVIIPFGQAMPDCMAALTRGGLDEAVKDALKNKPFGICVGAQLLFDHSEEGNTDGLGWFG
GKVRFPARDLRDPOGCRLLKVPHPMGWNTVROTKNKLFGQIPQWTRFYFVHSYVFAPENPETILGESDYPSPFACIVGKONVPATQFTEKSHDAGL/MLKNFLMW

SEQ ID 2429

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TC

SEQ ID 2430

MTHRTARQILHEVFGYPEFRGRQEDVINLTAGGSGSLTVLIMPTGGGKSLCYQIPALMREGVAVVSPALIAWMDQVASLHVAGTAEAAVNSGTSADFAREIADKLAQRLKLLVYAPERLV
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 KVEDAAQFLRENGLNALPHYAGLSMDVREENORRPTHEONIIVVATVAFMGIDKPDVRVFAHLMQPSVEHFYQSRGRAGRDGLPAVSWLYCLNMDVLLRERIEAGNSDEVQKQIEMOK
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 QALQITEAAKVLKGFEVMLRPLRDKPATFTLLKDWLRTEREERLQALKVRWMLQAEAGIPAYMIPGDKTLRDLVEKMPQNLNGLHDITYLGEAKTERFGHGILKVCQNAADFSDHA
 VIRPQTEREQQLRKLKEAWRYEQARAENCALHTVLSDESLEADMLAATPETTLEAVHGLGSVRAAKYGRDILAVCRPPFSDGIDETPAKHKRCIMRALIQWCNETAKHEQSEPYRILSKAAL
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SEQ ID 2431

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SEQ ID 2432

VDAIHDAEQSAVHFFARFQADGVLHAFQARSCHAAGVGGFARSVEDAGDFKLLDRAQSRRHARFAGNDVAAVCQQGGFGFFVQFVLGRAGQGDFGNAFRFLVFKVLQTLPLFGVGNFA
ADFFQFDQGGELRFGHTDVGEEDEAVGVGDGHFRFTQLDGFPSGVLRHVAGTGNQAFAPFTTVAGLQHLRGEIDAAVAGRLGADEAATPFQTFAGQDSEPIADFFVLSEBVADFASAYZ
DVAGRNIGVRADVAVEFGHKGLAEAHYFGIGFAFGVEVGTAFAAAHRRGGQGVFEHLFKSEEPQHAQIDGRVEAQAAFRVADGGTHLHAVAADVLDSFVVLPGYAREHDAFGDDAPQQA
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SEQ ID 2433

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SEQ ID 2434

LNPMPSEDRPFPSDGI F I SPAHL FVKIAAIL QXRGGSHANRHYLR YGQPAFRIEIRPDGGAACRKKYQNL FKKRRPRPRVPRRQSHPSRAGR DARLYGGTDARRLGRGSRRLKKQTVFRN
LRRCAFTIRPQRRRKHRLGLVRQSGYQLCPRP RPAGMPSESPAYGLEHRAFNPKPPAFSRHPKPHAFLPFQQLFPRKRSRHHIGRKKLPVVCVLRHRQRQRI RHAI SHRKKPCRAAD
VEKLFKLVSRTPRTRRKTMLLI PAIDLKEGRCVRLKQGLMEAEATVFS DSPADTALHWFQBGARRHLHVDLNGAFAGVQPNLPAIKDILAAVAKDIPVQLGGGMRDLKTIGQYVLDLGLNDV
IIGTAAVKNPDLVREACKAPGRI IIVGLDAKDGMAAIDGNATVTYGHVIDLAKRFDEGVNSI IYTDIGRGGMSGVNIDATVKLAQSVRI PVIASGGLTGLDDIRLCAAEKHGVAGAIT
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SEQ ID 2435

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SEQ ID 2436

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 EPRFVQAAACHKEGRIARCVLLAKREEVEAVAKERGISLPSLREIIDPASLVEOYVEPMCELRKSKGLTPEDARKOLODTFVLGLTMAANDVDGLVSGAVHTTANTIRPALOLIKTAPGA

SLVSSVFFMLLENQVLVFGDCAVNPNTPAQQADIAIOSADSAKAFGIDPKVAMISYSTVNSGSGPDVDTVIEATKLAREKRPDLAIDGPLYDAATVPGVGSKAPGSPVAGQATVLVFP
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SEQ ID 2437

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SEQ ID 2438

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SEQ ID 2439

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SEQ ID 2440

MSPPKIPWLGLLILLLALPLTLPLFLYVAPRSWQVGINRAVELLFPRMWDLLSNVLTMMAGVTLISIVLGIACALLPQRYRFPGRKTFPQTAITLPLCIPAFVSCFTWISLITRVBEGPFGT
VHMSLSGSPFLAYLPEVAALKRISISYEEVLSLSGKSRQLTPFSAILPOLKPAIGSSVLLIALHMLVEFGAVSILNYPFTTTAIPQYEMSYNNHTAALLSAVILFAVCGLVVPGESIFBKG
AKIYHSGCKGVARFPYPVKTLKLPQIGAIIVFLSSLLILGIIIPFGVLIHMMVGTSGTFFALVSVFDAFIRLSVLSALGAILTILCALPLVWASVRYRNPLTVWIDRLPFLHAEVGLVIALS
LVYPSINFTPAVYQTFIVVLIATFMYLPLPAQTLRTLSLEQLPKGMEQVATLGRGHFFIFRTIWLVSILPLGITAAPALVFLKMLKELTATLILLTADDVHTLSSTAVWEYTSDAQYAATPY
ALMLVLYSPFVLLKXAFK

SEQ ID 2441

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SEQ ID 2442

MKTSTRYALLAAALTAATPALADITVYNGQKEBAQAQAVADAFTRATGCIKVKLNSAKGDQLAGCIKEGGRSPADVFVYSEQIPALATLSAANLLEPIASTINETRGKGVPAARKDHWALS
 GRSRVVYDTRKLSKDELEKSVLNYATPKWKNRIGYVPTSGAPLEQIVAIKVLKGEAAALKWLKGLKEYGKPYAKNSVALQAVENGIDAALINNYTHHAFAREKGVQNVHTRLNFVRHRD
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SEQ ID 2443

GTGTATTCTTCCTTTTTTATAAATGCAAATAATTATTTTTTAAATTGTTATTATCCGATCCGGTTATTGTTTGTCTGACTTGTATTTTTTCCGTGCATCGCGCCCG

SEQ ID 2444

VYSFFFINANNYFLNLLSDPVTVCSDLYFFRASRP

SEQ ID 2445

TTGTGCGGAATCTGCGAGAACCTCTCCCTTTAAAAACGCGCTCTGAACAAGGTTGCGGGAATAGTATTGCCATCCCGGCAGATACAGTTTGTCTGGGATCTTGCCAATATTGTTCATCCAGACT
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SEQ ID 2446

LSBCHRTSPFTTSPBEGCRNSIALPADTVCRLANIVHPDCSARRPCCRDVLLIHYISHISFRFLPSDWRWRISFPNASAAARWISIALCTAPIFFRTEQVPSAAGKPOLQTNCSHPLPM
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SEQ ID 2447

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SEQ ID 2448

MTDTDTQADRPEOMMRQAVDKLFEQHDGKLESMGREGELVLIWRAEADIGNGGILOFVCLNWGFPAAEKTCVSLKKIGAVHSAMLIHRAADALGKEIRHLQSEGGNLEKEMDI

SEQ ID 2449

ATGACAGCAGCAAACTGGTCCGGACGTTTCAACGAAACCCGTTTCCGAACTCGTCAAAACAATACACCGCCTCCATCGGTTTTCGACCAACGCGCTTCGCGAATGGGACATCCAAGGCTCGCTCG
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ACAGGTTACGCTTCAAGTCAAAACGCTGGCGGGAATGTCACT

SEQ ID 2450

MHDKTSWGRFNPVPSLVKQYTASIGFDQLRAEWDIQGS LAHAQMLTRSGVLSNDLTDIRRGMSEILEEIRSGKIEWPLDLEDVHMNIERRITDKIGDAGKRLHTGSRNDQVATDILM
 LRDQITVYIQLNLIQNLQTALLDLAEQNAEAVMPGFTHLQVAPVPSFGHMLAYVENLGRDFERMTCRKVRNRMPLGAALAGTTPYIQREITAEILGFBQI CONSLDAVSORDFAIEFTAA
 ASLYMVHLSRLSEELILWMSRPGFIDILADRFCTGSSIMPQKNPDVPELVRGKSGRVIHGLIGLITLMSQPLAYNKDNQEDKEPLFDATDITLIDTLAIYADMGRGVTVKPGNRAAVAQ
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SEQ ID 2451

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SEQ ID 2452

MKPIKKA VFPVAGMGRFLPATKANPKEMLEIVDKPLIQYAVEEA EAGCTEMVFPVTGRNKR SIEDHFDKAYELET KLEMRHKDKLLEHVNTILPNNITCLYIRQAEALGLGHAVLCARAA
 IGDPEPPAVILADLIDAPKGA LQKMQVEVYGRSGNSILGVEVTEPSPQTSYGIVETEQLKQFORITGIVEKPKPEDAPSNLAVVGRIYILTPRIFDLITGLPRGAGNEIQLTDGIAKLLDHEF
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SEQ ID 2453

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SEQ ID 2454

SECID 2434
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PRALSGGTDLAVLDFAPQVQAVQAFVQIKRFHAGHIDRKVGYARIAETIHLGLTVVFTQSGDKRIFLQIFI*IFMPLGQKRRQAGKRLQFHRVPKIIIPNIAQLIPYAVFPSPGKHEGIF
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SEQ ID 2455

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GCGGTTTGCT

SEQ ID 2456

1GGMNTVOTVWHIRMYRYSELNLNOYGVASPCRTICTVCGSPPCPDNLNIHYSITRFERADNEMPSECHLRFGRRHFVCGARAF

SEQ ID 2457

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SEQ ID 2458

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SEQ ID 2460

SEQ ID 2461

SEQ ID 2462

SEQ ID 2463

SEQ ID 246A

SEQ ID 2465

SEQ ID 2466

SEQ ID 2467

SEQ ID 2468

SEQ ID 2469

SEQ ID 2470

SEQ ID 2471

SEQ ID 2472

SEQ ID 2473

ATGTCCTTTGCTTTACATTCCGCATACACAATGAATACGCAACCGCAGCTTCCCATACCGATTCCAACACGCTGATGCTCGGCCGATACGCCGAACGCGCTATTCGAATACGCCATGA
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SEQ ID 2474

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SEQ ID 2475

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SEQ ID 2476

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SEQ ID 2477

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SEQ ID 2478

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SEQ ID 2479

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SEQ ID 2480

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SEQ ID 2481

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SEQ ID 2482

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SEQ ID 2483

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SEQ ID 2484

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SEQ ID 2485

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SEQ ID 2486

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SEQ ID 2487

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SEQ ID 2488

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SEQ ID 2489

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A

SEQ ID 2490

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SEQ ID 2491

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SEQ ID 2492

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FVELPPL

SEQ ID 2493

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SEQ ID 2494

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SEQ ID 2495

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SEQ ID 2496

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PFVELPLL

SEQ ID 2497

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AAA

SEQ ID 2498

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K

SEQ ID 2499

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SEQ ID 2500

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SEQ ID 2501

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SEQ ID 2502

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SEQ ID 2503

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SEQ ID 2504

LDLGNFRFRFVGGGLPAPQRAGVQRDDVVGIRVAQRGPVSEDDGVVEVLPIGSGFEPRAQVRHFFTHCGFVVEIQVFVKGGQAHPRGEGVDDAEAGIAQITFFVPCGRFVAVHFGEEFDVFF
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SEQ ID 2505

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SEQ ID 2506

VELCVQNDVGFRFDLHAFGQGRGNADGGAGGERLGDKFRHHFVEDGKIAQVGVGVGFDDVVQRTACRFGDGLQVLEHLARFGVEIAVADESHRGGGIERNLTAHVNGAAGAHGLAVCADGGG
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SEQ ID 2507

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SEQ ID 2508

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SEQ ID 2509

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CC

SEQ ID 2510

LCSEFRYRMRKQRTAEGSAVCGITRISEFDAHAGGQFAGTVDFDIVDFADVVAVAGIQIDIGCNGIAYARQYAEAGGGFAEAVAAQVGGSAVEAQABAEIRFDGRLGVEVVNDGRADAV
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SEQ ID 2511

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SEQ ID 2512

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SEQ ID 2513

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SEQ ID 2514

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SEQ ID 2515

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SEQ ID 2516

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SEQ ID 2517

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SEQ ID 2518

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SEQ ID 2519

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SEQ ID 2520

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SEQ ID 2521

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SEQ ID 2522

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SEQ ID 2523

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SEQ ID 2524

NHTISFPNRLTALPPLSLYTHIPWCIKKPCYDFNSHSLKNGLEPAAYIDALLTDLDLEPLNHWGRPVETIFFGGTSPSLFQAESIDRLLSGVRSLRLQPEAKITLEANPGTVEIEKF
QGPRDAGITRLSIGVSPFNDMLSLGRVHNGREALTATATALKLFDKVNIDLMYALPNQVPTALDDVQTAIATDATHISAYHLTMEPNTFPGHTPKGLPDQREALDIEDAVHGTLEGA
GFHYETSAFAPKPMQCRHNLNMYQFDYLGIGAGAGHKISYFDRIERTVRRHRPNYDALMQLSQPGEAVERKTVAAEDLPEFPMNMLRLTDGVPAAHLQERTGVPAAKINQVETARQK
GLLETDPTVFRPEKGRFLNLDLQCFI

SEQ ID 2525

ATGAACCGGACCGCACACGCATACAGCACTCACCGACCTCTCAACCGCTACGCTACGAATACTACACCTCGACGCGCCAGCATACCGGATGCGGAATACGACCGCGCTGTCGCG
AACTCGAAGCGTTGGAAGCAAACTATCCGAGCTCAAGCTGCGCGACAGCCGACCGCGCGTTCGCGCGCGGAGCTTTGCGAGGCTTTGCGGAAGTCCGCGACGAAGTGCCTGCTGTC
GCTGACCAACCGCTTTTCCCGCAAGATGAAAAACGCGGTGTCGACCATGCGGAAATGTACGCTTCGACCAACCGCGTTCGCGGACGCGCTTGGACGCGCGGCAATCCGGAATACGTTATCGAA
CCCAATTCGACGCGCTTCGCGCATGAGCTGCTCTACCGCGACGCGGTATTGTCGAGCGCGCAACGCGCGCGCAGCGCAGCAGCGCGCGGAGAGCTTACCGGAAACGTCAAAACCGTATCCCA
ACATCCCGCTGCGGCTGACGCGCGAAACGTCGCCGAACCTATCGAAGTACGCGCGGAAGTGTGATGCTCAAAGCCGATTTCGCGCTTTAAACCAACGTCAGACCGAAACCGGCAAAA
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AACGCCACCTTCGCAATACGAGCAAGATATCGCGCAAGACGTCGCGCTGCGCGATACCGTCTGTCGTCGCGCGCGCGGAGAGCTGATTCCCGAAGTCTGCGCGGATTTCGAACGCC
GCCGATGTCAGGAAACCGCGGTTGCGGTTTCAGACGCGCATCGGCACTCAGCAGGACGAGCTGTTGCCGAAACACCGCTTCGCGCAACCGGAATCCGTTCCGCTCCATAAGCCCTACCG
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CGGACCAAGCCCAAGCCCTAATCGAAGCGCGAGCGCGCAAGGTGTCGCGCGAGCTGTCGCAAAACCGGACTACGTCGTCGCGGAGAAACCGCGCGCAGCAAGCTGGAAGGCAAGTGC
CTTGGCGGTTTCGCTGCTCAGCGAGCGCAACTGCTTACCTGCTCTGC

SEQ ID 2526

MNPFAQRHIELTOLLNRYAYEYTTLDAPSIPDAETDRLFRELEALERHNPFLKLPDSPTQVRGGEPLAGFAEVRHEVPMLSLTNAPSQDENGVPDHAEMYPDQVRVRLDGLDGGNPEYVIE
PKFDGLAISLLYRDLVLVQAATRGDGTGDEVDTRNVKTVSNIPRLHGENVPELIEVRGEVIMLKADFAALNQRQTENGQKPPANPRNAAAGSLRQLDSRTTAQRKLFHFPYSVARQGGGL
IAEBHIQELAYFQALGSLPNGNPGCPKNIGEVLAIFYEHMQKRPELPEYIDGTVVKNLSAQHGLGISRAPWMAVAHKFPAREALTIIVRAIDVQIGRTGAVTPVARLQPVFVGVTPT
NATLHNQDEVSKDVRVGDTPVVVRAGUVIPEVVRVIFERRPMQETAVAVSDGIHQDDLFATPESAKQTESVPLHKPYRLPARCPCIRSETEREBGEAVARCSGMLCQAQRAQGLIHF
ASRKAMIDIGLERQIEQLVAQDLVRHFADLYRIDIPTLQKMKETADKGSSENGDAETVSGDLSKYNTQNGKKOPTKWAQNLILAGIESGKTPELARFLFALGIRHVIGERTAKTLAQAFG
TLERVRRAPFVLACLPDITVVARSHAFPAQAEQAMIDELLAGVAPQAQAVSLPAAYAGPQRMITRLPGFKISENKAQALMELAGQSBGLQNDKALPADWQAMRSKAQNTALLER
LKTFFAQMPSEDEAAQSGDINKAVAGTFFVLGTLPFTFKRDQAQALIEAAGKVSQSVSKTQVYVAGETAGSKLEKANALGVSVLSEAEHLTLIC

SEQ ID 2527

GTGCGGTTCGGGTTCATGGATTTCGTACAGGTTACAGCGCATGGACAAATGCCGTCTGAACGGTAAACGTTGGAAATGGTCGGATTTTACC

SEQ ID 2528

VRSGSWIRTSQSDGMDKRLNGKTCWKWSDFP

SEQ ID 2529

TGTCACAAACCCCTTCGACAAAGTCGCGGCACAGCGCGCAACGCTTCGCGATGGCTCAAAACGCGCGGTGTCGCCCTTTTCATCACAACACAGCTGCTTCCTTTCAATGCGCATGC
AGATACATCGCCCATACGACGCGGTGTAATCGCGCTTTTCGCCGCGCAACACAGCAGTACCGGAACATCTATCTTGTCCAACAAATGCGCGCATCGGCCCTTTCCGCGCGTCCAAAGCTT
CCTGTAAAGGCTTGAGGCGTCCCGCAGCGCGCAATCGCGCAGGATTCTCGCGATGATTTCGCGCGCATCAGGCGTGTGCAAGCTGGAGTTGTGAGAACTGTTGATATGTTTGGCATA
ATCCGTTCCGAACGCGCGGACCAATTTTCCCGCAGTGCAGCGCGCAAGCCCTTCGGGATAGTCTTCGCGCAGCCCTCAGCCGTGCGAAACTCGCGCTCAGGCAGAGCGAAGGACTTTGTGCG
GGAATGCGCGCGCGCCAGATACAGCGCGCAATCCCGAGTGACCGCGGAGAATGTCGCGCGCAGTATCGATTGAGCGCAATGCCCTCGCGCAGCTGCCCAATATCGAAGGGTTGCG
CGAAGGCGCGTCCCGTGTCCGCGCAATCGACGCGGACACCGGCCACGTTGCGCGCAGCGCGCATCAATCGTCAACGCGTGGCGGTTGCCGCCCAACCGGTGATCAGGTAAC
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SEQ ID 2530

CQTFPDKVAQRGRFRMAQKRRVRLFHNNQSPASQPMQILAHQRCNRVFAAEHQYRNILYVQMPRIIRPRRVQSFL*GLRRAAARQIGQSDADDGGIRRVQKLEL*KLFDMPGI
IRSERADHFAQCRKPGKPGIVFGSRQPCETRRQAERTDFVGMARRQIQRDQAE*PAENWRRIRIDLGNVAGSCLNIEGLRBEGRVPSVSGQIDGHRPRCQARHQIVERVAVRPPPTVYQVN
FFGSIRHEFLSLLAAHRRRAH

SEQ ID 2531

GTGATTGCCATGATTACATCGTACTGTTCTCGCCGCCGCTTCGCGCTTGTGCGCTACAATATGTATCAGGAAACCAATACCGCAAAAAAGTCGCGACCACTTCGGACACTCCGACA
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CATGCGCAACCTGCAAGAACAGGATGCCGTCTACATCGCAAGCAGAAACAGGCAAAAGCTCCCGCTTCAAAACCGAAATCGAAACCGCTTGGAGAAATCGGCATATTCGGCAACTCC
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CGGCTGACCAATGAGACGACATTTCCAGATTGCCGAACCCATCCGCGCATTCGCTATCAGGCAITTTATCGTGGGTATCCAGGCACTCAGCGCAACCGGACTTGCCTCGAGGAAGACTC
TCCGCAITCAACCGCGCAGCGCGGACGATTCGCACAAAGCATGGCGGTGACAGCGCTGCACACGACCTTCGCGCTTTATCGAAGTGGCTTCGCACTGAGCAGCATTCGCGCGCGGTG
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GTCGGGCTCGACCATGTTCTCCATCTGCTCGCTCAACACGAGCGGTTTACCAATGCGCTTTTGGACAAACGAGTCTCTACAAAGGCTTCAGTATGCTGCTCGACATCCCGACTCTCGGCA
GTCGAAAAACCTTCGACGATTTGTTTATGATTTGCGGTACGCTGTCGCTCAGTTGAACCTGAATCTGCTCAACGACAAAAAGTGAAGAGTTTCGACCCATGCTCAAGAGCTAC
GCACTTATGATTGGCGCTCAGTCCGAGATGCTCAAGTGGTATCGAACCGCGCGCAAAACCGCTTCGCGCTGTTTCA

SEQ ID 2532

VIAIYIYVFLAAVAVVAYNMYQENQYRKKVRDQFGHSDKDALNLSKTSHVDRGKPSGGPVMMPKPQPAVKKPAKPD SAMRNLQSBQDAVYIAKQKAKASPFKTEIFALEEIGIIGNS
AHTVSEPTGHSAPKPADAPAKPVVPQTAPKPLITLKLKSKVELPWFVDVRPDIYSIALTEAKELHALPRLSNRCRYQIVGCTMDHFPQIAEPIPGIRYQAFIVGIQAVSRNGLASQEL
SAFNRQADAFQSMGGQTLHTDLAAPIEVSALDAPCARVDQTIHLVSPSTISGVELRSVITGVGVLEDDGAFHYTDTSGSTMFISICSLNNEPFTNALLDNQSTKGFSSMLLDIPHSPA
GKTFDDLLFMDLAVRLSGQLNLNLVNDKNEEVSTQWLKDVRTTVLARQSEMLKVGIEPGGKTALRLFS

SEQ ID 2533

ATGGCAATCACTTTAAATTTCCGGATGCGAGATGCGCAAAAGTCGCGGTACTGCGGTAAATCGGGCTTCGCTTTCCGGCAGTCTGACGGAAACGCGCGTTATAACGTT

SEQ ID 2534

MAITLNFQMQDAQSAGTAVKSGLRFRQSDGTAGYV

SEQ ID 2535

ATGCCGTGCAAAACACAGATTTCAGACGGCAATTCGGAATAATTCGCTTATTTTCGACACACTGCTGTCAGACCTGCAATTTTCGTTATAATTCAAACGTTA

SEQ ID 2536

MPSENHRFQTAFRKISAYFDLLSDPAIFVLIQTL

SEQ ID 2537

TTGCCCGCCGAGCAGGAAGAATCATGGACAATCAGCCGGAGCACACTGGCAAAACGCGTGGCTTCAAGCATACGCCATACCCGTCGCCCAATTCAGCCCGAGGGAACGGGAGAA
ACGGTTTCCTGATCGTGTGCACAACATTTGCTGCGCGCTTCGAATACGGCAGGATGCGGTGGAAGAGCTGTTTGCAACCGGCTCGACCCCGACGGACATCGTTCTTCAGCTGA
TACACACTTTGCACGTGTCCAGCCATTTCTGATTGCACGCGAGCGGAAACGTCGATTCGATCATGCGCGACATGGCGTACCAGCGCGCGCATCTCTGTTTCGGGGCGGGAGAA
GTGCAACGCGTTTTCATCGGCACTGAACGGAAGCTGCGATTTCGAACCGTTTCCGGAAGCGCAATACCGTTTCGCTCGAAACACTGTTGCGAGCCCTCTCGCGCGCTACCCATCAGC
GCGGTAACGGGACACCAAGACATCGACCCGCGCGCAAAACCGACCCCGGCAATTTTTCGACTGGCGCGGATACGGGAAAAAGGGTTTCCTGTCAGAGAAATCGCGTCTGAAACAC
AGATTTTCAGACGGCATTTTCGGAATAATTCGCTTATTTTCGACACACTGCTGTCAGACCTTCAATTTTCGTTA

SEQ ID 2538

LPAGQEEHGGQSRSTLAKRLASKHTPYVQAQFQPEBGNRNGFPDRAAQHFAAARIRHCGGKAVQCPARPRRTSVLQPDTHFARVQFPDCTRRRRNAGVRIMRRHGVPRRILVSGAGE
VQRVFRHRTGRLRPTVCRSAIPFARNTVGSPLPLPHHGNGTPRHRTRPQNRPRPFRRLAADTKRVSQKCRKLTDTDFRRHFGKPLISTHCCQTLQFSL

SEQ ID 2539

ATGGACAATCAGCCGGAGCACACTGGCAAAACGCGTGGCTTCAAGCATACGCCATACCCGTCGCCCAATTCAGCCCGAGGGAACGGGAGAAACGGTTTCCTGATCGTGTGCACA
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TTTCTGATTGCACGCGAGCGGAAACGTCAGTTCTGATCATGCGCGGACATGGCGTACCAGCGCGGCACTCTGTTTCGGGGCGGGAGAA
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CACCCGCGCGCAAAACCGACCCCGGCAATTTTTCGACTGGCGCGGATACGGGAAAAAGGGTTTCCTGTCAGAGAAATCGCGTCTGAAACAC

SEQ ID 2540

MDNHAGAHWQNLQSIHTSPNPFSPRETGETVSLVILHNLSPPEYGTDAVEKLFANRLDPDGHFFSLIHTLHVSSHFLIARDGETVQVPSGDMAYHAGASSFRGREKCNFSGI
ELBGGDFEPFAEQYRSLETLAALCRRYPITAVTGHQDIAPGRKTPDGHFPDWRIRERGGFPVDRNAV

SEQ ID 2541

TTGGGTTTACTGTCGCCCGGAATTTTAAAGACGTATTCCGAATGCTGGGAATCCTACCATGTTGAAAAAATGTTGAAATGGACTGCCGTTTPTTTTGACCGTATCGGCAGCCGTTTCGCGB
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CGCGGTACAACACCTATACGCGCGGGGGCTTCGCCCAACCCCGATTGCGCTGCCCGGCAAGGCGGCATGATGATCGCGCGCCCAACCGTTCGCGCGGAAAAATACCTGTATTTTCGTGTC
AAATGGACGGCACGGGCTTGAGCCAGTTCAGCCA

SEQ ID 2542

LGTYVARILRRPINAGNPTMLKKMLKWTAVFTVTSAAVFAALLFVPKIDNGRAYRIKIAKNQGISSVGRKLAEDRIVFSRHVLTAAYVLGVHNLHJTGTYRLPSEVSANDILQKRRGRPD
SVTVQIIEGSRPSHMRKVIDATPDIGDHTKGWSNEKIMAEVAPDAFSPNGEQFFPDSYKIDAGGSDLIQTYQATAYKAMQRLNEAWAGRGDGLPTKNPYEMLIHASLIEKETGHRADRDV
ASVFNRLKIGIRLQTDPSVTYVINGAAAYGKIRKADLRDPTNTYTRGGLPPTPIALPGKAAMDAAAHRSGGKIPVFPVQNGRHGLEPWPQ

SEQ ID 2543

TTGCGGGTTTCATGCTTGCAGTTCGGGTACGGGTATGCGGTCTGAAAAACACAACATTTTCAGACGGCATGGTTTATTTTTCAAAATATATTTCGGGACGGCGGGCTGTGTGTTCCGTCAAAT
CATGGCTGAACGTGGCTCAAGCCCGTGCCTCCATTTTGGACACGAAATACAGGTATTTTCCCGCGGAACGGTGGCGGCGGCATCCATTGCGCCCTTGCCGGGACGCGCAATTCGGGGTTG
CGCGCAAGCCCCCGCGGTATAGGTGTGTGACGGCTGTGCGGGCGCAGGTTCGGCTTTACGGATTTCGCCCTGTATGCCCAACCATGCCGTAAATCAGCGACGGGTTCGGTTTCGAGCG
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AGCCCGTCTGCTGCGCTGCCATGCTCGTTTCAGCGCGGTTCATCGCTTGTAGGCGGTTCGGTAAATCTGCAAAATCGCTGCGCCCGCATCGATTTCGTAGCTGTGCGGAAAAAATC
GCCCTTCAGGATTGCCGCTGAAGGCATCGGGCGCAACTTCGCCCATCAGTTTTCATTCGTCCAGCTTTGGTGTGCTGTCGATTCGGGCGTTGCGTCGATGACTTTCCTCATATCGCA
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AATACGCTCT

SEQ ID 2544

LRFHACSSGKMPSENTNPSDGHVYFFKIYLRTAALCSVKSWLNLKPVPSILDTKYRYPAGTVGGGIECRLAGQRNRGNWQAPARIGVVRVAAQVGFDFALVCRTHAVNHGRVGLQA
HTDFQAVDEGSDMVAVGLMPRFLFDQARENHQFIRVPIRQPVLPACPCLVQAALHRLVGLGLVNLQIAAARIDFVAVGKGLPFRILAAEGIGRNFHQFFIAPAGVVSVDVGRVDDFPFHER
KTRTFDNLHGNGIRPAAAHFLQDIPSRHFRROSVRPRMQPVVHTQNVGRRRQNMPEHDAVFGKFPADRRTWLIPGNLSDVCPAVVFRDKKQREGNGCRYGQKNGSPFQHFQHGRIPSIR
NPS

SEQ ID 2545

CCGCAACCGTCAAAACATATAGTGGAT

SEQ ID 2546

LTAHYKIGKSTRIGLDFENVFNKRCRTPDLHVGTPRSLTATVKHIVD

SEQ ID 2547

[illegible]

SEQ ID 2548

MVI SNPRELEKLDRI PNLI NIIRVAI VFLMTHILGLETGRANLHASWTAWAFYLHLA IACMLIFFSTLNPQWQHQALRIPSPFSAVADITMIGVLTLYLFGGIDSGFGILILFFVGS
 SCILSYGRPYLLYASYASILLI PNALASDNINMYPLILDAKTNTNTFFVVAGSYFVAMTASLSVRYIRDRAGLAHENHVA YRRIRGLAQIVIANVQOEAVVIVINVERQITLIFNKAKDILLPH
 LEIGQTSILDFPAILWDKTSSRTYEHHIDTPELTARIRAVPMMKNQKLLILYIRPQSEIQAELSVKLAALGQLTANLAHEIRNPMSATRHADGGTFLPDEVA DILPMSQVKILRATQE
 KAVRRIGHTAQEPVDVVRICATHKNEALVESGAPFDQDLYRLMNVSLPMSLREMRNRETPYLLYKHSNNRNPYITLSPAAQCMLLNYSPYGNFRELENILERAVALCVGTFYTTQIDDL
 QIQDVHHKPRTEFTEFVADTFLSEIAAPASGRLLFPDPDTMQIQDVLDKIEDIIGQVLKQTEGNRTQA AKRLGISPSRMYRMYERLNTD

SEQ ID 2549

ATGAAACCGCAATTCATCACCTTTGGACGGCATAGACGGTGC CGGAAAAATCCACCAACCTTGC CGTCATCAAGGCATGGTTTGAACGGAGGGGGCTGCCCGTCTGTTTCA CGCGGAGCGCGG
GCGGAACCGCGGTCGGTGAGGCGCTTGCGCGAAATCTCTCTCAACCCCTGAAACCAAGCCGGTTTGC GTGCGGAAACACTGATGAGTGTTCGCCGCGCGTATGCAGCACATCGAGGAAGTCAT
CCTGCCCGCGCTTTAGACGGCATCATGATCGTGTCCGACCGGTTTATCCGATGCGACCTTGCCTATCAGGGCGGCGGGCGGGGGATGCCGTCTGAAGACATTGAAATTTTGAACATTGG
GTGCAGGGCGGTTTGCGCCCCGATTTGACCTCTCTGTGTGGATGTGCCGTGGAAGTATCGATGGCGCGTATCGGACAGGCGCGCGAGAAAGACCGGTTTCGAGCAGGAGCAGCGCGGAATTCCT
TTATCGGTGTGCGCGCGCTTATCTCGACCGAGCCGCGCCTGTGCCGAAACGGTATCGCCGTATCGACAGTAACCGCGAGCTTGGATGAAGTCAGAAACAGCATAGAAAAAGTGTGGACCG
ACATTTCCGCTGT

SEQ ID 2550

SECRET 2330
MKPQFITTLDGIDGACKSTNLAVIKAWFERRGLPVLPFTREPGGTVPVGRALREILLNPETKAGLRAETLLMFAARMQHIEEVLPAISDGIHVVSDFRTPDATFAYQGGGRGMPSEDIKILEH
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TTTACGGTTCGGCTGTCGGTCAGTCCGTCGTTGCCAAAAATCCGCGCTTAATCAAGAAATCGATGAGTGAATAGCGGTATCTTGGACTGCATTGTCAGGGAATCGCGGACATCATC
TGCCCGAGTTTACGGAAGAGTTAGCGGCATCATCTGCGCGGTATAGTGGAT

SEQ ID 2566

VDMLKLTLLPFAALALCANAPAPGDASLARWLDTONFDRDIEKNMIEGPNAGFKPYADKALAEHPEAKKDQAAEFNRYRENVLKDLITPEVKQAVRNTLLKNAREITYTQERIDGMLA
FYGSPVQGSVAKNPRLIKKSMSEIAVSWTALSGKILARHHLPEFTTELRIICGGIIVD

SEQ ID 2567

TTGCCCTGCGCTTGCCTACTATTGTGACGGTCTGCGGCTTCCGCGCTTGTCTGATTAAATTAAATCCACTATACCGCCGAGATGATGCGCGG

SEQ ID 2568

LPRLAVLFVRSAAFPFPCPLNLHIHYTAADDAP

SEQ ID 2569

ATGGAAAAAATCTTTAGACATCTCGTCTGCCCGCTTACCAAGGCAGGCTGGAATATCATCAGGACAAACAGGAATTGTGGAGCCGTCAGGCGAAGCTTGCCTATCCGATTAAAGACG
GCATTCCTTATATGCTGGAACCAAGACGAGCGTGTAGCGAAGAGGAACCTCAAGCA

SEQ ID 2570

MEKKFLDILVCFVTKGRLEYHQDQELWSRQAKLAYPIKDGIPYHLENARALSEEELKA

SEQ ID 2571

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GCAAGCCGCGCGCTCGTCGTCGCCACCGATCATCCGACATTCAGACGGCTGTTCAGGCGCACGGTATCGAAGTCGTCATGACTTCAAACCGGCACGAAAGCGGCACGACGCGCTTGC
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GTCCAAATGGCGACCGCGGCCCAATTCACGATTTCGACGAATTCAGTAATCCCAATGCCGTCAAAGTCGTCTCGACAAAAACGGCAACGCCATCTACTTCAGCCGTGCCCGGATTTC
CCTATCCGCGGATGCGATGCGTGTCCGGAACCGGAAATGCCGTCTGAAACCGCGCTCTACGCCATATCGGCATTATCGCTACCGCGTCCGCTTCTGCAACGCTATGCCGAAATGAG
CGTCTCGCGCTGGAACCATCGAATCGTGGAACTCGCGCTCTGTGGCACGGCTACCCCATCGCGCTGAAACCGCCAAAGAGCCCGCGCGGTGTGGATACGAGGAAGAT
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SEQ ID 2572

MTEFVLLIPLRLDSSRLPGKALADHKGPMVVRVAEQAAKSKAARVVVATDHPDICTACQAHGIEVMTSNRHESGTTTLAEEAAALKLPHLIVNVQDEPLIAPELIDRTAEVLVERN
VQMATAGHELHDFDELMNPNAVVLKNGNAIYF SRAPIPYPRDAMRAGKREMPSETAVLRHIGIYAYRVGFLQRYAEMSVSPLETIESLEQLRVLWNGYPIAVETAKEAPAAGVDVQED
LDRVRAVFQTV

SEQ ID 2573

ATGCAGCAACATATTGAAAGTGGCAACACTTGAGCCGTGAAGAACAGAAATCCTTGCCGAAGTATGGGGTCTCGTGC AAAACGATGATCAGGAGGTTCACTATGAAATGCTCAAATTGA
ACGCACCTGATGAAGTCAGCGGTGAATTTTGGTTGAGAAATGGCAGAAACACTCAGCACCTTGC CGCCCAATCGTTCCCTCGACCTTAGAATGAACGGCGCAGGCTGTGCGACCGCGGTATC
CATCTTTCCGTCATGATTGAAGACAATCCGACATACCGCAGCTTTGGCGG

SEQ ID 2574

MQQHIKQWHL SREEQKILAEVWGLVQNDQEVHYEMLKLNAPDEVSGEFPFRMAETLSTLFPNRSLLDRMNGGRLSTAVSILSVMIEDNPDIPQLHA

SEQ ID 2575

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ATTCTAAGTCTGAGGGAACGATTGGGCGCGGCTGACTGACTGTTCTGCCATTCTGAACCAAAATTCACCGCTGACTTTCATCAGGTGCGTTCAATTTGAGCATTTTCATAGTGAACCTCT
GATCATCGTTTTCACGAGACCCCATACTTCGCAAGGATTTTCTGTTCTTCACGGCTCAAGTGTGCCACTTTTCAATATGTTGCTGCATATCTTTTCCCTT

SEQ ID 2576

VSVYQIIEGGNPLRPLRYVGI VFNHDKDGYGGRQPAAVHSKVEGTIGRQGAECFCHSEPKFTADFI RCVQFEHFIVNLLIIVLHETPFYFKDFLFFTAQVLEPLFNMILLHIFSL

SEQ ID 2577

TTGATATTATGCTTACCATCGTTTATATACGCCGGAATCCCCCGAACACGGGCAACATCATCCGCTGTGCGCAATACCGCGCGGATTTGCACCTTTGTCAAACCGCTCGGCTTCC
CATTTGATTCCGCCAAATGAAACGCGCGGCTGACTACCAAGATTCGCGAGCTGACGGTGCACGAAACTTCGAGACTGCTCAAGTCGCTGGCAGGCGGACGTATTTTCGCCCT
GACCAACAAAGGCACGCGCGCGCGGATGAAACCGGCTTCAAAGGCGGAGCTTTTACTGTGTTGGCGCGGAAACGCGCGGCTGCTCGCGACATCTCGACAGCTGCCCGCGCGCA
AAATTCGCGCTGCGGATGCGCGCGCGGAGATGAACTTTTCAACACCGTCTCCGTGATTCTTTTGAAGCGTGGCGGCAACAGGTACGCGAGGCGCGCTT

SEQ ID 2578

LIFMLTIVLYQPEIPPNTGNIIRLCANTGADLHLVPLGFLDSAKMKRAGLDYHEFASLTVHENFDCLKSLAGRRIPALTTKGTARPDSTAFQKGVLLFGPETRGLPADILDSLPAAQ
KIRLPMPGRSRMNLSTVSVILFEAWRQHYAGGV

SEQ ID 2579

ATGACCGACATCTCATGACGATACCGCCACCGAAGCGTCCGACCCGTGATACGGGCATTCCCTTCGTGCCGTTTCCCAACCGCCGAAACAGGCAGTTACCTCCTGTGTAACAG
ATACCGTCAGCTCAGGCTTGTCCGGGAAAAAGCAACGTCATCGTCGATTTTACTTCCGGCGCGGCACAAATACCGCGCACAAAAGCGGAGGAGAACTCATCGCCAAAGCGGTCAACCA
CACC CGCACCCACCGCTATGGGATGCAACCGCAGGATTTGGGCGCGACAGCTTCGTCCTCGCTCGCTCGGACTGACCGTTACCGCTTCGAGCAACATCCCGCGCTCGCTGCTGCTT
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CTGCCCTACGAGCGGACAAGGA

SEQ ID 2580

MTDILIDTATFAVRTLIRAFPLVPVSPPEQGSYLLAEHDTVSLRLVGEKSNVIVDTSGAAQYRRRTKGGELIAKAVNHTAHTVMDATAGLGRDSFVLASLGLTVAFAEQHPAYACIL
SDGIRRALINPETQDTAARINLHFGNAAEQMPALVKTPQKPDIVYLDPMYPERKSAVVKEMAYFHLVGEAQDEVLLHTARQTAKKRVVVRPRLGEHLAQAPAYQYTGKSTRFDVY
LPYGADRG

SEQ ID 2581

TTGGTACACGGACAAAAGCCCGTCCGACGCTTGGTACACAGCCGACAAAAGCGGACAGCAACGAGGAGGAATACCTGACCAAAGCCCTGTGCAAAACCTGCTGTAACATTGG
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SEQ ID 2582

LVHGKARADGLVQPPDKAAEANEVEYITKALSQNLSTLDAALARFPEDAWFQRIKQDAQKHFA

SEQ ID 2583

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SEQ ID 2584

MEKSLLEDVAVRNISIQEKKCLIGYNQKSYFISED

SEQ ID 2585

TTGAACGAGGCAAAAATAAACGGCAACATCTCGGATTAACAAAATTTCAGAATCAAGACAGGGCAATACCATACCGGGTTTGCGCCAACCCGCTATAAAATTGCA

SEQ ID 2586

LNEAKINGHLGLTKFRIKTGQYHTGFAPTRYKIA

SEQ ID 2587

TGGCTCGTGTCAAACGGCGGCTCTGATCTCGGCGGTTTCGTTTGGCGATTTCGCTATCCGTACCGCAAAATGTTATAC TGGGAAAAAATCACCAGATTGTATTTTACGGCGTATTTGGCGGA
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 AGATTGAAAACAAATCGCGGCAACGAGGCTGCCGCGTCCGTTGTTGGTCAAAGAGTTAAAGGATGCCGTGCGC

SEQ ID 2588

SEQ ID 2386
LPRSGSGSLRGLFCFLPYSPIRTANVLKCHRLRYTAYLPIGWKQRMSRIHQAFALDGGKALIPYIAGVDPDTRTTLALMHGHWASGADILELGVFPSPDMADGPVQRAAERLANGIS
LRDVLDDVVRKFRFETDQTPVVLGMYLNIPIHKMGYREFAQEAAKAGVDGVLTVDSPETIDSLYRELKQNEVDCIFLIAPTITTEDRIKTI AELAGGFPVYVSLKGVGTGAASLDTDEVSRKIE
YLRQYIDIPIGVCGFISNAESARKIGRVAAIIVGSRIVKEIENNAGNEAAAVGALVKELKDAVR

SEQ ID 2589

TTGTCCATGAGCTGGT TAGATAAAATCTGCCACC CAAATCAAGAAATCGTGGGAAAGACGGTGCTTCCAATGTTC CGAGGGTTTGTGGCGCAAATGCCCGTCTTGTTCGGCAACCGTTT
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TGTGCCGTACAGGACAAAGTTTCGCCACC

SEQ ID 2590

LESHWLDKILPPKIKNRKGDGASNVPEGLMRRKPCSCSATVYSTELQONNOVCPKCNHNPLSARQLNLLLDEEGREEVAGNVKPTDPLFKDKSKKYPRDLISAARKLTGEDDALVVMKGM
NGLPLVVAAFEPRFTIGGSMGSSVGERFVQGVRRVADNCPFVCAVASSGGARMQEGVNSLMQMTTSAALHLLTEKRLPPLSVLTDPTMGVVSASFAGLDVVLAEPNALIGFAGPRVIEQT
VRETLPEGFORAEFLLEKGAIDQIVDRDMKRRISDLITLLCROQKVSAT

SEQ ID 2591

TTGGAGAAACCTTATGCGCCGCGCCATCCTCTGTGATTCTGACCCTGACTGTGCGCAGCTCCCTTGTCCGCGGGCTTCAGCCAAAAAGACACGCGGATCAACACCCGCTACCGCGAAACGCGCG
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CTGTCTCGACAGCTGCAAAATTTATGCCCGCGCCGACGGCAGCATCCGCTACATTCTCAATATCCGCTCCGACAAAGGCTACGACAACTGACTGCCAAGGCATCTCTGCGCCGCTCC
TCCATCGGGTTTCGCAACGGCAAACTTCTCTCACAAGTATTCGGATACGGCGATACGGTCAACAGCCGCTGGATACAGCCCGGAAACGGATGGAAACCATATGGCGGCACACTTG
GGCGCAACGACGCATTGCGCGCGCTCTGTATCAGGCATTTCTGCGAGGCGCGCTACGTCACGACAGCGCAAGGTTTGGTACAAACGCTGAAAGAACGTCGCGGACGCTATGCCCGCTGCAT
GAAGCCCGCAGCAATA

SEQ ID 2592

LEKIMRRRAILLIILTVGTSLAAGFSQKDTINTRYRETPEEAAREFKEHTAEZLPLLPDAHSDGMFDIVDVENYKGQPKILLDSIQIMPAPDGSIKTYILNIRSDKGYDNLTAEGTFCARS
STGFCNFKLSSYKVFVGYGDTNSENKTOPRNEAWPKIGTGLGRNDALRAVLVYQAFCEGGVPADTQGLVORLKERAGRYAPSMKPHDK

SEQ ID 2593

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ACCGGATCGGAGGAGCGGGCGCAGAAATATGCTTCGGCAGTCAGGTGTGCTGAGCCTTTGTGCGAGCGGATATTGAGAATGTAGCGGATGCTGCCGTTCGGCGCGCGGCATAAATTCGAGGCT
GTGCGAGCAGGAATTTTCGGCTGTTCGGCTGAATTTTATCCACATAAATGTCAAACCGCCGCTCCGAGTGCGCATCCGGCAGAGGCGGCAGTTTCGGCGGTATGTTCTTTAAATTCGCGGCG
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GTCTTCCTCAAAATGAAATCCGCTTATTTTATGTTTGGCGGGAAGGGCTGCAAGCAATCGGGGTATAATCTGACC

SEQ ID 2594

SEQ ID: 2594

VRLLHRRGIASCTFFQALYQTLRVGGYAAALAECLIQDGAQCVPKCAAYRFPFGVSGLYPAADVRIAVSEYFVGKGFVAVAEPPDGGAGAEYAFGSQVVAFPVGADIENTVAADAAGRGHNLQA
VEODFRLPAVTFIHINVLKPAVRVRIGORRPPGGMFFKFAAGGFFGFRFAVAGVDRRVFLAEAGGKGRADSGOGNQDKGAHHKFLQIENGFLWFGGKGCKQSGYNYLT

SEQ ID 2595

SEQ ID 2595
ATGAACAGCGAAACTTTAGACGCTAACCGGATTGAAATGTCGCCCTGCCGATTTTGCGGGCAAAAAAGGCTTTGGCGCAAAATGCCGCGAGGGCGAGGTTATTGACCGTTCCTGGCGACCGACGGCG
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SEQ ID 2596

MSSETI.DVTGLKCPILPIRAKKALAO MROGEVLTVLATDGGAPGDFEAFRCROTGHVLLDSSEODGVPTLVVVKHK

SEQ ID 2597

SEQ ID 2597
TTGAAGCGTGGCGGCAACACGGTTACGCGAGGCGCGTTTGAACGCGAGGTTCAATGCCGTCGAAAAACCGTTCCGGACACATTCCGAACCGCTGCCCGACGCGTGGCGGGTTTCGGAAACGCGTCCGTAGGGCA

SEQ ID 2598

SEQ ID 2598
LKRGGNTVTOAAFERRFMPSENRSDTFRATAAACGGSEVRRA

SEQ ID 2599

SEQ ID 2599

TTGATGTTATTGCTGTGCGCAATTGTGCTTGTGCTGCTGTAATGCCCAAAACCGCGCAATCCGGTGTCAGGCATCAGGATTTTGCACGCGTAGCCGTCGATTGTGTTTCGGAGTGCCCTGCGTCC
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GTGACGCTTGAACGCGATGGCGCGCAATTATTATTGTGAGCCTGACGCGCGACAGTTGTCACTGTGAAGACCGAGCGGGCAGACAGTCCCGCGCTTTTGAACATTTCTCAGGGCTTGTCCGA
CAGCGCCCGCAAAATGCCAATATA

SEQ ID 2600

SEQ ID 2600
LMLLSAFVLAACNAQNRQSGVRHQDFARVAVDLFRSACVLTQGSFEFVSKFAAVGHFVVGKEDLSRLPPAVAREPDVQALWTLERDGGITYLSLTRDSCSVKAERADSAALLEHFSGLVR
OPPEKNMI

SEQ ID 2601

TTGACTATATATGCGCATTTTTCGGCGGCTGTCGACAAAGCCCTGAGAAATGTTCAAAAGCGCGGCACTGTCTGCCGCTCGGCTTTCACACTGCAACTGTGCGCGGTCAGGCTCAAATA
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TTGGAACCGGTTGGAACCTACCTTGAAGTACGACGCGGCACTCCGAAACAAATCGAGCGTACGCGTGCAAAATCTGATGCGGTACACCGGATTGCGGTTTGGGCAATACACGACG
CAAGCACAATTCGACAGCAATAACATCAATCAGGACATCCGCAATTCAGACGCAATTTATTTGTGCT

SEQ ID 2602

LTIYWHFSAVGGQALRNVPKARHCLPARLSHCWCRASGNNKCRHRVQASTTTPVHRVLQORADGTGLPFRQGNVQRQTWKIPVKNYLSGRRHSETRRLRVQNPDAVHRIAGFGHYTQ
QAQMPATTSIRTSAPQTAFICA

SEQ ID 2603

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GATTTTCGCGATGCCAACGCGTTTGTCCGATGAACAGGATTGACAGCGCGCTGTTCGCGCTTATGCCCGCAGCTTGAAAGGCAAAATGCGGAAAGCGCGGATAAGTGGGAAAAGATA
CGGCGCTTATCTTTGGTGTCCGACAAAGTCGCAACCGCGGATTGCTCCGATGCTTTGTCAAAATACGGTGGCGGGGCTTTTGTGAAGCGCGGTTTCAGCAATGCGTACTGCGCCCA
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CCAACCGGATTGAGAAAGTGGGCGAATATTAAGCGGTATCTGCGAACCGTTTGTGCTGATTACGCGCGGATTGACGATGCACTACTGCTCTATTGATTTTAAT

SEQ ID 2604

LYGSRRLPCAQTADGAQKTAAYKQDPKVTYHLTRPAGFSDCQRVCPDETGFDRRLFRPYARSLKQMAKARISGKRYRRLSLVSAQVGNRPVPHVCQNTVAGVFFEARPOQCLLPA
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SEQ ID 2605

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TCAAGAAAACAGCTTTTACCTGCGGATTGCGCTTAAAAAACAAACAGCGACGC

SEQ ID 2606

MAYSADLRNKAHLNHSGLTKIRTRRAADGTNGTPIRPAHLHRESFPLSRGGATPYRFLIRYITDNAKTPAKPQRLTCQETRTCTGALKNKQAA

SEQ ID 2607

GTGACGCGACGCTTTGAAACAGGCAAAATCAGTATGCTTGGCGGAATCGGCGAGCCCTGAAGAAACCGTATTGACCGCACAACCGCGGATTCCCGGATTACCGGTACAGGCACTAT
TGAACCTAACGCAACGCTTCCCATACGGAACCCCTAATCTCCCT

SEQ ID 2608

VQAPPETRIQISYANRESGSPRETVLTAQTADSPDLVQAVLNLTHRSNGKPLILP

SEQ ID 2609

TTGTCAATCCACGGAAGTGGGAATCCGATTCGTTTCACTTTAGTTGTTTCAAGTTTCAGGCACTTCCAAACCGTCATTCCCGCGAAGTGGGAATCCGGA

SEQ ID 2610

LSFPRKWSDFSFSFCFQVSGNFQTVIPAKVGIRK

SEQ ID 2611

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ACACATCGGTTTCTCCATCCGCGCGGTTGATTGGGTGGGATGACTATTTGCGAGCCCGCGCTGCAAAAGCTGATCGACATCGCACTCGAGCGCAATACCACTTTGCTACAGCGGT
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GCAACCTTGAATTAACCGTCCGATACCCGAAGACTTCCCGCGCGGTTTTCGCTTGGCAAGCAGTTTGTGTGAAAACCTGCGTGGCGGTTTGAATTCGGAATTTGCTCGAAGCTTCCG
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SEQ ID 2612

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SYNVLGAASYELDLFGRVRSSEALQGYFASVANRDAHLISLIATVAKAYPNERYAEKAMSLAQRLKTRREETYKLSERYKAGVISAVALRQOEALIESAKADYAHARSREARNAL
ATLINRPIPEDLPAGLPDLKQFFVEKLPAGLSSEVLLDRDIRAAEHALKQANANIGAARAAPPFSIRLTVSGVTGSVELGGLFRSGTGWAFAPSIITLPIFTWGTNKANLDVAKLRQQAQ
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SEQ ID 2613

TTGTTCTTTTAGATTTTTGGTTTCCAGACGGCATGCCGACTTATGCGCTGCAAGTACGGGAGAAATAGGGGTTTCCCGTTATGGGAACGGTGGCTAGGTTCAATACCTGCTGTAC
GGGTAATCCGGGAATCGCGGTTTGTGCGGTCAATACGTTTCTTCAGGCTGCGCGATTCCCGCCAGGCATAGC

SEQ ID 2614

LFLFRFLVSRHADFPSEVRGELGVSRVNGALGSLPVRVNPGRFRVRSIRFLQCCPIPARHS

SEQ ID 2615

ATGCAACCTTGACCATCATCGACCCGACGATATGCACCTGCACTGCGCGACGCGCAGCGCTCAAAGCGTTGCCCTTATACCGCCCGCAGATGGGCGCGCGCTCATCATGCCCA
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CGCAAGTGGCGAATCTCAAAGTGGTTCGAACACATCAACCGCGGAAGCGCGCGCTTGTGGAAGCGCGGACCAAGTTGCGCGCCAGCTTACCGCGCAACACCTCTCTGCTCAA
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SEQ ID 2616

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LEZHAQKQILFVHGEVVDPEIDIFDREAAPFGRVMKPVLAQVPMKVVFEHITTAEARLVLGAGDNVAATVTPQHLLNRRNDLLVGGVRPHHFCPLVLRKRETHRQALVAATVGEKAKHP
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SEQ ID 2617

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SEQ ID 2618

LTVQSLHRRPADFAARHRDKFAVAVRDACNGLALFDKGNRVGVFRNAVPECAVFRGEGFEVQRAFFKHFVGLKDSGHRAEHTGAAAGVFFGFGVRRVGAEEFVRLLAGNGDQC
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IGGRACGVFEEDDAGGFGFAHEFGRGLVQVQRHQRKRAAFQRRHNRARFVGRVGYADDWRFEVGHDDGAPHLAGGIRNGFERVAVAVQVQVHIVSGDDGQGLHGCSPDLDFWPDGMP
TLCRLKSGEN

SEQ ID 2619

ATGAAACAGCGCGCGCGCTTCGCCGAGCTTCGCGTACAGCGCTTTACCAATCCCTTATCAACCGCACCGCGCGCGCGGAAATGCTAAACATCCGCGAATGTCGCGACTTTGCCA
AAGCGGACGAAGAATGTTCAACAACCTTCTTCGCGCACAAACCAATGACGCGGACTACATCCAAACAAATCCGCGCGCTGCTCGACAGGAGCAAAAGACCTCAACCCCATCGAAG
CGCGCTTTGCTGACCGCTTCGCGCAGGCTTCGCTATGCGCGCAACCGCTTACCGCGCTATTCACGAAGCCATCGAAGTTACCAAACTTCGCGCGCAGGAGCGGCAAAATTC
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SEQ ID 2620

MKTARRRSRELAVQAVYQSLINRTAAPEIAKNIREMSDFAKADELFNKLFFGTQTNADYIQKIRPLLRDEKOLNPIERAVLLTACHELSAMPETPYVPIINBAIEVTKTTCGTDGKHF
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SEQ ID 2621

TTGAACGGTCAAGCAAAATGCGCTGAAAGGTTTCAGACGGCATTGTGTATTTCCGATTTCGAGTTTCGAGTATCAACGCGCTTTGGGCTCGTCTGGCGGATTTGGCGCGGAGT
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AGGCGGTGAGCAAAACGCGCGCTTCGATGGGTTGAGGTCTTTTCGCTCCCTGTCGAGCAGCGCGCGGATTTTTCGATGTAGTCCGCTGCATTTGTTGTGCGCAAGAGAGTTTGT
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ATCGGATGTTG

SEQ ID 2622

LNGQAKRLKGQTAFFVYPIRIFRVSTAFGLVMADLGGFEVDADEFVVRRAEAGFGNDFGVNDGVRGHSGLVAGGQNGAFDGVVEVFPVVEQRAFLDVVRCIGLCAEEFV
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IGML

SEQ ID 2623

ATGCGCTGGAACGGAAGGGCGCATCGGTGTACGCCCTGTTGTTATCTTCGCTTCAAACTGTTCTTCGAGCAGAAGGTTGACGAGGTTGGCGCATTTACGCGGACTTTGGCGGCA
TCCGAGGCTTTTCTCAATCCGTTCAATTCGCTGCGCTGTTTCGCTGGTCAGGACGCGTTGGCAATCGGATGTTGTAGTTCGAGTGCAGCGCGCGGATCCCTGCGCGGATTCGT
TGGCAACGAGCTCGAATGTAGGTTTCGCGCAGGATGACGACCGCGATGGAATCAGTGCCTCAAAATTTTCGGAAGAGGCAAGGTTTCATCAGCGGATGGGATTTCAAGCGCGCGG
TACGCTGGCGAGCGGTGATGTTTCGCTGCTACGCCAATTCCTTGGAGGTCGCGCGCAGAGCTTTGAGCATTTGCGCTGCGGATTTGCTGTTGAGCGCTGCTGATGATGCGG
AGGTGTTTCGCGTTCGAGGTTGGGGCGGATGTTTCATTTGGGTGCTTTGTTATTCGCGGTTTCGGAATGCGCTTCGAGGTTTCAGTCTTCGCGCTGCGAGTTCGCAACGCTTCGAAT
GTGCGCTTTCGCAAGCTCCACGCGCTGCTTCGCGTGGGAAAGCAGTGCAGCGGTTTCAGGTTGTTTTCG

SEQ ID 2624

MPSETERAHRCTPCLLFFVFKLFPEQKDEVGAFYGDGFGIRGFFSNPFLNLRVVGQDGVGNRNVVBCDAADPCAGFVGNQLEMVGFATDDADGNQVFPGRGKVHQRDGFKRAG
YGGDGVFVCAQFLGAAADFEHLAADFVGEACLYDADADEVFAVEVGDDVHVVSFGRGFGNPSBGFSLAAASRQRFGHCRRLQAPTCLRLVGRKAVRFPQWFW

SEQ ID 2625

TTGCCGACTGGCAGCGCAAGACTGAAACCTTCAGACGGCATTCCGAAACCCGAAATACCAAGGACACCCAATGAACACCATCGCCCAACCTCGAAGGCAAAACCTTCGATCGGCA
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TGAAATCCCATCGCGCTGATGAATTTGCTCTTCGCAAAATTTGACGCACTGATTGCCATCGCGCTGCTATCCGTCGCGGAAACCTACCATTTTCGAGCTGGTTGCCAAGCAATCCGCG
GCAGGATCGCGCGCTGCACTGACTACAACATCCGATTCGCAACCGCTCTGACACCGGAAACGACGCGCAGGCAATTGAACGGAATTGGAGAAAAGCTTCGGATCGCGCGCAAG
TCGCGTGAATCGCGCAACCTTCGCAACCTTCGCTCGAAGAACAGTTTGAAGACGAAGA

SEQ ID 2626

LPTGSRKTEPFRHSETPNTKGHPMTIAPNLDGKHLRIGIVQARFTNEIGSQMLKVCCTRLQELGVADENITVATVPGALETPIALMNFASSEKFDALIAIGVIRGETYHPELVANESG
AGIGRVALDYNIPIANAULTTENDAQAIERIGEKASDAARKVAVECANLWNLLEEQFEDER

SEQ ID 2627

ATGAAGCATTTGCAACAAGCACTTTCCTCGGCACTTCGACGCTGCAATCGCCACCAACACCGCTCGCAAAACAAACCGCGCGCTTCCTTTACCGGAAAGCCCGCTTTTGAAGACG
ACAGCGCTGCGCTTTCCTACAGCGCGCAGCAACCGACGAATACACCGACGACCCGCAACCTTCAGCATGTCAGCTTCGCGGACATCAACAAACCAACCTGAAACCGCGCGCACTGCT
TTCCCAACCGAAGGCGCGCTGGGAGCTTCGCAAGACGCGACATTCCAACCGTTGCGGACTGCGCGCAAGC

SEQ ID 2628

MNAFAQALSSALDRCIATNTVAKQNRPVGLYREAPVFENDSGWRFFSGDETDEYTDPDFNSTVSLADITKTNPETALLSQPEGSANWELADGTFQTVADWQPDQ

SEQ ID 2629

TTGGAAAGCAGTTCGCGCGTTTCAGGTTGGTTTGTGATGTCGCGAGGCTGACGATGCTGAAGTTGTCGCGGTCGTCGCTTATTCGCTGCGCTTCGCGCGCTGAAGAAACCGGAC
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CGTTTATTCGGGGAATACGTTGGGGGGGGGAACTTGCAGATTTACACGATTCGCCGCTTGTCCGAGACGGCGCGGTTTGGTGTACAAATGTGCCCGTTTCAGCCTTAAGGTGT
FTCTGTATTTTGGAGTATGGAACGCAATTCGGGCTGTTTTTTCGGGAAGACGG

SEQ ID 2630

LKGQCGGFRVGFVDGEADDAEVVGVGVFVAAEETPAAVVFNKGGFAVKADGPFVLPDGVGGDAAVECRGKCLCKVHCGNTLGGGKLADFTTIPALSADGGGLVVQCAPFAALRC
FCIFGWKRIKRAVFCGR

SEQ ID 2631

TTGACTTTAACCCGAAAAACCTTTTCTCTCTACCGCGCGGTTCCGACACACTCCCTTCAGACGGCATCCGCGGACGAGTGGTCAAGCCGAAAACTGCAGCCTCCGCCAACCGCA
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GCCGCGCAAAATTTGGGCTTTGTTCAGCAAGGGACGGCACAGTCAAAATCGAACAAATCGTCCGCGGCAATCCGACCGGTTGCCGAAAAACAAAGACATCTTTATCGACTTGAATCTTT
TCGTACGGAACAGCAAGCACAAGCTTATCTGAACCAAGCGCGCAAAATTTCCGCGCTTCGTATCAAGCCGCAACCTCTCGGTTGAAAAACCGCGTTACGAATACGTTGTCAAAATGGG
CCGCTTTCGCTCGCAGGAACGCGCGCGCAAGCGCAAGCGCAGGACCGGCTATGTTTCGGGCGGTACTGACCTCCGCT

SEQ ID 2632

LFLTRKTLFLTAAPGTHSLQTASADAVVKPELHASANRSYKVAEPTQTGNASWYGGFRPHGRKTSGGDRYDMNAFTAARKTLPIPSHVRTNTKNGSVIVRVNDRGPPHGNRIIDVSKA
AAQKLGPFVSGTAHVKIIEQIVPGQSAFVAENKDIIFIDLKSPGTEHAQAYLNOAQNFAASSSPNLSEVKRRYEVVKGPFASQERAAEAQAQGMVRAVLPSG

SEQ ID 2633

TTGCCGTCTTATGCAAAACGAGAAACCGGTTTTTGCCTTTCGACTGTTTTGGATAAGTCATCACACCTTAAAGTTTGTCTATCCCAAGGAGTGGGAATCCGATTCTGTTAGTTTGTG
TTTTCAAGTTTCAGGCAACTTCCAAACCGCTATTCGCCGAAAGTGGGAATCCGGAATGAAAGGCAACAGGAATTTATCGTAAATGAC

SEQ ID 2634

LPFLCKRETGFCVSTVLDKSSHLKVCHSHSGNPIRSVLVVPKQATSKPSFPRKWESGNERQQEFIVND

SEQ ID 2635

ATGCGTTTCATCATCCAAAAATACAGAAACACCTTAAGGCTGCAACCGCGCACATTGTACCAACCAACCGCGCGTCTGCCGACAACCGGGAATCGTGTAAATCCGCAAGTTTCC
CCCCCCCCAACGTATTCGCCGA

SEQ ID 2636

MRFFTFPIQKHLKAANGAHCTTKPPPSADNAGIVVKSASFPPPNVFPQ

SEQ ID 2637

TTGCGGAAGACCGTAATGAAAGACGATGTTTTGAAACCGCAGGCACATCTGCGATACAGAAAAAGTTAGGCTACCGGTTCCCGGATATGTCGCTTTTGGCGCGGCTTTGACCCACAGGA
GCCATCATGCGAAGCACAAACGAGGTTTCGAGTTTGTGCGGATTCGATTTTGAATATACGGTGGCGCGGATGCTGTTTGAACGCGTTTCCGAAGTTGACCGAGGGCGAGTTGTGCGCGTT
GAGGCGAGTCTGCTCAATGAGGCGCTGCTGCGGAAATGCGCGGAAATGAATGTCGCGGACGCTGCTGTTTGGGGCGGCGAGTTGAAGAGCAGCGCTTACGACGCGCTTCGATA
CTGGCGGACCGATGAGGCGGATGTTTCCCGCGTCACTTCGATGCCGATTTCAACACCGCGGAAAGAGTGGTGGCGCATTTTGTTCGAGAAGCGCTCCGCGCGCGCGATTTCCAAATC
AGGCAAAAGACGCGAAACTGCTTTTCAGGAGGCGTTTCAGGCGCGCGCTTTCGCTTTCGCGAAATACCGCATCGAAGAGCAATCGGCCATGCCGACGACGATGTTTGTCAATTTCTG
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AAGAAA

SEQ ID 2638

LRRFTVMKDDVLRKQHTAIQKKLGYAFRDMSLRLRALTHRSHEAKHNERFEFVGDSILNYTVARMLFADFPKLTGELSLRLASLVNKGVLAEAAEMNVGDGLYLGAELKSSGFRFRPSI
LADAMEAMFAAVSFDAFNTAEKVVRHLFAERVRRADFQNAQDKGTALQELQARRFALPKYRIEBQIGHADDSMFVISCDELGLGFPVCRAGKTSRKAABQEAKEALKWLEELPLKRI
K

SEQ ID 2639

GTGGATATGAAGCAATATGGATATGAAACCTTCTTGCAGGGGAACGCGCGCGCGGATACCGTTGCGGCTTCGTGGCGATTGTGCGTCTGGAAGCTGGGCAATCAACGCTGA
TGAACCATCTCATCGGTGAGAAATCAGTATTACAGCAAAAGCGCAGCAGCGCAACCGCGTAACGGGATTTATACCGAGATACCGCGCAGTTCTGTTTGTGCGATACCGCGG
CTTTCAAACCGACCCGCAACCGCTCAACGACAGGCTGAATCAAAATGTTACCGAGGCGCTCGCGCGTGGATGTGTTGTTTCTGCTGCGAGGCGATGCGCTTACCGATGCGCG
CGCGCTGTTGAAACAACTGCCAAGCACACGCGGTCATTTAGTGATCAACAAATCGACAAGGACAAGGCGAAGAGCCGTTACCGCTGGAGGCGTTTGTTCGCCAAGTGGCGCGG
AATTTGAATTTGCGCGCGCGGAGGCGGTCAGTGCAGAACAGGTTTCGCGATTGCCAACCTGTTGAGACTGCTCAAGCCGATCTGCCGAAAGCTGACCGATGATTCGCGAAGACATGTT
TACGGACAATTCGCGCGCTTTTTCGCGATGGAATCGTGCCTGAAAAACTCTTCGCGTATTTGGCGGAGGAGCTGCCCTTATGCGATGAACGTCGAAGTGGAGCAGTTTGAAGAGGAGAC
GTTTGAACCGCATCTACATCGCGTTTTCGTGCAAAAGAAAGCAAAAGCGGATTTGATCGGTAAGGCGGGGAGCGTTTGAAAAAAATTTCCACCGAAGCGCGCTGGATATGAAA
AACTGTTTGAATACAAAGTATTTTGAAGTCTGGGTCAAAGTCAAATCCGTTGGCGACAGCATTCGCTTCTGCGGAGCTGGGTTG

SEQ ID 2640

VDMKANMDETFLAGERAAGGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTTNRNVTGIYTDTAQFVFPDTPGFQDHRNALNDRLAQVTEALGGVDVVVVEANRLTDAD
RVVLKQLPKHTFVILVINKIDKRAKDRYALFAFVQVRAEFPAABAVSAHGLRLIANLLELLKPYLPESVPMYPEDMVTDKSARFLAMEIVREKLFVYLGBELPYAMNVEBQFEBG
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SEQ ID 2641

TTGCCCGCGCGGACCAAAAGAGGCGGACGCTGATTTTCAGCGGCAAAACCGCGGGGATACAGGCAAAACCGCTTACCGGAGTAAAAACCGCAATTTATGAAGTCGCTCGCGCGG
GGTTACGAAAGACGGTTGGGAAGGGCTGCTAATCCGAACCGCAAGGCGGGGAAACCGCGCGCGGATATTCGCGAGCGGGTGAATACCGCATAGACCGTTTGGACGCGTT
CCGCGACATACGATATTAACGCAAGACACAGAGCCATTTTCTTAGTAGAGGGCGAGATACACTCAAGCCGTGGCAAAATTCGCGGCTACGGGATATATTTGAACCGCGAGCTC
AACCGCTGGTAAAGAACGCTATTGAACAAATCAGCCTTTAAGTCTGAAGAAGAGGCGCAGGTCGCGGAGGCGCAGCGCGCGCAAAACCTGTCGCCCAAGCTTACAGCGCGCGG
CGAGGATATTCGCGGATCCGATGGAATTCACGACGCGCTCTTGGCTTCGCGTGGGCTACCGCTTCGCGCGGAGGATATGTCGCGCGCGGTTTGGAGGATACCAACAGCGTTACGA
CATCCCGGATATGACGGAACAGTATTACGTTACGAGGAGGCGGAAAGTTTAGAGACAAGAGCGGGGTGACGACGCGCAGGATTTCCGCGACGCTTGTATTTGTGCGCAATA

SEQ ID 2642

LPRPGTKEADLISDGKSRGIQAKTAYGSKNRQFMKSLGAGFSKDGWEGLLIRTERQGRETRPHGDIADGVEYIDRLDAFRQTYDIKRTTEPFLVGEENTLKPVAKIAGYIYLMRQL
NRWVKERIEQNQPLSAREEAQVREARHENLSAQATTGGGRILPDPMDYRSGSWLAKLGYRFGGRHYVGVFEDTKQRYDIRMTENSIVTRTRRSLETRAGCTPATISATACILCRI

SEQ ID 2643

GTGTACGACGCGGACGATTTCCGCGACGCGTTGATTTTGTGCCGAATATAGAAGAGTGAAGAGGCGATAAAAAATTTGGTCAAGGCGATAGTTTGAATATTTCCCGACCAAAATTTATG
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CAACACGCTGAAGCTGAATTCGCGCGTGTATCTTCCGCTGGACAAATCTCGCGCGCTCGCGCGGACAAACCGTATTTCTACGACAGCAGCGAGCTTTCCACTACCGCGAACAGCACAAAT
GTTTGAATGCTGTTTGAAGTCTGCTGAAACCAATGGAAGAACACCATCTGACTTTGGGCTTCGCTTACGATGCTTCCAAAGCAGTATCCGCGCGGAGACAGCTTTCCCAATATG
CGGCAAGGATTTCCGAATCCACGGGATTCGATGAAAAGAAATCAAGATAAGTACCGTTTGGGTAAAGCCGAGTCTGCAAGGGTTCGCTGCGGCTATATCGAAACCTCGCTTCCGCGAA
ATGCGTGCAGAAAAATCAACGCGACGATATTCACATTTCTTTGAACGACCGTTTTCATTCGCAAAATTT

SEQ ID 2644

YDGDGDFRDGLYFVFNIEBWKDKNLVKGIGLKYSRTKFI DEHRRRRRMLGLLYRYENEKYSNDNADKAVLSFORQGVATDNNTLKLNCVAVPAVDKSCRASADKPKYSYDSSDRFHYRQHN
VLNASPEKSLKNKTKHFLTLGPGYDASKAVSRBPOLSHNAARISESTGDFEKNQDKYRLGKPEVVBGSVCGYIETLRRCRCVPRKTKNSNIPHFPERPFPRQIIF

SEQ ID 2645

TTGAGACGACCGCTTTTTC AATCGGCAAAATATTTTGTATTTACGCTTTGGGCGGCAGGTACGACCGGAAAAAATTCACACGTCGGGAAGAACTCGTCCGACGCGGGCGGTATGCCGACCGTTCGT
GGAACAGCGGCATCGTGTTCAAACCGAACCGGCATTTTTCGGTGCTTACCGCGCCTCCAGCGGCTTCAGAACGCCCTTCCTTCCAAAGAACTTTTCGGGATAGACATTTATCAGCAATTATCC
GAAAGGCTGGCAGCGTCCCGCCTGAAATCGGAAAAGCAGCCAAACCGGGAATTCGGTTTCAGTGGGAAGGGCGATTTCGGCTTTTGGAAATCAGCAGTTTCCGCAACCGTTATACCGAT
ATGATTCGCCGTTCGCCGATCAAAAACCAAAATGCCGGATTCAGCAGGACGATTCAGACAGATTGATATACCGGATATTACAATGCCCAAAATATGTCGCTTCAAGGCATCAACATCTTGG
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ACAATATCGGCAACTACCGCTACGTTACTTCGGGAATCTTGCCGCAAGCTGCGGAAAGCAGCGCAAAACCGGCACGCGCGCAGCAGCAACTATGGAAGGTATGCCGACCGGCGAGGAACCTT
CAGCCTCGCGCTCGAAATGAAGTTT

SEQ ID 2646

LNDRFSDIGKYPDFSLGGRYDRKNFTTSEELVRSGRYADSWNSGIVFKPNRHFVSYSRASSGPTPTSPQELPGIDIIYHDYPKGWRPALKSEKAANREIGLQWKDGFGLBISSPFNRYTD
MIAVADQKTKLPDSAGRLTEIDIRDYNAQMSLQGINILGKTDWNGVYGLKPEGLYTTLAYNRIFKPSVSNRPDLSLSYALDAVQPSRYVLGFGYDQPEBGWGANIMLYSKGNPDEL
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SEQ ID 2647

ATGTCGATAATTCCTTATCGACCGCCCAATTTCGCGGGGTATTTCGATTTCATTATTGTCGGCAGGATTTTCGGCATTAAAGAGCTGCCGGTTTCGCAATATCCGTCGGTTGCCGCC
CGACCATTTACTTTGACGCCAATTATTCGGGTGCGTCGCGCAAGTGATGGAAGGCAGCGTACTTTTCGCGATCGCAACGGAATATGAACGCCGTGGAAGGTTTGACATATATGTCACCTTC
CGCGGATTCGAGCGGCGAGCGGACGGTGCAGCTTGACCTTTACGCCCGATACCGCAGAGAATCTGGCGCAGGTGGAAGTGCAAGAACAGCTTTCCGAAGTATTGAGCAGCGTCCCGGCAACC
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CCGAATTTGCGAATATCGAAGCGGTGGCGGAGTTCGGCTGTTTCGGCGCGCAACGCGCGTTCGCGGATTTTGGGTTCGCTTACGAAGAACTCGAAACTACAAATTTGCTGCTTGGCGATGTCCG
CAGCGCGTTTGTGGCGCGAAGATATCCAAATTTCCGAGGTTTCCATCGGTTGCTTCCCGCTGTGCGCGGACAGAGGTTACGGCTACCGTAACGGCGCAAGGGCAGTTGGGTACGCGAGAA
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CGCGTCTGATTTCCGTGTTCTGTGCTCTGCGCATGTTTCAGCGGGCGCGCGGCAATATTTACAAACAGTTTGCCCTGACGATGGCGTCATCAATGCACTTCTCCGCTTCTTTCGCGCTG
ACCTTACCCCTGCTTTGTGTGCCAATATGTTGAAGACAATPCCGAAAGGGCATACGAAAGAGAAAAAGGTTTCTTCGCGTGTGTTCAACAAGAAATTCGACAGTTTGGACGCGACCGCTAGC
AAGGCGCGGTTGCCAAAGTGCTCGCGTAGACTTTTCGCGATGATGCTTGTCTATATCGGCTGCGGATGCGGTGTTGTGGGCGTTCCTGCTTTATTCGCGCTGCGACTTCGTTCTTCCGACCGAAGA
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CGGCCATACCGCATTCTGTGGCGAAGCGCAACGAGCTGATTCAGAAATATGCTGCGACGCGTTTGTTTGACCCGACGACCGTCCGTGCGCGCGGTTTGAAGAGACTCGCGCAGGTGAAATATC
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CCATCGGCAACGACCTATTTTCGGGGATGTTTGGTCGCGACGATCTTGTCCGTGTTCTTGTTCGCTTTTATGTAGTATGTCGCGCAAAATTCCTTCAAGAAGAACTGCACACGAGCATGAAAT
GGCGCTACAGCATGCATCAAAAGCGGTTAACCAGGTTTCGGACGATAAACATAT

SEQ ID 2648

MAKFPIDRPIFAWVISIFILAAGIFGKISLPVSGYPSVAAPTITLHAIYPGASAOVMEGSVLSVIERNMNGVEGLDYMSTSDSSGSGSVSLTFTPTDENDLAQVEVQNKLSVLSLTLPAT
VQQYGVTVSKARSNPLMTVMLSDDVQSTEDNDYAOQNVVPELQRIEGVGQVRLFGAQRAMRIVWDPKKLQNYNLSFADVGSALSANOIQISAGSISGLPAVRGQTVTATVTAQOQLGTAE
EPGNVILRANTDGSNTYLDKDAKVGLGMEDYSSSTRLNGVNTQMAVLSNSNGNAMATAKAVKERLAVLEKYTPQMGSWKTPYDTSKFVBLSETEKVHIHTLEAMVLVFFVMYLFILQNTRYT
LIPTIVVPISLGGFAPISYMGMSINVLTMFAMILVIGIVVDDAIVVENVERIMAGEGLPKPKATKKAMQISGAVIGITAVLLSVFVPLAMFSGAAGNIYKQFALTMASSTAFSAFLAL
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TVSGFSFGSGSQNMAMGFAILKDWNTERTASGSDAVAGKLTGMMGTLDKGFQISVVPPILELNGSGSLINLQDRNNTGHTALLAKRNGELQKRASGLFPDPTVVRAGGLESPOQLI
DINRAAAAQGISFADIRTALSALSSSYSDPFNQGLQRVWVQADEADMGQPADILLITVPAKSGVAVPLSTLATVSWENGTEGQSVRPNGLYPSMKLSASPATGIVTGAAMAAYQKMWDE
LGGGYSFENGQSRBEAKSGQTLTLLYLGLAAVAVFLVLAALYESWSTPLAVLIVPLGLITGPNKVPINLEGLLGSVSPSFAANDIYPOQGVFTVMGLSAKNAITGLTIFKARDLQAQGSXAV
FAALFAARLRFRPRLTMTSPFSLIGVPLVLTAAAGASSASORAIGTIVTFMGLVGTLLSVPLVFLFYVVVRKPKFETAHEHEMAVRHASKAGITGSDDKQY

SEQ ID 2649

TTGGGTAAGCGGCAATCTTCAAAAGTCGTCTGAAAATCAGAAGTTCTAGATTCCCGTTTTCACGGGAATGACGGAATTCAGACGGCATCTCCGCCCCGTCATTCGCCGCAGGCGGGA
ATCTAGTCGCTTCGGTTTCAGTCATTTACGATAAATTCCTGTTGCCTTTCAATTCGCGGATTCACCATTTTCGCGGGA

SEQ ID 2650

IGSGNLOKSSKSEVLDLRFHGNDGLSDGILPPHRSRAGGNLVRVSVVTYDKFLLPFISGFPLSRE

SEQ ID 2651

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SEQ ID 2652

MGASLIOPCRVSEEGLRVVKDFCQGRKGRCQYRRPMTVPBE

SEQ ID 2653

SEQ ID 2535

ATGCCGCTCTGGAAGCTTGATCTGCACCCCAAAGTCGGACTAAACCGCCAACTGATTAAAGGTGCAGGTTTTTTTGTATTCAATATAAAACAAGATTTCCGGCTCATTCGCCGCCAGGCGGGA
ATTCCGGACATCTCAATGC

SEQ ID 2654

MPSGSLICTPKVGLNRQLIKVQVFLIQYKQDFRRHSRAGNPDIOQ

SEQ ID 2655

GTGGGAATCCGGTTTTTGTAGTTTCAGTCAATTTCCGATAAATTCCTTAGCATTAATGTCGGATTCGCCCTGCGCGGAATGACGGCGAAATCTTGTTTATATTGAATCAAAAAAAC
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SEQ ID 2656

VGIRFFQSFPPINCLSECPDSRLRGNDGGLVYIESKKPAP

SEQ ID 2657

ATGAGGAAAAATCCGACCAAAATCTGCGGCATCACCACACCGGAAGACGACTGTATGCGGCCACGCGCGCGCAGACGATTGGGACTGGTTTTTACCCCCAAAGCCCCCGCTATCG
ACATCATTAAGCACAATAATCGCGCGCAGTTCGCCCTTTGTCAGCGTTGTCGCCCTTTTCGTCAACGAAAGCGCGCAAAACATCCGCGCATCTTGCAGAGTGGCGATACACAT
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GCTCAGGCACTGCTGTGATGCTATCACCTTCGGAATACGGCGGCACCGGACACCGCTTCGACTGGACGCTGTGGCGGAATATTTCGGCAAGCCGTGGGTGCTTCCGCGCGGCTGA
CCCCGAAAACGTGCGCGACCGCTCCGATCACCGGAGCGGAAGCGGTGACGATTCGCGCGCGCTGGAAGCGTCTAAAGGCAAAAAGACCCGCCAAAGTCGCGCGCTTTATCGCAAC
CGCCAAACCGCTATCCCGT

SEQ ID 2658

MRKIRTKICGITTTPEDALYAAHAGADALGLVFPQSPRAIDIIKAQKIAAALPFFVSVALFVNESQNRIRLAEVPIHI IQPHGEDDAFCRQDFRPHYKAIRVQTASDIRNAATRFPH
AQALLFPDAYHPSFSGTGHFRFDTLLAELYSKPPWVLACGLFPENVGEAVRITGAEAVDVSGGVEASKGKDPKVAAPATATANRLSR

SEQ ID 2659

GTGCGCTGTGCGCTTTTCAGACGGCATTCGCCATCAGTCGATTTTGATGTATTGCAGACAAAGGATTTCAATTTCTCAGCGCTTCGCGGTGTTCAAAACCACTTCGTCGCTTCGCGC
GCTTTAATCAGGCAACGCGCAACGCGGAAATCCAAGAAATTTGTTTTGCGCGGTATCGATTTTCATCGACCGCGACGATTTTGACGTTTTCGCGCGGTTCGCGCGCAACAGACCGA
CGGTGCGCGCAAAATACTTGTGTCGCTTCGCGCAATTCGGGATCGACGACGACGCGAGCTCCAAACGTTTGGTCAGGAAACGGATGCGCGGTGATTTGCGCATACGCGCTTT
GCGGTAAAGATAGTCGCGCTTTTCGCTGCGGTGCGCTGCGCGCCAGTTGACGATTTGGACGATTTGCGGCGGTCTTTATTGACAGTTGATAAGCTCGTCTTTCAATGCTGTC
CATCGCGCGGTGATGATGATTTTGTGTTTGTGCTACTCATATTGTGTCGGA

SEQ ID 2660

VRLCRFRHSRSDVDFVDRKDFNLTAFRRVQNHVAFARFNQATQRNRNFRVLRIGDFTDADDFDGLLAPVAAQQTGDAEKYLVGRFAQPGIDDDSLQTFQETDAAVDPAHTAF
AVKIVAVFAAVACRPPVDDLDFGATFIDQLIKLVFQCLPSGGRNVVFGFTHIVCG

SEQ ID 2661

ATGAGTACCGAAACCAAACTACATACGCGCGCGGATGGCAGGCATTTAAAGACGAGCTTTTCAACTGGTCAATAAGAACGCGCGGAAATCGTCCAAATCGTCACTGGGCGGCGAG
GCAACGCGGACCGCAGCGGAAACGCGGACTATCTTTACGCGCAACGCGGTATGCGGAAATCGACCGCGCATCCGTTTCTCGACCAACGTTTGGAGGCTGCGCTGCTGATCCGGA
ATTCGCGGAAGGACGCGACCAAGTATTTTCGCGCGGACCGTCTGCTGCGCGGCGACGGCGCGAGCAAAACCGTCAAAATCGTGGCGGTGATGAAATCGATACCGCGCAAAACAAA
ATTTCTTGGATTTCGCGGTTCGCGGTTCGCTGATTAAGCGCGCGAAGCGGACGAAAGTGGTTTGAACACCGCGGAGCGCGTGAGGAAATGAAATCTTTCTGTCGAATACATCAAAA
TCGAC

SEQ ID 2662

MSTETKNYITPAGQALDELYQLVNRKEPEIVQIVNMAAGNDRSENGDYLYGKRRMREIDRRIRFLTKRLEAAVVVDPELREATDQVFFGATVGLLRGDGREQTVKIVGVDEIDTAQNK
ISWISPLARCLIKAREGEVVLATPEGREETELSVYIKID

SEQ ID 2663

ATGTGCGCGCTATTAGTTTGGTCAGTCATGAACCCGTGAACAGCTTCTGTACGACGCTTTGCAGATGTTGCAGCACAGGGGGCAGGATCGCGCGGCTTGAACGGCGGAAGCGGTA
CCTTCATATGCAAAAGCAAAGGATGTTGAGCGAAGTGTTCGCGACGCGCAATATGCGGATTTGACCGGCAACGCGCATCGCCACGTCGCGGCAACGCGGCAACGCGG
CAGCAGCGCGGAGCGGCGAGCTTTTACGTCAGCTCGCTTTTCGCGCATGTTTGGCGCACAACGCGCAACCTCACCAACTGCGGAAGTGTATGAAACGTTGTGAACAAACCTGCGC
CACATCAACACCGGCTCCGATTCGGAAGTTTGTCTCAACGATTTGCGCGACGAATTCGCGCGGGAAGTCTCTAAAAACGCGGACCGCGACCGGCTCAATGCGGACAAATTTTCAACGCG
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GCAGCGCAAAAGCGTGTGCTGTTGGAGACTTCCATCGTTCGCGGACGACGCGCGGAAATCGTGAATGTTACGCGCGCGGCGCGCGGCAAGTCTATATCGCTCCGCGCGCGCGCG
AAGTGGCTATCCCAATGTGTCAGGCAATCGATATGCCACGCGCGAAGAGTTGATGCAACGCGCGGCGGCGGAAATCGCGCGGCAATCGCGCGGCGGCGGCGGCGGCGGCGGCGG
CTTGGCGGATTTGGAAGCGGTGCTCAAGCACTCAACCGGAAATCGAATCTTCGATTCGCTCTGTTTCAACGCGCATTTATCGGACGCGGACATCGATGATGCTTACCTCGACCGCGCTG
TCTCGCGGAAATTCGCGCTGCGCGGCTGGAATCCACCGGAGGATGGAACACGACATCAGCATCAGCGATGCGCGCGGCGGCAAGAA

SEQ ID 2664

MCGVLGLVSHFPVQLLYDGLMLQHRQDAAGIATAEGGTFHMKGKGMVSEVFRTRNMRDLTGNAHLAVRYPTAGNAGSSAEQPFVYSSPFGIVLAHNGNL/TWTAEIYENVCKHLR
HINFGSDSEVLINVPHELRRVSKNADPHRLNADNIFNAVAEVHRLVRGAYGVVAMLAGYGLAFRDPYGRPLALGSQTDSEGRKSYAVASESVAFNALAYDLERDIRPGEAVFVGFEG
TILARQCSDRAKLSPLCFEYVYFARPDVSDGVSVYQSRLLMGVSLAEIKRELVDGIDVVMPIPTSRPSAMELAVHLNKPYREGLIKNYIGRTPIFPGQSTRRKSVRQKLSPMETEF
AGKSVLVDSDIVRGTTSREIVEMVRAAGARKVYIASAAPEVRYPNVYGIDMPTREELIANGRSAEIAAEIGADGIVFQDGLDEAVVKALNPKIESFDSCFNIGYRTGDIDDAYLRL
SAKSGCAGLKIHPSRMEHSISISDAGDEE

SEQ ID 2665

GTGCGCTTCAGACGATACCTGATTTATGCCGTCCGAAACGCTTTTCTTTCCTTGACACACCCGACAGACAAAGCGCACCTGCTGACTTTACACAAATATTGTCACAAATTCGGGC
AAAAAGCGCGGTTTGTCTTTATAATTCGTTTCAACCT

SEQ ID 2666

VAPQYATLIYAVRNAPSLDTPQTKRTCLFLHKYQQFGQAACVCFIIPHP

SEQ ID 2667

ATGGGTGGTTTCTCTTTTTTGGCAAACTCTTTGCCGACCCCTTCGCGGACCTCGCTTTGCTCGTTCCAAACCGCGCTGTTGCAATTGGCTCTGTGATTCATTCCTGTTTCGTCATT
GCTGTCTGATCCAGAAATGCTCCGTTCGCTGCTGACCGCGCGAGTTTCGCGGTGCGTTCGGCTTTGCCAACCGCATTTTGGCGGTGATTCGCTGATTTGAAAGCGGTTTGTATG
TTACCTGCTGATCATGCTGTCTCAAAAACCGACCTGCGCGATACCGAAGATGCGAACAGTCTATACCGTACCGTTTTGCTATGCTTTCCGAAAGCGGTGTTAAACCATACCGGACAA
CGACCCGGAATCCCTGACGACGACTAATCCGATACGTGGCTTCAGACGACATACCTGATTTATGCGCTCGGAAACGCTTTTCTTCTCT

SEQ ID 2668

MGGFLFPQTLCLRTLRRLCLVPTPPVCIGSVIHPVRHCLSDPENAPFAADRRSPGGRSGLCQPHGRCIRCIERRPDCYPADHACPKNRPARYRRHATVLYRTVFRIAPRSVKPYGQ
RTRIPRRLIRIRGVSISIPDLCPKRLFFP

SEQ ID 2669

EQ ID 2669

ATGAACATCAAACACCTTCTCTTGACCGCCGCCGCAACCGCACTGTTGGGCATTTCGCCCCCGCACTCGCCACCACGACGGACACGGCGATGACGACCAACGGACAGCGCCACACCAAC
ACGGCAAAACAAGACAAATCATCAGCCGCCCAAGCCGAAAAAGCGGCTTGGGCGCGTGTCCGCCGCAAAATCACCAGCATCGATCTCGAACACGACGACGGCCGTCGCGACTATGATGT
CGAAATCGTCAAAACCGGACAGGAATACAAATCGTTGTCGATGCCCGTACCGGCCGCGTGATTCTCTCCGCCGCGACGAC

SEQ ID 2670

SEQ ID 2670
 MNIKHLLITAAATALLGISAPALAHHDGHGDDDHGAHAHQHGKQDKLISRAQAEKAAWAVRGKITDIDLEHDDGRPHYDVEIVKNGQYKVVVDARTGRVISRRED

SEQ ID 2671

SEQ ID 2671
ATGCTGTTGTCAATTAAAGTAGTATCTCGTCATTCCCGCAAAGCGGGAATCCAGATCATTTGGGTAGCGGCAATCTTCAAAGTCGTCTGAAAAATCAGAAGTTC

SEQ ID 2672

MLLSIKVVSRRSRKSGNPDHWVAAIFKSRLKNQKF

SEQ ID 2673

SEQ ID 2673

ATGTAATAGCGTCGCCCACTGCGCACTCCTCGCCTCCGCCGTCATCGCCGCCTGCATCGTCATTTCACGATCGCGGCGTGATTGCGGAAGCAGGTTTCGATGTTGGCATGGGTGGTTCCTTCTTTTTCGCAAACTCTTTGGCGCACCTTCGCGCACTCGCCTTTGCGTCGTTCACAACCCGCCCTGTTTGCATGGCTCTGTCATTCAATTCCCTGTTCGTCATTCGCTCTCGATCCA
GAAATGCTCCGTCGCTGCTGACCGGGCAGTTTCGCGCGTCGGTCTGGGCTTTGCAACCGCATTTTGGGCGGTTGATTCCGTCATTTGAAGGGGTTCGATTGTACCTGCTCGATC
ATGCTTGCTTCAAAAACCGACCTGCCCGATACCGAAGATGGCAACAGTCTTACACGATACCGCTTTTTCGTATCGCTTTCCGAACGGGTGTTAAACCATACGGACAACCGACCCGAAATCCC
TCGACGACGAC

SEQ ID 2674

SEQ ID 2674
 MNSLPIDLLASAVIAACTIVSTMRCVIAEAGSHVAVVVSFFAKFLAFAFPADLAFASFQPRFLFALALSFSILFVIACTIQKMLRSLITGAVSAVGLGFANRIIGGVFGALKGVILIVTLLI
 WLSKTDLPDTEWQOOSTYVFFPVSLSAEVLAHTDNAPESLDD

SEQ ID 2675

SEQ ID 2675
ATGTCGGGAAACAAACAAACGGAAGTCCTGACCGGTTACGAACAGCTGAAACCGGCGCAACCGCGCGCGCTGTAACGGCAAGCTCCTCGTGTGCCGCTCTCTGCATCTGCTGGCAGCG
CACTCAGTTCCGATCCTCGCGACAGCAATCCCGCACCGCCAGCGCGCGCGCAAGCGGAAGCGCAACCGGCAACACGCGCAACAAACCCCTGCTTGAATCCGCGCGCGGAAACCG
GGAAACCGCGCGCGCAACACCGCAGCACTTGGCAGCGCAAGACAAGCCTTCTGCGCGCGCAGCGAAATCAGCGAGCTGAAAACGTAGGCGCGCGCGTGGTCTGATTAAACGACCGCGCTC
GAAGACGCAACATCAAAGGTTTGAAGAATCCGAGAAATGCAACAGGCAGAAACCGCCAAAACCGAACGGAAGCAGCGCAAAACAAACGCGCTCGCCGAAAGAGTGTGGCACTGCCGACA
GTACGGATACGCTAGCGGTTGAAAACCGAAACGCACTCGCGAACCCAAACCGCAAAAAGCGGAACGCACTGCCGAAGCCAAGCCCAAAGCCAAAGAAACAAAACCGCGGAAAAGTTC
CGCAAAACCGAAATCTGCTGCCGAAAACCAAACCGGATACGGCAAAATCCGACAGCGCGGTAAAAGAGCGAAAAGCCGACCGCTGAAGGCAAAAAGACACGCGGAAAAGGACCGT
TCGGACGCGCAAAACACGAAACCGCGCAAAAACCGACAAAGCGGACAAAACCAAACCGCCGAGAAGGAAAATCCGCGAAGCGGCTGAAAGCCAAAAGCCGCCATTACGCAAGCCGT
AAAAGAACGCGCGCTTAGGCTCCACGCGCAAAATGAAGCGCGCGGATCGATTGCAACCATCACGAAATCATACCGACAACGCGCAAAGTTTACCGCGTCAAATCAGCACTATATAAAA
CTTAAGGATCGCGAAGCACTTTGAACAAATCTGCGCGTGACGGCATCGCGGCCAGGTAACGAATGAA

SEQ ID 2676

SEQ ID 2676
MSENKQNEVLTCYEQLKRRNRRRLVTASSLVAASCILLAAALSSDPADSNPAPQAGETGATESQTANTAQTALKSAAENGETAADKPPDLAGEDKPSAADSEISEPENVGAPLVLINDRL
EDSNIKGLESEKLLQAAETAKTEPKQAKQRAAEKVSATADSTDTVAVEKPKRTAEPPKQAKERTAEAKPKAKETKTAEKVADKPKTAAEKTKEPTAKSDSAVKEAKKADKAEKKTAEKOR
SDGKKHETAQKTKRADKTKTAEEKESGKAGKAAIQAGYAEKERALSQRKMKAAAGIDSTITEIMTNGKVVYRVKSSNYNKARDADRLNKLRVHGIAGQVTNE

SEQ ID 2677

SEQ ID 2677

ATGAAACACATACAGACTGGCTCTCGCATTTTGGAAACCGCCACAGCGCGGTTTGATCGACATGGGTTTGGAGCGCGTAAGCGGAAGTAAAAAGCGCATGAACCTGACACCGCAATGCC
CCGTGCTGCTCGTCGGGCAACAAACGGCAAGGTTCTGGCTCTGGCCTACCTTGACACAGATTTCACAAACAGGCAAGGCTTCAAACCGCGCACGCTGACCAGCCCGCATTTATTGCTATTACAA
CGAACCGCATCGCATCAACCGCGCAACCCGTTTCGGACGATACGATTATTGCCCTTTTCGAGCGCATCGAAGCCGCCCGCGGCAATATCGCTGACTTATTTTGAATTCATAGCTCTGGG
GCTGTCGACATTTTTCATACGCGAACAAGTGAATGTAATGATATTGGAAGTTCGGCTTTGGCGGACGTTTGGACGCGGTCAACGCGTTTTCGACGGGATTCGCGGTTGGTTACTAGTGTGGATT
TGGACCATCAGGCATTTTGGGCGATACGTCGAAACAGGTTCGGCTTTGAAAGGCGAGCGGTGTTCCGCGAGCGGCAAAACCGCATCTGCGGTCAAAACCCGCGCCCGCATATTGGTCGC
ACACGCCGAAGCCATAGGCGCGAAACTGTCTGATGGTACAGCGCATTTTCGAGTTTTCACGCGATGAAACATCCAATGGAACACTACCGCTTCCGCGCGCAGCATTCAGACGCCGCCACCG
AACCGCATGCGCTTCCCTTCCCGCATTCGCGCGCGCATACACAGCTTCTTAACCGCGCTGCGGTTGCAGCTATTGGAATGCTCTGACGACAGAGTCGCGGTGGACATTTGTGCAATCA
AACCGGGGCTGCTGCTGGTTGAAAAATCCCGACGCTTCCAAGTCTTCCCGCGCGCGCTGACCGTTGCGATGATGGAACCAACCCCAACCGCGCGCGCTTGCAGCGCAACCTAAT
CAACCTTGCTTACGCGCAAAAGCGCACCGCGGTGTTCAAGTATGCTGCGCGCGCGCGCTGACCGTTGCGATGATGGAACCAACCCCAACCGCGCGCGCTTGCAGCGCAACCTAAT
GTGCGCGCGGTATGACGCGCGGATGCACTGAAAGCAAATTTGGAACAACACCACATCGAAACATACAGACATTCGCGCGGTCCGCGACGCTACCGCGCGCGAGCTCAAAGCGGGCG

SEQ ID 2678

SEQ ID 2678
 MKTQDNLSHLSTAHSGGLIDMGLERVSFVKRNMNLTPOCPVVVAGTNGKGSVCAYLTQIYKQAGFKTGTLTSPHLLHYNERIAINAEVPSDDTIASFERIEARGEISLTYPFENALA
 AYDIFIREQVDVIMILEVGLGRLDAVNAPDGCNAVTVSDLDHQAPLGDTEVQVFGEKAGVFRSGKPAICQMPAPASLVAHAEAIGAKLLMVQDFEFHAMENIQWNYRFRPQHSQDGP
 RRNALPFPALRGAYQLSNAACALTFLCCLDDRLPVDIGAIKRGILLVENPGRPOVLGPRPLTVLDVGHNPHAARALRRNLINLAYAQKRTAVFSMLSDKDDIGVSETVKDQFDEWYIAPLD
 VPRGMTADALKAKLSHHIENIQTFAAVRDAYRAASKAGEDDRIVVFGSFHTVADVMSVL

SEQ ID 2679

SEQ ID 2679
ATGCGCGCCTTTTCAGACGGCATTGAGGCCGTCGCCGATCCTGAACATCCTGACCGTATCACTCCACTCGGCTTCCATTGCCGCTGCCTGACTTGGTFTTTACGGCCGGATGATGTGGTTCTG
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AGACAAAACAGCGGCAACACTCTCGGCGCAGCAGTATGGTTACGCCCTTATGCCCTTATTCCTTACAATGGGACACAGCGCGCAAAACCGTCCGCCAATGCATCATGCCCGACATGACGGACAAA
GAATCCTACCGCGCGCTGAAAGTCTGGGTGCTTTTGGCGGCAGCCGAAAAAACCGCGCAAAACCGATATCAGAC

SEQ ID 2680

SEQ ID 2680
MRAFTALRPSRIILNLTIVSLHSASTIAVCLTWFGMMWFGLAALAASYAISLRITNLKRRHAITAITIDRGRARIVSGKDKTAATLAGSSMVTYPALFLQNDYGGKTVRQCIMPDMTK
ESYRLKVVVLWROPKKTAEITSD

SEQ ID 2681

SEQ ID 2681
TTGAGAAAGCACACCATGTATTTTGTGTGACCGCACCGCCGCCGTCTCAAGCCGACCGCGCGCTTTTGGAAATGCGCTCAAAGACCGACGAAATAATGCCGACCTGACCATAGAACAGC
TTCGCCGCCAGCTGTCCGCTCTCCCGCTTCGCGAGTTCGACGAACCGGAAGCGTCGTTCTCTACTTCGACGAAGCGCTACCGCGAGATTTTGTAGGCGGAGCTGGCAGGTGGGCATCGA
CAAGGACAAATGCCCGCAAGATATGGGGCTGAAGGCGTTTGGGAATTTTTCGACATTGAAATCCACGATATGGTTTGGATATGGAAGAAGCGGATTGACATCACGCCCGTGTTCGAC
AATATGATG

SEQ ID 2682

SEQ ID 2682
LRKHTMYFVDRTAAVLKPTARFLEWLKSTDENMPDLTIEQLRADCSVFLVTPQFDEPAVVSFYDERYRQIFEARLAWGIDDKDKWPDQMLKAFWEFFDIEIHDVLMOEADLNTTPVFD
NM

SEQ ID 2683

ATGGCGTTCATCATATGTCGAACACGGCGGTGATGTTCAATTCGGCTTCTTCATATCCAAAACCATATCGTGGATTTCATGTCGAAAAATTCOCAAAACCGCTTCAGCCCCATATCT
TGCGGCCATTTTCGCTTGTGATGTCACCACTGCCAGCTCCGCTCAAAAATTCGCGGTAGCGTTCGTCGAAGTAGGAAACGACGGCTTCGCGTTCGTCGAACCTGCGGAACGAGGAAGA
CGGAACAGTCGGCGCGAAGCTGTTCATGTCAGGTCCGGCATATTTTCGTCGGTCTTTTGAGCCATTCCAAAAGCGCGGTTCGGCTTGAGGACGGCGCGGTTCGCTCAACAAAATA
CATGGTGTCTTTCATCATCTTTCGGGTGTCGGGTATGCCGCTGTAACGTTCGGTTTCAGACGGCATAGCATCAATGGGTGATGCTTGTTCAGGAACCTGCTTGGCGCTTCGCTGT
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TCATGCCGCTTTCGCGCAAGTCTTTCATCATCTTTCACACTTTCGCGGACATTTTCGGGTTCGATGTCGGAAGTTCGGCTTCGTCGAAACAGCATCACGCGCGCTCCATGCCAGCCCGCGCGC
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CCCTTAACCTTCATCGGTGCGAGGTGATGTTGTCACACGCTCAGGTGCGGGTAGAGGTGAACTTTGAAACACAAAGCCGACTTTCGCGGATTTGTTCAAAATCGGTTTTCGGGT
CGCAACGTTGACGCGCTCCACCCAAATCTCGCGCTTTCGATGCTTTCAGCTGTTGACGCTGCGGATGAGTGTGATTTCGCGCTGCGCGAAGGCCCGCAGACGACGACCTTCGCGC
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SEQ ID 2684

MALEHIVEHGRDQIRFFHIQNHIVDFNVEKFPKRLQPHILRPFVLDVPTCQLRLKNLFPVAFVEVNDGFRFVELRNEEDGTGAKLYGQVGHIFVGAFFEPQKARGLEDGGGAVNKI
HGVLSQSSCGVGLCRINVRPSDGLASMGHDLLELIGAPVFRVGEKRRFRFPKDLFFIDENHAGVNFAGKPHFVGYAHRHAAPRQVPHHPQHFADHFVGECSRLVKQHHARLHQBPAR
NRHALLAAGLKGREGVFPVQSDAPQLHCLFLRLPLNLHRCBGDVGQHVREVEITLHKADFFADFPVQIGFVGNVDAVEPNLAAPDAFLVDGDEBCGFAAARRPADDDHFA
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SEQ ID 2685

ATGGACATATGATCAAAATTCAAAACGTACACAAACATTTCAAAGACCTGCACGTCATCAACGGCGTAAACTTGGAAATCAAAAAGCGGAAGTGTCTGCTGCTGCGGGCTTCGGGCA
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AGTCGGCTTTGTGTTTCAAAGTTTCAACCTTACCCGACCTGACCGTGTGGCAACATCACCTTCGACCGATGAAGGTTAAGGGCAAAATTCGCGAACAGCGCGGAGAAAAAGCAATG
GAGCTTTTGGAAACGCGTCGAGCTGCGACACAAAAGACGCGCTTCCCTTCCCACTTTCGCGCGCGCAGCAGCAACGCGTGGCGATTCGCGCGCGCGGATGAGCGCGCGCTGATGC
TGTTTGACGACGCGACTTCCGCACTGACCCCGAATGTCGCGGCAAGTGTGAAAGTGTGAAAGCTTGGCGGAAAGCGGATGAGATGTCGTAACCCAGAAATGGGTTTTCG
CGCGAAGTTCGCGACCGCTGATTTCGTCGATAAAGGCAATCTTGAAGACGAAACCGCGGAAGCGTTTTTCACAAACCGGAAACGAAACGCGCCAGCAGTTCCTGCAACAGTGC
ATGACCCAT

SEQ ID 2686

MDTHIKFKNVHKFIDLHVINGVNLKIKRGEVVVVCPSGSGKSTLIRTVNQLESIESGKIWDGVNVADPKTDINKIREVGFVFPQSNLYPHLVLNDITLAPHKVKQONAEQAEKKAH
ELLERVGLAHKDAFPSPQSGQQQVIAIARGLAMEPRVMLFDEPTSDLPENVGELVKMKDLAESGTMCMVTHEMGFAREVADRVLPVDKQILEDETFFRAFTFNPKHERAKQFLQGV
HSH

SEQ ID 2687

ATGAAATACACAGCCGACTCTCTGACTTTTCTTTTAACTGCCTGCATGAACCCGAACGATGCGCTTTTCCAAAACCGCGCTTATCAAAATGCGGAGGCGCAATTTGAACGGTTTCAACGCCG
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CAAAAACGACTCGCTACTGGAAGGCGGAAAGCGGGGTGACGTACTACACTGCGATGCGGAAAGGATTCACGCGCACAGTTTCGCTCATGTGTCGTAATGAAAAACGAC
AAAGGCTACGTCGAAAGTTTACCGGGGATGAATAAGCCGAATCAGGAAGAGTTTAAACCAATTCGTTGCGGATTTGAATAAGTTTACCTT

SEQ ID 2688

LNCRQAALKPFTTYVYKIRINXIHNRIPDFSPNRSEPTMYTAALLTFLI/FACMFPNDAPFQNNRYQMPHAQLNGSNVPHYGYSONPDHLLVDQVRVPDAYRASPARDWIAKEQYRKN
DCVLEKAESEGGVYTYTCDAREGPNTRFVITYVVMKNDKGYVKVYRGMKNPNEBELTKLVADLNKFPY

SEQ ID 2689

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AGAAAGCATACATGATAAATCAACCGCTATCTGCGACGCGGACCCCAATATCCGACCAACAACATCTGAACGATATTTTCGCGCGCGCGCTGATTGCGCTGAAACAGTTCGCGG
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SEQ ID 2690

MESNLQKTERLIRINRILHAQYSQDYFETGKVRKINLSHTLKNVPTHEILSYRLNHEAVNDYLAADTRGIDFFYRVKTAESIHDKINRYLARGTQYPNNILNDIFGARLIWPSETVAG
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SEQ ID 2691

ATGAAAGAACACAAAGCCCGCAAGCGTTTCGGGCGAATTTTTTCAGGACACCGGGATTATCGGGATATTGTCAACCGCTGCGCGCGGAGCGGATGATGTCGATTGAAATCGGCG
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SEQ ID 2692

MKEHKARKRFPQNLQDTRIIQDIVNAVPRQADDVVIETGPLAAITPELAKKLNRLHVVEIDRDIVCRILTFADKLVHIEGDVLPQDFNGISGKKKIVGNLPYNISTPPLFLAEVAD
DVADHFMQLQKEVVERHVAAPKSNDSYGRGLGVMLQVFFDMELLIDVPPESFDPAPKIDSASVVRMTIPVHRIGKADDPDFAKLVKLAQFRQRRTIRNNLKLADDDDLQAVGISPDRAEHI
APEKYVALSNYLADRAV

SEQ ID 2693

ATGACCCGACGCTTCGCGCGCAACACGGGATCGAAGGGATGGGTTTCGATTCAAGCAGATTTTCAGACAGTTCATCTCCAAACAGGCAAGCGGACAGCGCGGTTTCACCAAAAC
GCCAAACACGGCAAGCTTCAACAGCATTATCAGCGCTCGCGTTTCGGTTACAATCGCGACATCAACCGATACGTAAACACATTATGTTCCAAACACAGGACGACACATAAAGC
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SEQ ID 2694

MTAAGGNTGSKGWSISSEFSDFNPPTGAADSRFAPNRQTRQAFKQHYHALFVSVMTPTSNGYCKHIYVPTHTRTKAPPTVSS

SEQ ID 2695

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CTTCGCGCAACTGATTAAAGTTCGCGCGCATCGCGCGGAAACCGCTTTGGGCAATTTGTCGCGGATGACGCGCAGAGCTGGCGCGGCTTGCAGAGAGATGTCAACCGCTCTCC
TCCGCTTCGCGAATCGCAAAAAACCGCGAAGCTATGCTTGAAGCTCGCGCGCAAGCTGCTCGCGCATACGCTAACCGGACGCGGCTGTTCGCGCTCACCGCGCGGACGAAACGG

AAGACATCGTCGACGACGCTGCTTGCGCTGGGTTACAACGAACGCGAGGCGAAAAGCGGGCGGTCAAAGGCGTTCCGAAGGGGACGGACGTGGGGCGAAGGCGTGCGCCTTGCCCTGAAAAACCT
 GCTGAAA

SEQ ID 2696

LHP T L Q D S A H M I S R L T G K L V E K N P P Q I V I D V N G V G Y E A D V S M Q T F Y N L P P V G S E V Q L T Q L I I R E D A H L L F G F A T A E E R K T F R Q L I K V G G I G A K T A L G I L S A M T A D E L A R A V A E D V K R L S
 S A P G I G K T A E R M V L E L R G K L V A H T V T D G L F A A S P A A D E T E D I V S T L L A L G Y N E R E A K A A V K G V P K G T D V G E G V R I A L K N L K

SEQ ID 2697

TGGACATATCCAAGCTGCATTTTGACGCAACGGCCATGGTCGGCAAAACGGAGCAATTCGGCAAAAGTTTGACAACGATTCAAAAGGTTTAGATCAGTTTTCGGACCGGTTGAAAAGCTTGG
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 AGAAAGCAGGTTTCAAGCGAACCAAAACAGACAACAGGATGCCAAGCTGATAGCGCAGTATTGCCGGTCGGCGAAAGAAAGCGAGCTTGTAAAGAGGCGAAGCCCTACGGACGAGCAATAC
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SEQ ID 2698

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SEQ ID 2699

SEQ ID 2699

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SEQ ID 2700

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SEQ ID 2701

SEQ ID 2701

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SEQ ID 2702

SEQ ID 2702

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SEQ ID 2703

SEQ ID 2703

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SEQ ID 2704

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SEQ ID 2705

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SEQ ID 2706

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SEQ ID 2707

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SEQ ID 2708

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SEQ ID 2709

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SEQ ID 2710

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SEQ ID 2711

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C

SEQ ID 2712

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SEQ ID 2713

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SEQ ID 2714

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A Q A T L A K A D A D L A R Y K P L V S A D A I S K Q E Y D A A V T A K R S A E A G V K A A Q A A I K S A G I N L N R S R I T A P I S G F I Q S K V S E G T L L N A G D T T V L A T I R Q T N P H Y V N V T Q S A S E V H K L R Q I A E G K L
L A A D G A I A V G I K P D D G T V Y P E K G R L L F A D P T V E S T G Q I T L R A A V S N D Q N I L M P G L Y V R V L M D Q V A A D N A P I V P Q A V T R G A K D T V M I V N A Q G G M E P R E V T A Q Q G G T W I V T S G L K D G K
V V V E G I S I A G M T A A K V T P K E W A S E N Q A A P A G V Q T A S E A K P A S E A K

SEQ ID 2715

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SEQ ID 2716

EQ ID 2716
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SEQ ID 2717

SEQ ID 2717
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SEQ ID 2718

SEQ ID 2718
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SEQ ID 2719

SEQ ID 2719
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SEQ ID 2720

SEQ ID 2720
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SEQ ID 2721

[illegible]

SEQ ID 2722

SEQ ID 2722

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SEQ ID 2723

SEQ ID 2723
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SEQ ID 2724

SEQ ID 2724

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SEQ ID 2725

SEQ ID 2725

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TTTACCACATCCGGAAGCGGGGAAACCGTTTCGTTTGAGGACCGGATTCGGACGACATATATCATTTTGTGTCGCTCCGCTTCGCTTTGAAGCGGTTTGGATTGCTCTTTGACCAATGAA

SEQ ID 2726

SEQ ID 2726
VAQALSAKPNETVKRIFFMQNTSFDNESYDSDSDFASAGTENRIGLTVPLELAGRRLDAVLAKLLPDYSRSLTSWIKEGAVIVNDKPSQPKDKMIGEQQIVTVPSEENLAFVPEPM
DLIDIVYEDTIVIVNPKAGLVVHPAAGNWTGTLINGLLAHCPELSQIPRAGIVHRLDKETSLGMVAKTLPAQNSLVRLQERTVKRITYRAVANGIVFDGKIETQIGRDPHNRLKMAVK

FGGKPAVTHVKVLERYLAHSYIECSLGTGRTHQIRVHMREANPLAGDPVYGNPRHPCGDTVKEAVKSLGARQALHAYRLSFTHPESGRTVSFEAPTDDIYHLLSVLRLEAGLDSSLSNE
EEHQDKFGADDDDDNEDDYDEVVYVRE .

SEQ ID 2727

TTGAAAGGCGGGGCGAACSCAGGCAGCCGAACCGGAGCAGCCGGGCAATCGTCCCGCCGATTTCAAACAAAGGCCGTCTGAAGGGGCCGGGCAGAAACCGCCGTTTCGGTTGCCCGGTT
CAGACGGCATTATGATGAAAGGCGTT

SEQ ID 2728

LKGGANAGSRTGAAGQSSPPI SNKGRLKGPGRNRRFRLPRSDGDMKGV

SEQ ID 2729

TTGACGCTCAAACCTTCCGACTTCGATATTTTGTTCAAACACCCCAAAGCCGTCATCATCGCGGTAATCGCACAAATTCGCCATTATGCGCGGCAACCGCCTGGCTGCCGTCCAAACTGTTGA
AOC TGCC TGCCGAAATCGCGGTGCGGTGATTTTGGTCGGCTGCTGCCCGGGCGGTACGGCTTCCAAATGTGATGACCTATCATGCGCGCGCGGCAATGTGCGCTTTGTGCGGTTCCCGTTACGCT
TGTTTCCACCCCGATTTCCCAATGTCTGACTCCGCGCACTTCTCTGATGCTTGC CGGTGAAATGCTGGAAATCCAAGCGGCGGTATGTTGATGTCCATCGTCAAAATGGTTTTGTCTCCC
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SEQ ID 2730

MTLPKSDPDILFKHPKAVIIGVIAQFAIMPATAWLPSKLLNLPAELIAGVGVILVGCCPGGTASNMVMTYLARGNVALSVAVTSTVSLTISPLITPAIFPLMGLAMELETQAAGMLSTIVKRVLLP
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SEQ ID 2731

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SEQ ID 2732

NDACFFVIPAAGIRRFGIVFKRSGRILAGAGMMPLVTFSELYMLQOGTAHQAPHCVLPERGCPPIRFYRYKQTGFNRKGMGIKSISDTSRAMPSNDSPISDGIV

SEQ ID 2733

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SEQ ID 2734

MKTTITSTLMLAPKGNFLTADWPAPANVKTLLTTRNGGVSQGAYQSLNLGTHVGDDPETVRNRKEIVQQQVGLPVAYLNQIHSTPIVVAEALDGTDPDASVDDTGKAVCAVMTADCLPV
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 GATGRMASLIVLDGNAV

SEQ ID 2735

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CGTTACCGCTGCGCGAGTCATCAACGAATATCTTTTGATATTGACGTTGAAGCGCAGGTATTGAAACGCGGCGAGCGGCTGGCAAACGATGACCGTGTCCGTCCGCGCGCATTTTGGAT
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SEQ ID 2736

MNKIFLTAALAVLGACGPHLKADGISPPPIYRSHIEGGQALQFPFLETALYQASGRVDDAAGAQMTRLRIDSVSQNKETYYTVTRAAVINEYLLILTVEAQVLKRGEPVGKPMFTVSVRRILD
 YADNEILGKOREEETLWARMRODVASQIVRRILTFPKAE

SEQ ID 2737

[illegible]

SEQ ID 2738

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ORKLOCI.SAFDVPAPVGGORRRNAVCTPOVETARAHOCCGSKFYVHRLPFSKA

SEQ ID 2739

GTGGCGGCACATATCGGACGCATCGATACGGACGCGCCTTTGAAACCTCTGTACGCTATCCACGGCAGGAGAAGAACTGCTGCGTATCGAGGCACTGGAGCGCATTTGAGGCGCGCGCGAAGA
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SEQ ID 2740

VAHHIGRIDTDAPLKPLYVHNGEELRLI BAVDALRAAAKKQGYLNREAYTADASTFNNELIQTAGNAGLFADLKLELHHPNGKPKGKGEALQDFAARLPEDTVTVLVLLPKLEKTRIQS
KMFALAAARGEVWEAKPVGAALPQWIRGRGLKIGLIGIEADALALFAERVEGNLLAARQIEDIKALLYPKHAVNIDEAQTAVANVARFADQPLAGAMHKGDPVPRCRLLDGLEKKGREPV
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SEQ ID 2741

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SEQ ID 2742

LGITALPQRHDKLFYRPCVAVFRAFDSDVLGAGFERVKQADDGNPLDRKCRFLVAPKPEAVADGLDALPLFQSGKPNQRPVFNRPQKQHRFFAFFLQPVQPAYARDIALHPR
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FLLLPVCPKPRCRHNPCKGGRTRSSVCRPARRVSIPLQPSISKDIR

SEQ ID 2743

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SEQ ID 2744

LRLHLNFENRYNLLCNPFHSVSKQAVFIS

SEQ ID 2745

TTGTACGTGCAAGAAAAATAGGGCGAAAAAGGAAAAAGGGGAAGCTTTGTAAAGATTGGGTGCGTTACCCAACTTTTACGAATACCCCTTTTCTCTTTTATGAAGCTGTTTTTCAATA
CCGCAAAACCACTAACGGAG

SEQ ID 2746

LYVQENRAEKRRKGLCKDWVRYPIFTNTPLFLFYELFFNTANPLTE

SEQ ID 2747

ATGGACAAATAGACCAAACTGCGCTTGGGCGGCTGATTTTACTGACACCGCGCTTTAAGCCTCATTATCGTATTGATTGTCGATTCTGCGCGCTTGCCATCTGCTTGGCGCGCTCA
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GAAATCAATCAATGCGCGCAAAACAGTCGCGGCTCAGAAACGTCGCGCAGCT

SEQ ID 2748

MDNFKLRLGGLILLTAVLSLIIVLIVDSWPLAILLAIVIAAAGGFVWTSRRQQRQPIERLKKPIDPEKGRINEANLRRMYHSGGQHQKDAITLICLSQKCSVDRAHMFKKRPTRQ
EINQMAAQSRGQKRPFR

SEQ ID 2749

ATGCGCTGTAAGTCTGTTGGCGTTTCAGACGSCATATTCGATGAAAGATGATGATCTGAAACCGCGCGCTCAACCGCGCTTTCGCCCATACTGTATGAGATGCTGCTGGTGC
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TTTTCCGCGCACTTGGCAGGTCAGGCGGAGCCTTGGCGATGAGGACATGGAATTCGCTTGTGCGACCTTAAACGGCATAACGCGCTTTCACCTGCTGCGCTTTCGCTTATTTGG
GCGTGCATATTCATGCTTTCATCTATGCTTGTCTTATGCGGATTCGCGCCTTCTTCGCGATTTCGCGCAAGGCGCGCGCGCGCGCATTTGTTGCGTATTTGCGGTGGGGT
TCGCGCTGCTGAATCCGACCGGAGTTTCGATGACTTCTTTCGCGCAAGAGGTTGCTGATGTAAGAAACAATCT

SEQ ID 2750

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SEQ ID 2751

ATGCGCTGTAAGCAGCAACAGACTTCAGACGSCATTTGTCAGAAAGATGCTTTCGCGCGTTAAGCGTTCGCGAGCTTCTGACCGCGGAGCTTTCGCGCATTTGATTGATTTCCTGA
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TTGCTTCTGATTTCGCTTTTCGCGATCGATTCGAATTTTTCAGAGCTTCGATTAACCTGCGGCTGCTGTCGCGGATGTCCAAACAGCGCGCGCGCGCGCGCGATGAC
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SEQ ID 2752

MPSETPTDFRRHLCKDALRLTVRTPLTARLFCRHLIDFLTCRAFFEHVRLVHRTFLRQADQGNRIFVLVLSAAVVHTAQVCLVDSAFFGIDVEFFQTFDKLALLSAGCPNKAARSGGDD
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SEQ ID 2753

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SEQ ID 2754

MSSGNIRIHSMTGFANAAECGSKRINLDIRAVNHRFLDIQIRMPDDLRLHENGIREQISSHLARGKVBCKIQIQDAENGNSLEARNVLVQGLAEINKNLAKHYDLAKLGVADILRFPV
LASQKWEALAKTIVELADKALDPTAARRREGKLGHEHLQRIKNEETIDALSEIPFALVEAHKERTRLAERAVGSINDRLQEFALFIQKSDIDEFSLRLTHIAEVRRIVTEHK
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SEQ ID 2755

TTGATACATTTCCCTTCTTCGAGCAACAAAGCGGTGATTCCAATCTACCGCTGCGAAATCTCAATTTTTCACACCGCAAAACGCTTTCGCGCATACAGATG

SEQ ID 2756

LHFPSLQQQKRVPIYRCRIFNFSHPKTLAAIQM

SEQ ID 2757

SEQ ID 2757
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SEQ ID 2758

SEKID IP 2758D
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GAREAVYAKQSMEEFMTVVRQMRLATLLHSCNFIVNTSILFLSTAALGTLWHNGQVGVGAVATATAMALRANGLSQTIVMESARLFENIGIVNDGHATLSKPHITLDPQALPLMVPQGA
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GGFLSEHVEHQD

SEQ ID 2759

SEQ ID 2759
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SEQ ID 2760

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SEQ ID 2761

SEQ ID 2761
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TGAT

SEQ ID 2762

SEQ ID 2762
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SEQ ID 2763

SEQ ID 2763
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SEQ ID 2764

SEQ ID 2764
MIFASRWLQVPIYAGLTVVVRAICAYKFLKSLKHLVNNLDSVDENAIMLAVLNLDVVMIANLLTMVQIGGYESFVSRRLRIDDHPRPEWLSHVNAPVLKVRLSMTIIGIHPSICSKHLSIP
PICRKS

SEQ ID 2765

SEQ ID 2765

GTGGTTGAGCCATGTGAATGCACCGGATATGAAAGTAAGGCTGTCGATGTCGATTATCGGTATTCATCCATCCATTTGCTCCAAACATTTTATCAATTCCGCCAATCTGTGGGAAAAGCAGC
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SEQ ID 2766

SEQ ID 2788
VVEPCECTGIEGKAVDVDYRYSSTIHLLOTFLNSANLSEKQLMHQCLVHVCFLISALAMANADKIVYGTTHKPH

SEQ ID 2767

SEQ ID 2767
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SEQ ID 2768

SEQ ID 2768

MNNAPALPAIQSGNSGLEQYIHTVNSTPMLSQBEETRLAERRIKGLDNAAQQLTSLHLVVVSTIARGYDGYGLNAQDLIQEGNIGLMAVKRYEPGRGARLPSFAVHWIKAEITHEFTLENN
RLVRVATTKPQKLFNRLSMRKNLNLVLSPEAKQIADDLGVKLSVLEMBQRMTHGDIAIMADNSDDSDSPAPIDWLADHDSEPSQLSKQAHYALQTEGLQNALQDDRSRRIVESRW
LQDDGGTLHLQAAEYGVSAERIRQIEAKAMQKLGFLTERAAV

SEQ ID 2769

SEQ ID 2769
ATGGCGGGTAATCGGAAAGCGTTATTCATTTCGGGCATTTCTCTTCGGCTGAAACTGCGTATCGGGCGTTTGGTGTTGGGATGCAGTATATCACTGCTTGGCTTGTATTTTGTATGTGT
GGCAGGAGATATACGCTTAAGGTT

SEQ ID 2770

SEQ ID 2770
MAGNAKALFIWGISFRLKLRIGGLVCWDAVYHCLACILYVWQETYAKV

SEQ ID 2785

SEQ ID 2785

GTGGATTGGATGAACACGCTGTTCTGCTGGGTGGCGCACTGTTGTCTCGAGCGTGTTTCGACCATTGTGCCGACGTTTGGGAATGCCCTTGCTGCTGGGTGTTCTTGCCGTGCGCA
TGCTTGCCGGCGGGAAGCGTTGGCGGCATTGCTCTCAATAAATGTCGTGATGGCGAATTTCATCAGCCAGCTTGCTTTGGCGGTATTCTGCTCGACGGCGGTTTGGGAGCGACAGCTTTC
CAGTTTTCGGATTGCGTTGAAGCCGCGTCGCTACTGCTTCGTGGGGCGTGTTTGCCACTGTGCTTCGCCGTGGGACTGTTTGCACACTTTTAACTCGGTTTGATTGGAAGATTCGGCGTG
CTGATGGCGCGGATTGTGCGTTTCGACCGATGCCGCGCGGTATTACGCTTTTGCGCAACAGCGCGCTGCGCTTGAACGAAACGGGTGACGGCGACTTTGGAATACTGAATCGGTCGCAACG
ACCCGATGCGCGGTTTTTTTGGTTACCGCACTGATTACCAATGATTATGACAGCCGCGGAATCGGTTGCGGCAAGCGTTTGTCGGATGCTTTGGCGCTGCAAACTGGGTTTCGGTCTGACCGG
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ATATTGGCTGCGGGAAGAAAGAAATGTGCAGATGTGCGGCTTTAAAGTGGTTGCCGAATCTGAAGCGGAGGGAACACCTCCGATACCGTCCGAAAGGTTTCCGATTCTGTTGACGCAAG
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CAATGATCGGGTCTATGGGGCTGAAAGTACCGGCT

SEQ ID 2786

SEQ ID 12786

VDDMNSFLFDGALLFLSVSVTTLSARLGMPLLVLVFLVAGMLAGEEGVGGIAPFNVVMANFISQLALAVILLDGGRLTQLSSFRIALKPPASVLASHGVFATVFLPLGLFATFYYLGLDKFGV
LMAATVSGTLAGAVFSLLRNSGVRLNERVQTATLEISGANDPMAVFLVLTALITMIMQPAESGAAPFVMLALQIGFGLTGWAGGKTLAKLVRRNLNLAEGLYAISMVLSGGLLVFPATFNH
GSGFLAVYLAGITVGNQRNRAZHVLRVMDGLAMLAQATFLVMLGLLVSYPAGVLDRAAELATAAFIMLVARPLVSPFGGLKWFNYSLRKAYTISWGLRGAVFLSMAMLVHGVFVNSHLL
FDVAFVAVVLSLLIQGTFIPVMARLLKVMNPKEPKDITMLAEKETVRMSAQITVGEESABGHDPDTEVSDSPFCALIRNGSRITEMQDGLQADLAWYITLADGKVKHAKY
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SEQ ID 2787

SEQ ID 2787
ATGAAATAGAAATCGAAAGATTGTAACACGGCATTTCCTCTCACGAAACTTTATTCATGTCCGCCACCGCCTTCAGACGGCATTTTCCTGTTTCATGCCGCTGATACCGCCCAAACCC
GGGTCTCCTATATAATGTCGGACTTTGGCGCGCATTCAGGATTTTTTATGGCATTGGCTCACTATTACTCTGCGGACTACATCGCGCGGCTTTTGAGCAGATGTTGGCC

SEQ ID 2788

SEQ ID 2788
MKIISKDCNTAFSSHETLPFVHRHRLQTAFCFMPDPDTAQTRVLLYNVGLCAAFQDFLHHLPHYLLCRTTSPFFWTEL

SEQ ID 2789

SEQ ID 2789

GTGCAACCTTACTACCGAFTTCGGCAAAAAACCTTTCACCGCGTACGCAAAATCAACAACAGGTTTCAACATTAAAGGAAACGCCAATGAACACAACCGACTGCCGACGCCCTTCATCT
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ACCAAAACGACAGCAAAATCGCGCTTACAGCGGCATTCAAACTCAACCTTTC

SEQ ID 2790

SEQ ID 2790
VQPYRRFGKTKTFHLRKINKKVSNIKETPMNTTLPPTAFILCCLCAAASAAADNSTMTKGQKVYESNCIACHGKKGEGRGTAPPPLFRSDYIMNKPVILLHSMVKGINGTIKVGKTYNGFH
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SEQ ID 2791

SEQ ID 2791
ATGCCGTCGGAACACCCCTTTTCAGACGGCATTTCACACCCACCCCAAAGAAACCATGAACGACACCGCCCAAATATACCGCGGGCTACGGCCGCGCTACATCGTCCGACGCCCGACG
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CTGCTGCGGAAACCGGGCAGCAACCCCGAACCGCTTCGCTTTTTCAGGGCATCACCGACGAACTGCTCGGG

SEQ ID 2792

SEQ ID 2792
MPSEHPFSDGISYPNPKETMNTAQITAGYGRRIYIVRTDGTTYEASTRKKRVDFACGDRVRI SFVNABQVVIEDFLPQSQLLYQDAWTKLIAANVTQLLIVTAAPVSPSVRLLRALL
AARAAGIRAVIVLNRADLPETALWLEKLKPYETLCYPIVETRVLENADSLRPVLVGGSNILLGQSGMGKSTLANALLGSGTARTGDISAALDSGKHTTHARLYDLNGETQLIDSPGLQEF
GLHHLOADLPHYFPDFRHLVGQCRFHNCTRAEPCCAFKAAAEAGASPERLAFLOGITDELLG

SEQ ID 2793

SEQ ID 2793

ATGATTATPACTCTTTACGGGAACACTGGGGGCGAGCAAAACCCCGCGTCGTCCTATGATTTTGAAACAACGAAGACGGATTGTTCAAAATGGAATTGGAAGACGGCAGGAGCGAGACC
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CGCAGGCGGTGACCGGCGTAGAAGCCGCCAAATTTGGAACCGCCTTAAAGAGCCTTCAAACTACTATAAATCCGCAAGCGCGCACCAAAAGTTCAGAAAAGTGCCCTTGGCGCGCTTGGCG
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ACGGAGCAGCAGCGCATCATCAGAAAACGCGCCCTTTTGAGCATTCGCGCAATCTGAAACCTTGAAGACTTTGTGCGGCATTTGCGCGAAGAACCCCGAAAGCAAGCCCTATTTATAACACAGTCC
GACAGATAAACCTTTGACCAAACTCGCCGATGTCATGACAGCGCGGAAATCAGATTGCACATGCTATTCAAATCAAGGAACACCCCTTGAAGAAATAACAAAGATATATGTGTAAGAAATA
TGTGAAAAACGGGTTCCTTTCAATCCTTTACAAGGACGAACGGCAAAGGACGGAACAGGCGGCACATGTCGCGAAGCGGACAAAGCCCCAAGTTCCTGTAATGGCGGAAAGTCC

SEQ ID 2794

SEQ ID 2794
 MYLFTGMNGAGKTPRVVSMILNNEEDGLFKMELEDGTEADRPLYPCHIDGLDKRRKFNARELAEGQIMSAPLRDVIPEGAVLIVGEAHYTPVRAAGRPVPPYIQELTELRRHGHFTVILKTR
 HPSQLDITPVNRNLSKVHLERKAIGMKQYYWYKCYPTSLDNAPGVSQVEANMKPKPEAFKYKKSASRRHQFKKKKVPMAVWALLAVGVFGWKSQYGMQVYSKATDSRIEQAQKESVQTH
 TEQTASSETAPPFHSNDNLKPEDPVPTLPEKPKSKPIYNTVRQVKYTPQIAGCIDGGKSDCTCYSNQGTPLKEITKIMCKEYTVKNGLFPNPYKDERQTEQAQSAKADRPVLVHGGS

SEQ ID 2795

SEQ ID 2795
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GCTGTTGCCGAACGATGCGCCGACCTCATCGTCCGCCACGCCATGACTTACGGCAATCCTTCGATAGCGGATGTAATTGCGCGAGCTGAAATCCCAAGGTGATGGCAGATTGCTTCGGATTTC

CCCTGTATCCGCAATATGCCGCTCCAGCAGCGGAGCGGCGGTAGATAAACTGTGCGCAACACTGCTGCTGCAACGCAACCAATGAGCGTCCGCACCACTTTTCGCGCTTTTATGATGATGC
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TATCCCGCAGAGTGGCGGCCACACCGCCAACTGCTTTGCGAAGCACTGGAAGTACCGGACTGACCGAAGACGAATATACCGTATCGTTCCAAAGCCAATTCGGCAGGGGCAAAATGGGTACACCGAGCA
CGGAGATTGTGTCGCGCAAACTGCCCAACAGGGGGTAAACGAGCTGGACGTATTCGCCCGGGCTTTTGGCAGACTGCTTGGAAACCACTGGAAGAAATCGCCTGATGGGGCGGGAACA
GTTTATTGAAGCGGGCGGAAAAAATACCCTACATCCCTGCCTCAACGCAACCCCGACTGGATAGACGCACTCGTGCACCTTCCGAAGAAAACCTTGGCGGCTGCGCT

SEQ ID 2796

SEQ ID 2796
MPSEAASDSILPLYPACTIFQKPIMLPFLPEPSLSYVQQRNTAVLLNLGTPDAPTAQAVRPYLKSFLLDRIIVELPKNLWYPIILHGLVLFRPKKSAHAYEKIWFKEGSPLEVVYTAQAA
ALAEKMPDLIVRHAMPTVGNPSIADVLAEIKSQGVGRLLAIPLPYQYAASSSGAANDKVCEQLLRNQMSVRTISRFYDDAGYIDAMKNHILRYWAEHGRGKKIMLSFGVGPQKHLYDLGP
YPDECRHTAKLLAEALLETDEYTVSFQSQFGRAKWVTPSTQDLPGKLPKQGVTELLDVFCPGFLADCLTMEETALMGREQFYBAGGKNRYTIPCLNDNPWDALVALAEENLGWR

SEQ ID 2797

SEQ ID 2797
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 TCTTCGCTGGCTGGGCGGAACGGGACAAAAAGCCTTTGAAGATTGAAAAACCCGAACGGCTGTCGCGATCGTGTCAAGGCGCGATGTATGAGGATTTGCGCGAAGAAATCTTTGCGCGGTT
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 AAATCTTTGGGCGCGCAATTTGAACACCATCCACCATGTCATTTCTACCAAGTCATCATGGCGAAATGCGCGATGCGCTGCGAACAAAGGCAAAATTTGCCGACTGGCAGGCGCAATTTCCACGA
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SEQ ID 2798

EQ ID 2798
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 SLRWAERSKKAFEDLNPNPALFGTIVGQAMYEYDLREESLRGLEEFFDPGLAVGGLSVGEKPKEMYRLHVAVGPMLEPKPHYLMGVGTPEDLVYGVAGHIDMFDCVMPTRNARNGLFTRPG
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SEQ ID 2799

EQ ID 2799
TTGCAAGAGAGATGTGCATTTCCTTTATGCAACATTTGTGGCAAGATTTGGGGATACCGTCTGAAAAACCGTGGGAATTCATTATATAATCCGCTCTTT

SEQ ID 2800

LOERCAFLYATLNQDLGIPSEKPWEFIYNAVF

SEQ ID 2801

SEQ ID 2801

ATCGCGGTATTATTTTAAATCTTTCGGAGCGCTTGTATGTTGAATATTACCTTGCCGAGCTGTTTCAGTCCGCCAATACGAATCCCCCGTTACCGTGGCTCAAATTGCTGCGTCTATCGGTGCCG
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ATCGGTGATAAAGAGAAACAGAAAAACAAAGTTCGGTACGCCGAAAGCGGAAGACTGGGTCTTTGGAATTTGGATGATTTCAATGCGCAATTGCAGCAAGAAATCACTGATGCGCTCG
TCAATCAT

SEQ ID 2802

SEQ ID 2802
MPLPFLNSERILMNIITLPCDSVRQYESPTVVAQIAASTAGIAGAANAAGVAGVNGKLVADCAPIVEDSAVQIITPKDQEGIEIIRHSCAHLVGHAVKQLYPIAKMVGIPVIEGFFYDIATEK
PFTPEDEVAAITARMKELIAQDYDVVKIMTPRABAIKIPOERGEYKLRILIDMPEVBAAGIYHHQEVDMCRGPHVPNTRFLKNFKLTKLAGAYWRGDSNNEMLQIRYGTAWATKDELKDY
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GRSWCGTQLQDFVLPERLDAYEYVTENNDRARPVMLHRAILGSLERFIGILINENHAGSFLWLAFPVQVMNITENQADYCREVAAKLQAAGFRAELDLRNEKIGYKIRDSQYRFPFYQIV
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SEQ ID 2803

EQ ID 2803
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 GGGCGATTTCATCAAACTCAGATGCGCAACATCAACCGCTTCCTTCCGACGGCGATAAAGTCAAAGTGACATTCGCTTTCGCGCGCGTGAAATGGCTACACAGCAACTCGCGCGCAACTT
 TTGGAACTGTAAAGAAGATTTCGCTGAAGTGGCGCAATTCGAGTCCTTCCCAAAATGGAAGGCGCTCAAAATGCTGATGATGATTCGACCCGAAGAAAAAA

SEQ ID 2804

SEQ ID 2804
VRLISESGEQLGVSVREALAMAEQDVDLVEISPTAKPPVCKLMDYGRKYQQAKKRDEAKKNQKQVQIKEIKFRPGTDEGDYQIKMRNINRFLADGDKVKVTLFRFGREMAHQQLGAQL
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SEQ ID 2805

SEQ ID 2805
ATGCCACGGTTTTTCGCCCAATTGAAAACCTACTCCGAAGCGGCAATCGGAGTAAGCGGAAAAATTATAGCTTTATTTTTCTTCGGTGCAATCATCATCACCATTGACGGCCTCCATT
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GCTTCACGAAC

SEQ ID 2806

MPRFFAAIENLRSNGNSRKRKIALFFLRNHHHLTAPHPFGKGLDLRHPFSQIFFYTFQKLRALLVSHFTAAETQCHPDFIANGKEAVDVAHLDLIALICTRTEFNFINLHLLLVFLGF
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SEQ ID 2807

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GCGGAAAAAACCGTTAAAGTACTGGGTAAACGCGGTGTGAAACGCGCTCATGCGTTCAAACGCCACATCTTGACTAAAAAGACCACCAAAAAACAAACGCCAAGTGGCGGTACCTCTAT
GGTAAATGATCGGATTGGCTTCTGTGTGCTAAAAATGTTACCTACGCT

SEQ ID 2808

LRQKTVALWQVFETDVLKPPNALSINWSPFPHKMKTKSSAKRFRKVLNGGVKRAHAFKRHLTKKTKNKRQLRGTSNVNDRDLASVAKMLPYA

SEQ ID 2809

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SEQ ID 2810

LPTGAEMKPSAEGFGPTASVLQKCYNPLFTGTPETMKKNTPKSPREALSRLSTQSMQEMPLDALAAVQEGNELVRYCQTKLAQVEQKLQVLADGTEKLNLESDE

SEQ ID 2811

ATGAGAAAAACCAAAACCGAGCCTTGAACCAAAAGAACACCTGATGCTTCCGCGCTTGGAAACCTTTTACCGCAAAAGGGATTGCCCGCACCTCGCTCAACGAAATCGCCCAAGCCGCCG
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AACGCGCGCGTTATCGCAATTGCCCGCAAGCATCAGGCAATCTGGCGGAGAAAAATTACCGCGCTTTTGACCGAAGCGGTGGAAGAAATCAGGATTGGCTGACGATTGGACAAGGAACGG
CGGTCACTTCATCAAAATGACGTTGGACGGGCTGATTGGCGTTGGTTCTCTCCGCGCAAGATTTCGATTGGGCAAAACCGCGCGCATCATCGGATAATGATGACAACTTGA
AAACCATCCCTGCCCTGCCCGCGAAA

SEQ ID 2812

MRKTKTEALKTKHEHMLAALETTPYRKGIARTSLNEIAQAAGVTRGALYWHFNKEDLFDALFQRICDDIENCIAQDAADABGGSWTVFRHLLHFFERLQSNIDHYKPHNIFLKEHTBQ
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SEQ ID 2813

TTGCTGTGTTCCAAAGTCCGGATTCCCGCTGGCGGGAATGACGAATCCATCCGTACGGAAACCTGCACCCGCTCACTTCTACGAACCTACATCCCGTCATTCACCGAAAGTGGGAAT
CTAGAAATAAAAAGCAGCAGGAATTTATCGGAAATAAC

SEQ ID 2814

LLLFQGPDSRLRGNDISIRTECTTSLRTYTPSPRKWESRKKQQEFIGNN

SEQ ID 2815

GTGCGAGGCCCCAAGGCACTCACACTTATCGGTAACTCTGTTTGTAAAGAGCGTTGCGAAATATATAAGTATCCCTTCGCGCTGTCTAAGATATCTCTCGATATTTCCGACATTCGCTGCT
ATACTTTTCAGTTCGTCGCCCGCTTCGGCAGCGCGGAAGAACCGCAATATACGCTTAAAGAGATTTCGCGTCAACCGTTTTTGAATAATTTTA

SEQ ID 2816

VRGPRSHLSVICFVKERCEI IKYFRLSKISLDSIPCTYTFQVFRFGSGEEPNTYKLEICGQPFPEKIL

SEQ ID 2817

ATGCCACCGGTAACCAACCGGTGTACCGCCCGTCCCGCTCACAAAAATCTTCGCGTTAGCCAAAGGCTATCGTGGTCTGCTGTAACCAAGCTTTACCGCGTTGCCAAGCAGGCGGTAAATGA
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CGGTCTGAACCGCGCTCTATCGAAATGACCGCAAGTATGGCTGATTGGCGGTGTTGATAAGCGCTTTTGCACAATTTGTTGAAACGCAAGCTGCTTTGCGCTGCT

SEQ ID 2818

MPRVKRGVTARARHQKIFALAKGYRGRKNVYRVAKQAVEKAGQYAYRDRQRKRQRLWIVRINAGARENGLSYKFMNGLKRASTIEDRKVLADLVDFDKAAFAQLVEKAKAALAA

SEQ ID 2819

TTGCGAAATCTATGTGATTGATTCTTTCTTTAAAGTCTATTTTTTAAATAAATTTGCGTTAAATAACAGAAAAATTTATCCAATGGATTGGCGGTGAAGAAAAATAGGTCGTC

SEQ ID 2820

LRKPYVIDFLSLKSIPLNFKALKYRKFIQWIGREENKV

SEQ ID 2821

TTGCGCGTGAAGAAAAATAGGTCGCTGAAGAGTCTGATATGTCAGGCTATACAGCGCGCTCGTTGTTTCAGGTGGCATACTAATTTGACAGGCTTGATATATGAAAAATGTAAAC
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GAA

SEQ ID 2822

LAVKKIRSSSESDMSGYTGGLVSSGGISLIDRLDIMENVNRIVAEGIAVEAAQDFNALEQIKARYLGTGELTGLLKTGLQMSPEERKTIGAHINECKNRFPQAFNAKRDALNEAKLQAR
LAAEALDTPLPRAQEGGSLHPVTLTQRVVELFHGMGEVADGPEIEDDFHNPALNIPANHPARAMQDTFFVENGDLRHTSPQIRYMLDKKEPPIIRIAPGRVYRVDSDATHSPPF
HQAEGLVVEGVTADLKAFTDFIRRRFFERDDLQVRFRSPFPFTEPSAEIDINGENKWLLEVGGCGVHPNVLKVNIDPEKYTGPAFGIGLDRFAMLRVNVNDRLLFPNDNLNFKQF
E

SEQ ID 2823

TTGAATAATCTCAATAAACCCCAATGGATAAATTAACCCCGGAGCAGCGCAAAAAATGTATGCAGTCCAACAAAAGTACAGGACGAAACCCGAGCTTGTGTTGGCGAAGCAATGTGGG
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ACAGAAAAAGCGGTAATAAGGGAATCTGAGTTTGGATTGCCAAAAATGAGCGCAATATCCAAGGGATATAGAAGTAACAGCGCGCTGAAAGCCGAGGCTGGACGGTTTACGT
TTTTCGAGTAACGATGCTGCAAAAAATACAACCTGTGCGGAAAAAGTCAAGAAATCATCCAACAAGA

SEQ ID 2824

LNKSKQINPHDKLTPBQRKCMQSNKSTGTPELVAKAMWALGLRYRKNSGSIPGKPDFSPKRYKAVFVDGEFHWKGDWEQKAVINGNREFWLAKIERNIQORDIEVTGRLKABGWTVLRL
FWSNDVVKNTTCCAEKVKELIQT

SEQ ID 2825

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ACCTTATCAAAA

SEQ ID 2826

VPKSKSKSSQDELIYKNKIKEDGQDERLKEKAAQYRLFENNDTFQTALKPKFTTIDLPAGIGGFRIAMQNLGGEYVFSSEWDEKAKLYEANPGEVFPDITLERIKQYIPKQFVILCGF
TLRK

SEQ ID 2827

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AAAATCTGTATGTACGATTTCCTTATGAAAATCAGAAAGATAGC

SEQ ID 2828

MCCVGLPYQNKDFRNMRLSDYILNNKININLSKQVQRIIDYPSSEIDMLLASEKELKDYDVLYLKLVLGQQYVQGIKRSVLYDFLMNQKDS

SEQ ID 2829

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AGAGAAAATATTTTCAGAGT

SEQ ID 2830

MKKWTRDETILVALYLYIIPFKVSKDNPIQYVARI LGRTPSALGMKIGNLRLDPTLKVKNISGLSNGSKMDVVVWNEFSGDWELNKEFEGVISYQYQSNDESNIEIESPEIKPKRER
PARISVRVWQGFRRSVLAAYNNQCCITGLKQPELLVASHIKFWGEDKDNRLNPRNGLCLNALHDKAFDRGLLIDENPKIIFSPILLAKTEGFDLPKPYENRMIRLPERLNPSLEFLKPH
RENIFQS

SEQ ID 2831

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SEQ ID 2832

MQFSYSLKTOANPDLADKLEHLLTMAGLEVEIDTAAPAFSGVVVAEVKSVEKHPDADRLNVTQVDAGTGELVQIVCGAPNVKPGIKVPCSLPVAVLPGNFKIKPTKMRGVPNSNGLCS
TNELGLPDDGVDGLHILFEDAPVGTNIREYLDLDMFLTITPNRADCLSVKGIAREVSALTQCAFTTPEIQTAPIGSEKKQAVRIDAPADCGRPSIRVIENVNKAATPDWMKQRLERS
GIRTSIALVDIGNYVMLEIGQPMHVFADKLSSGLIVRRQNGETLACLINEKTVPPLADNPLVVADEKGLSLAGLGGAAASVSDGTQNTVLEAAWFPEIIVGKSRQYFGSDSSFRFER
GVDYRLQADAIERATLVLQICGGAAGEMVBAQGLPEAKQVGLRLGLRLKTVLGVDPABQVETILQHLGLQPEKTAEGFRITAPSFRFDIEADLIEEIGRVYVENIPDYTSGLRLM
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SEQ ID 2833

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CATTTGATATGACGCAATCAAAAACAGCTGCTTTCCTTCGCGG

SEQ ID 2834

MPLLSGLIFLLGILLMLIVRIILATGLTFVYAGYLALEKFKGTANAINSMPSDIINLLLSISGFGGLGCLFGAPSFPIGMHAFKRLTFVFPFG

SEQ ID 2835

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SEQ ID 2836

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SEQ ID 2837

ATGACAAACACCGTTGATTGACGATTCTGCAAAACGCTATTTACAGCTGGACGAGTTGTGCGGAGCTGTGCAAAATCAGCCCCATGTTTTCGCCAATGGCAACATGATCAGCGTGTGG
TGTGCGGTACGCGGAGAACCTACACCGTTTGGATGTGTGAACTGTGAAACTGAAAGAGCAGCTTTCACCGGTATGCAGAGGTGCGGAATCGGGTTCGGACGGCAACCGTCCGT
TACGCTTCAGGAATCGAGAGCGGTCTGAAAGACCTGTGTGAGGATTGTGATAAGGAGTTGTGC

SEQ ID 2838

MTNNVLTIPAKRYFTLDELCLLQISPYGFAQWQHDHGVVVVYGGERYTRLDVVLLKLESTFPAPYABGAESGSDGNRPVTLQEIQDGLKDLLEDLKELC

SEQ ID 2839

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SEQ ID 2840

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SEQ ID 2841

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SEQ ID 2842

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SEQ ID 2843

ATGAGTGTTCGGATATATGGGACAGGATGCTGAAATCTATCATAGTATAAGAACCGTCCGCTGTTTTAGCAGTGGATTGTGTGATGGGTATGTTATCATAGAGCCGATGAGGAGC
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SEQ ID 2844

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SEQ ID 2845

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ACATCATCACTTAAATTTTCGACCGTACCCATCTGCTCCATCCCTATCTTCCA

SEQ ID 2846

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SEQ ID 2847

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SEQ ID 2848

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EHEVVPDIMGKLSGGYMTLAAATISQKVETETISRGEAGVPMHGPFPANPLACAVACASVKLLLSQDQANIRRIESILKRLKAANDIRGVKDVRLGATGVTELEKGVDMARFOA
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SEQ ID 2849

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SEQ ID 2850

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SEQ ID 2851

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SEQ ID 2852

LFAHPEKNAVYIRWVLLIVNKYKVNMDKNEIQKINDKYPWHEDDFKSYEDIAKDVSLATDKPTIEHYLLEVYSEENGHFDQDNVHAMIGRIKNAI

SEQ ID 2853

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SEQ ID 2854

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SEQ ID 2855

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SEQ ID 2856

MDGVGKNRRGIRIKDMEHFLGKWLPLPAPVSDGIDLPMSRLKARSITAAALCALPHTFVRLKLGEABTEYGRRRVRDVLKLDGTAVVQARSACSVGSFAWQNLDCGTRPLGERLF
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SEQ ID 2857

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SEQ ID 2858

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SEQ ID 2859

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SEQ ID 2860

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SEQ ID 2861

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SEQ ID 2862

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SEQ ID 2863

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AAAATTTCCCGGATAGGCTCATAAGCTTCTCTTTTCAGACATCGCAAAACAGAGGATGTACCGACTGCGGGGCAAACTCAATCCCGCATACGGTACGGGCT

SEQ ID 2864

MLFWENLPASLDKTSKSPVAFSGTSKIKTSETGLPSGASNP TGSRVRMNPVACFTLAWRPWGMATPCPKPVEPSFRAKRHSKTSAMDWEDSRKSRPASSNSLFLIPTSLSKFTWDRG
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SEQ ID 2865

TTGCTTGTATTTCCTGTGCGCGTGTGCCAAAAATACCGCCGACGAAACAGGGAAGCGGAAAAATGAGGTACAGGCAGACGAGCGTGGG

SEQ ID 2866

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SEQ ID 2867

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SEQ ID 2868

MHSIYFPKFKQMSQTDARRSGRFLRTVEWLNMLPHVPTLPIITVILLIASAVGAYPGLSVDPDPFVAGRADDLIHVSVLLDADGLIKILHTVKNFTGFPALGTVLVSLGVIAB
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IGYVPTKEIVBQLGPYQSDLSQEEKDIRHSNETPLEYKGLINAGVVPVALSALLAWSIVPADGLLRHPTGLVAGSPFLKSIVVFIPLFALPGIVYGRITSLRGEREVNMAESHS
TGLYLVIIFFAAQFVAFNFWINIGQYIAVGAVFLKEVGLGGSVLFIGFILICAFINLMIGSASQWAVTAPIFVPMMLAGYAPEVIQAAAYRIGDSVTNIIIPMHSYFGLIHATVIRKYK
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SEQ ID 2869

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SEQ ID 2870

MPSISVRRLPDDNQYKLQAWAAGNSGADNRIGVEADRPVLAHVHNLPHNPQIVVGLAESEYLNRLSEGTGYQFGDLFDISMSLVIVANDLPVSPGLRDYCHNDIPLITSKLESPY
LMDVLRILYQRLTAASSVKHGVFLDVFEIGVLIHSHGLKSELALELISRGHSLIADDAVELFRIGPETLEBRCSPMLRDLFVRLGLILNRHIFGETSIRPKIILQLINLEADDEY
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SEQ ID 2871

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TGTCCGACGCGGCGAGGACGGGCTTTCGCGCTTACGCGGATCAGGTTGTCGCAACCGAATTCGCGCGCGCGGAGGCAAGTTGCAACTGTGATGTTGCTGCAACAGCGCGCGA
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SEQ ID 2872

LPPEPSPILRTIFMILFVFFKLRLMAPOKPARTVFAAQLQNVIAVRLNQNKGVASDGDGQNRNDDVDVEDGFGGADAQPVLLHLVVRLDQIDNELQDFPGADGSPAENHADIEYPOA
AHFQKIAQHRRTFFPQCFRTDAEQLDRIVGNQMAARNPQCFALITQTRMSGNHADFKHIEKVAFDGRCCQVQALQVNPQHILQIRAFEPGQGDVVVFAVVAQPRGNRQIVCHNDQR
HGNIEQVSELITRLPFEAVQIFRLRQTDHLDLVCMDEIQVSDQGEDGLVRLYADTVVTRJAGGPGKLQVLVVRQAADGDTGHILFPFGQDAGFFRRSNRHRPDAFLGKLQAGQF

SEQ ID 2873

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GCGC

SEQ ID 2874

MKIVLISGLSGSGSVALRQMEDLSYPCVDNLPLEMLPSLVSYHIERADETELAVSDVRSIGIDIAQAREQIATLRGLGHRVEVLFVBAEAVLVRRFSETRRHHPLSNQDMTLLLESKE
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SEQ ID 2875

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SEQ ID 2876

LTGLAARQVRLPVPYQQTITFPQSGEFFDNDIRTHLPAGTADGDNVAPAFILQTRQPTRNKPFDVANHFLRQLRSVQIIPNGLVHTGVRPQLGIVIRVGTQTAHIEHKIGVVRHTVFP
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SEQ ID 2877

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SEQ ID 2878

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SEQ ID 2879

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SEQ ID 2880

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SEQ ID 2881

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SEQ ID 2882

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SEQ ID 2883

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SEQ ID 2884

LACVAHEGDFGIVFLPFAFAVIGLGFPGGPFILFLGKRPGGKRGFGKQRRAVLDPDIEKRHPFQQLQCPVLDRFQYPCFSGLDDKGLPRFGFRHHNGAKYQVFPQKSHFLRRI
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SEQ ID 2885

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SEQ ID 2886

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SEQ ID 2887

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SEQ ID 2888

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SEQ ID 2889

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SEQ ID 2890

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SEQ ID 2891

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SEQ ID 2892

VFSIFYREDWYVYVNIIMFCGRDGMRLKESGSAF

SEQ ID 2893

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SEQ ID 2894

IDQATQCLQFDSINLIEHILPDVRFVLVPSRTRLHEHFFHHSWQTEAIPQTESKDXPWFALPQTSERKKPEHVLVIGAGIAGASTAHALASHGISVTVLEARKAAQASGNRQGLLYA
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SEQ ID 2895

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SEQ ID 2896

VPLNGATVNSFIPIPKPLTQFALIWTISYGTAFPTSASHTKPSANTHTRST

SEQ ID 2897

TTGTATGCCGAACCGAGGTGTTTTTGAATAATATTCCTGTTGAAATCCGTTTGTGAAAAACCGTGCCGCTGTGGTTTGTACTTATGGGGACGAACCTAAAAATCTGCCTGCCGAATTTT
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SEQ ID 2898

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SEQ ID 2899

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GTGAAATTT

SEQ ID 2900

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VKP

SEQ ID 2901

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SEQ ID 2902

LFACLPFVARVPKIPPHETREGENEVQADDGKVLPTLIVYRSRTGFEDVGRKGQRETCRQLDQVSEMPALERGHAEQSGREEGVGKDECDQDKDVHCGHDGLSVWALSAAMPSELH
CGTAYLANKGSL

SEQ ID 2903

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SEQ ID 2904

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 PLQAPSRRYFQEGGRSDGIPGRTDYAALGQTPPEPQPPFDQPVENAEVPAEIQDEFIRFWRNPVKVWLQQLAWSBPHIGRAWPEAPPEPQHAQIABTYTGAARBQDPSQTAARIA
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SEQ ID 2905

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SEQ ID 2906

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SEQ ID 2907

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SEQ ID 2908

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SEQ ID 2909

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SEQ ID 2910

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SEQ ID 2911

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 CGGACAGG

SEQ ID 2912

MNNRHFAVIALGSLNDNPAQQIRGALDALSSHDIRLEQASSLYMTAPVGDNDQPDFINAVCTVSTTLDGIALAELNRIEADPGRERSFRNAPRTLDLDIIDFDGISSDDPRLTLPHPRA
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SEQ ID 2913

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SEQ ID 2936

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MLQORS

SEQ ID 2937

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SEQ ID 2938

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SEQ ID 2939

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SEQ ID 2940

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SEQ ID 2941

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SEQ ID 2942

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SEQ ID 2943

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SEQ ID 2944

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SEQ ID 2945

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SEQ ID 2946

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SEQ ID 2947

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SEQ ID 2948

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GIFAVFGRT

SEQ ID 2949

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GAAACAGTTTCTCGAACCG

SEQ ID 2950

VCKLTKETRMKLTLMFREYCSLCHKMRDALKPFQDEYGFGLVVDVDENPVLEEKYNELIPVLLAGDERICHWFLEDRLKQFLER

SEQ ID 2951

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CCTGATTTGATGGTGGTAAACGCGATTGAGATGACAGACAAACATTTGTGCTCCGTGTGTTCTCAAACTATCTAGCCGATAGCGGCTTTTATTTATCTGATGCAAAAT

SEQ ID 2952

MSSRKHLKSCQKQKRLNSSDGLSKTVLRNVDTNRNRLRIVRRQKRSKLPAAAAARHAQLRLQIAHCRAGSDGFLDLNVGNGIADADKHFVLRVFSNYRTDSGFYRQI

SEQ ID 2953

GTGCTTCCTTTACCGGCAGGTCATCAGCCCCACAAAACGTAAAGAACGTTGATTGAAAAAATGCCGCTCGAAGTCTGCTTCAGACGGCATTTTTACCGTTCGAGAACTGTTTCAA
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AACCGTATTCTCCTGAAAAGGTT

SEQ ID 2954

VLPFAGHQPHKNVNDLKKMPSEVLLQTAFFTVRETVSTCPHPKTSKGFPHLPPTKRESAHCIFLPKQDFPHRPLPARTRIHPEKV

SEQ ID 2955

TGACCTTTCTTTATTTTATTTGTCGGTGGGAGAATCTTAATTTATGATTTTTTCAATAAAAAATTAGAAAAATTATTGTGAGATGTCATGTTGGCAATCATATCATGTTTGTCTGT
TGATGGAAGCA

SEQ ID 2956

LTLFLPYLSVGRILNLLIFSIRKRFIVRCHNQSYHVLLHLEA

SEQ ID 2957

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SEQ ID 2958

MRQTLRLRGKQMKLLAALIPLMSVAGRILFALGLNAVTVAGVDRLAANFQQAITHSTGAPQAMLQFYISGGGTVLNIFGAIAFILSPKQMTKLATSIGKKK

SEQ ID 2959

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TTTCAAGCTGCTC

SEQ ID 2960

NRILLTGSQSLAHLRDLRPEDWETIATDSASLDITDADAVCNMVKSPQDAIVNTAAYTAVDKAEGDAAAFVNASAVYNLALAAHRAHARFIHISTDYVFDGKIPYQESDFTNPS
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SEQ ID 2961

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SEQ ID 2962

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SEQ ID 2963

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SEQ ID 2964

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SEQ ID 2965

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SEQ ID 2993

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SEQ ID 2994

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SEQ ID 2995

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SEQ ID 2996

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SEQ ID 2997

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SEQ ID 2998

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SEQ ID 2999

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SEQ ID 3000

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SEQ ID 3001

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SEQ ID 3002

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SEQ ID 3003

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SEQ ID 3004

VFGLSLIVRSVPVPGYAIAPWRLLSVLVFWFLAPFGQKFPKNRKT VRYALTAGVFLAFDLALMHESIHAVGPGISTLLNSLQIFLSAIGVFFGERLGRQAASLSNAVGVVAMIA
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SEQ ID 3005

GTGGTGATGCACTGTTTTCGCTGGGCGATGCTTCCTATGCGATTCCGCTGCTTTCCCTGTCGCTGACGGGGCTGTGCTTTTTCGCAACCGGTGCCCGCTGTTTCATCGATTATTCG
GATTGGGCAAAACGATTGAAGCGCTGCACTGGGCGGGGTGGTCTGACGCTTTCGCGGATTACCTCGGTTCGCTGAAACAGCGCTCCGAGCTT

SEQ ID 3006

VVMQCFAMAMVAYAIPLLSLSLTGLLLSEPVAALFIDYFGLGKTEBGVQWAGVVL/LSA IYLGLSKQPSSEL

SEQ ID 3007

TTGGACTGGCAGCTCAAAACCGCAAGACCAACATCCGACAAACGGCGCGGAGCGGAAATGCCGCTGAAGCCCTTTCAGACGGCATCGGGCGGGCAGAATCAAAAAGCCGCT
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SEQ ID 3008

LDWQAVTKGKTKHADNGAERKNPSEALSDGIGAGRIKKAASAGMAMQIK

SEQ ID 3009

GTGGCGGCATATGGAAATACGGACATTTATTTAGTTGCATTGCCATTCTCGCGGAGCGGCTTTTGTGATTCGCGCGCCCGATGCCGCTGAAAGGGCTTCAGACGGCATTTTCCGCT
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SEQ ID 3010

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SEQ ID 3011

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SEQ ID 3012

MSVFPYAAHTVSRKCPILFNGMGFTNGNNRLPTRRIKSTDDLTGKSYAARTHPFSRQISCAAHIDNAGKAVHIVD

SEQ ID 3013

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SEQ ID 3014

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SEQ ID 3015

TTGTCGGATGCAGAAATCCGGATTTCATATCGAATCCGGATTTTTTATTTTGAACGGAATCTGTTTTGATTATGCGCTGAAAGTGGGATTTTGATGCTTAAGCAGTCAGACCGAC
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SEQ ID 3016

LSDAEIRIHIESGFFILNGNPFVFLCRLKVGILMLKQSDRLIFLYGLKNGAVGCRATLFDAPRRHIGLFLQN

SEQ ID 3017

ATGAACAAATGCTAATGTGCGGCGCGCTGCGCGCTGCTTGCCTGATCATCTCTTTATTTCAAAGCGACAAGAAACGGCAGGAAACCGTGAATGGAGTTCCGCGCTCGAATACGCT
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SEQ ID 3018

MNTHLMSGAAALLAGIILYFKSKRQENGWSSGLEAYIILAVGVFAALSIFMSFVAVFLIFVVLGCTANGVYKYLKTHPEISSESHFGDYGFSPFVTVLVLIRSFIAEPFQIPS
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SEQ ID 3019

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SEQ ID 3020

MKNIRNFSIIAHIDHGKSTLADRFIYQCGGLDLREHSTQVLDSDIEKERTITKAQTAALNYKARDQVYQLNLIDTPGHVDFSYEVSRLSACEGALLVVDASQVZEAQIVANCYTAID
LGVEVVPVLNKLIDLPADPERVEQIEDIIGIDAVGAVQCSAKSGIGVEDVLEIVAKI PAPTGDENAPLQAVIVDSWFDNYVGVVMLIRVNGTILKLDKVRPNSTKAETQVEQLGVPTF
KSVQRELKAGEVGLITGVKELQAKVGDVTVLVANPATEPLPGFQEVQSVFAGLYPVESHDEYALRDLEKLQNDASLKFPEPSQALGFGPRCGFLGLHLEIVQERLEREPDMDL
ITTAFTVYVYEVVLSKEKIEVENPSKLPDIGSIETILEPIITATILVPEYVGNVMTLNCQKRGVQVMQYMGROVHLTYDLPMEVVMDFDKLSTSRGYASLDYHFKFQPSDLIKLD
IMVNGEKVDLSLIVHRQSAVHKRELASKMRELI PRQMFIDIAQAIGSRILARENKALRKNVLAACVYGGDI TRKKLLEKQKAGKRRMKQVGNVEIPQSAFLAILQVSK

SEQ ID 3021

GTGCTGTCGAAACCGTTTCAGACGCGACGGAACACCGCTCCACTCAATCTGCGCTGTAGCGGTATTAATTCGCGCTTCTATCCGAAATTCACAGCAGGTAGCAATATGCTTTGA
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ACGCTATGCTGCTGATTCGAGCGCATCGGCAAGGTCAACGCGCGGTTGCAACGCGCTTGGCTTATTCGCTCAATTCGCAACCGGACTGCGTCATCAACCGCGACGCGAGGCTTTGGC
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SEQ ID 3022

VLSFVSDGTDKPPPLNPAVLACIIRRSIRNSQVSNMSLKTVAIVGAMQRIELIREMMENVKAVSFGFRFSAYEGELAKRIVLALSGIGKVNAAVATAMLIHQFAPDCVINTGSAGGLG
KGLKVDVIGTETEHVDVDTAFGYARGVQPLPARFASDGIILETKRAARTFEGAEVQGLIVSGDRFVHSSBGVAEIRKHFPEVKAIVEMEAALAQTHOLEPFPVITRAVSDADE
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SEQ ID 3023

GTGAGGCGGTTTGTCCGTCGCTGAAACGGTTTCAGACAGCAGCGCGGATTTTGGTAGAATGGGAAGGTACAGATTGTTTGAAGATTGGGGACGAGGATGTTTACCGATGAAATA
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SEQ ID 3024

VEAVCPRLKRFQTRRIFGRMGRYLPEDWGTMTDENMTAKEELFAWLRHNMKNKSGDLFTVTHFPAMKLDGKITRITDEPLIAEKCMELAFSMAKQAEFFSTNECNFAISLFD
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VILIGEIRDRETFMDYAIAPETGHLCMATLHANSTNQALDRIINFFPEERREQLITDLSLNLQAFISQRLVPRDGGKGRVAEVEVLNPLISELHNGNIHEKVMKSTTILGMQTFDQ
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SEQ ID 3025

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GAACAGG

SEQ ID 3026

MIYPWHQBWQRQIAEHWTSRPNALFVGKGTGKTAFARFAAKALLCETPAPGCKPCGCMCHLFGSGHPDFYEITPLADEPENGKLLRIKIDAVREIIDNVYLTSVRGGRLVILLHP
AESMNVAANSLIKVLEPPPVVFLVSHAADKVLPTIKSRCKMVLPAHSHGALAYLRDRGVAEPEERLAFHSGAPLQEBGELREIRAKLLEILAEPRILLKILDYAALFDKELFLA
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SEQ ID 3027

ATGTCAGACGGACAAAATATTCGGCAAAAATGATGTCGTTGCAGCTGAAAGACATGAATCTGCTGTACAGCTCTCTATATGCCGTTTGTGGAACACGGCGGTGTTTGTGTCAGACCGAGC
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SEQ ID 3028

MSDQNI PAKMMSLQKMDNLLYSYMPLEHGLFVQTDVFSIGDDILLAVEILNFPKLFPTKLVAMINPASTSSPKGVGLAFTKHENCLRVKDQIEVELGSTISGRPTPTM

SEQ ID 3029

TTGTTTCGCGCAAGCAAGGCTAAGGCAGTCAGGCAGCAAAATCCCGCAATGTATTAACACAGACGCGTAGAAATGCCGCTGCTTTATCCATCTCAAAATGAATATCATCTAGCCG
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SEQ ID 3030

LFRAKQGLRQSGSKSRNVLKQTRNAGCLYPSSKLNILLAVSRLYK

SEQ ID 3031

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SEQ ID 3032

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RILRGRAVNTQRHHECHLIRRTPLNDFTPGQYHQQRNKRIQDDKEH*NTVHAQCVDVQKRNPLVELGLIAAAQVETGKQQRVQSTGKRSHEGKHTBQRRTAVFTGRNQHACGD
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SEQ ID 3033

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SEQ ID 3034

MNATSQPTSNFWNIYIAIVLISFIALANLILLSQNVKRPKKEEVQTTGHEWDGIAEYDNLPKWWFNLVLTWLPFGIYLVNYPGVGDYKGLLWTSNHYQYEVKKADEQYKLYAKP
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GDKGQIGLGLPNLTDDVNLWGGTQKSIIEITNGRSSQMPAWGHFLDKDLHINTAYVWLSNKGDKAPVKKAEPAPAEAPAPSAPEAAQAASEAKPAAEKAKAEPAAKADGKQV
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SEQ ID 3035

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SEQ ID 3036

MHIIDSHCHLNFEGIKERLEPEVLSNMEANGVQALAIYSVRESFSEVPAVAEAHEHYCTI GVHPDSKEAEFPIAEHVRAAHPKVVGIGETGLDYVWCKGDLSSQHKRFADHIEAANQT
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SEQ ID 3037

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SEQ ID 3038

VPTIRKTKAIHPYACPRCCRLPANTFTFGWANSASKFCIAKGGREVKKDESGGYALCHLPDSRIVEENEYCRSQH

SEQ ID 3039

ATGGCTTCCATCCACGACCAAAATTAAGAAAGTAGTAACGACACACCGCGCTGTAATGTTTATGAAAGGTACGAAGCAGTTTCCGCAATCGCGTTCTCTTCCCGCGCGTGCAAATCTCTGA
ACGCGGACAGGTGCACCGATTACGTTGCTGTCAACGTATTTGAAATCCCGAAGTACGCCAAGGCATTAAGGAATACAGCGACTGGCGGACCATCCCCAACCTTTATGTGAACGCGGAGTT
TGTGCGCGGTTCGACATCTCTGATGGAATGTATGAGGACGCGAGCTGCAAGAGCTGCTGAAAGCC

SEQ ID 3040

MASIHQIKIEVVTTHRVVLFMKGTQFPQCGSSRAVQILNAGCTDYVAVNVLENPEVRQGIKEYSDWPTIPQLYVNGEFVGGSDILMENYBAGELQELKA

SEQ ID 3041

TGCGCAATCCATCAGGCTTTTCAGCAGCTCTTGCACTCGCTGCTCATACATTTCCATCAGGATGTCGCAACCGCGGACAACTCGCGTTACATAAGTTGGGGGATGCTGCGCCAG
TCGCTGTATCTCTTAATGCTTGGGCTACTTCCGGATTTTCAATACGTTGACAGCAGCAAGTAACTCGGTGCGGCTGCCCGCTTCCAGATTTCAGGATTTTCAGCGCGCGGAGAGAAACCGCATTCGG
GAAACTGCTTCTGCTACCTTTTCATAAACAATACGACGCGGTGTGCTGTACTACTTCTTTAATTTGGTCTGGATGGAAGCCATCGCTTATCTCTTTGATAAAGTTGACAAATTTGTTCAGG

SEQ ID 3042

LPNPSGQQLQLACLHHPQDVRTADKLAVHIKLDGRPVAVFLNALAYFGIFQYVDSNVI GAACRVQDLHGAGRETAIRKLITFHKQYDAVCRIYFFNLVVDGSHRLFLILIKLTKFVR

SEQ ID 3043

ATGGATTCCGCAATGCCGTCTGACGCTGTTTCAGACGCAATTTCTTTCCCGCAAATTAAGAAAGTATAATGACGCGCTCTCAAAATCACAACGCGGATGAACGT

SEQ ID 3044

MDSAMPSEKVSVDGIFPSGKLKKSIMTRIKITLHEDR

SEQ ID 3045

ATGAATATAATCGGCGGACATCTCAAAGGACCATAGACGCAACATTGCTAAACAAACGGAAGTATCCATTACATTAATTAAGAAATATGATGATGATTAAACAGTTTAGAT
TGTGGATAAAGGGAACAGAAATCAGAAAGTCTATATCGCATGGAGGCAACAGGCACTATTACGAAAGGCGAGCAGATATGCTTTCTCTACTATACGTTTACGTTTCAATCCCTT
AAAAATCAAGGACTACGGAAGGAGGAGTTTAAACGCAACCAACGCAAGCAGATTCAAACTGATAGCAGATTACATAAAGGCAATCAAGATACATTGATACCGTATCAGATACCC
AAAAACAAGCATAAGCAACCTGATTAACTTTAAACCAATTAACAGCAACGAGCAGAAAGCAATTAAGAAACCGTCTTCAATAGCACTGAAGAGACTTTCATAAGGAACATACATCAAGACT
TGATAGATACCATACAGGACAGATGGAACAGTAAAGATAGCCATATCCGAAACAAATCAAAACAAACGGAACAATAACCATTAACGCAATCTTCAAACATCCGAGCATAGGCAAGGA
CACCGCATCAGTTCTTTATGCGCACTGACAGAAAAACATTTTAAACCGCAACCAATTTGTATCTATGCGGATTAAGTCCCGCATCATCAATCAGGAGCAAGCGTAAGAGGTCCG
GGCAGATTGAGCGGATACGGAACAGAGATTAAAGATACGCTGTATATGCCGCGCTTTGTGCTTACCGTTTAAACGCAATTTCCGAAATTAATAAATATCTGAAAAAGCGGGTAAGC
CAAGATGTTAATATCGTTGCCATCATGCGCAACCTGGCGAAGCGCGCTTATACATTGTTAAACCGCGCAGCTTACGATGCGGAAGACACCGATTGAATCAA

SEQ ID 3046

MNIIGPDISKPTIDATLHKTNGSIHYIKPNNDGLKQFRLWIKGNIRKVIYIMEATGIYKERAADLSSYTYVYINPLKIKDYKSRFNRTKDKADSNLIADYIKRHQDLYIPYQIP
KNKALQKLNILKNLQOQKQIKNRLHSTEDFIRNIHQDLIDTIQDKMEQVKIAISEQIKKQTDNNHYNLQITPSIGKDTASVLYAQLTKEHFTANQPVSYAGLSPALIQSGTSVRGR
GRLSRVGNRLKSTLYNPAFCAYRFNAPKILNKLKAGKPKMVIIVAMRKLAKPAYIIVTKTQPYDAERHRLNQ

SEQ ID 3047

TTCCCAATCAATATCTGTACGATTGCGATATCTGCCGTACTAAACATCTAATTCAGCCAAATCTTTTATTCTGACTGCATAGCTAGTAAAGCTCTTAACCTCATACTTAAATCAATA
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AAACTGAACCAAGAGTGAAGACCCACATCTTTAGCCAACTAATTTGCTTGGCAACACCATATCTCTCTCAGTAAGTGGAGCATCAAAACTGATTGGATGGCAATGCAATTAATTTCT
AAATCTGAAGACTTACCCGCTCTTCCACGTTTATCTTGAAGACGATTGCGTACCCTCTCTCTTTATTTCTGCTTTTCCAAGACATAATTTATTAATTTCCCATAAAAATCATT
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AGCCCAAGATTGACTTTTATAAATCTCTGCTGGAATTTTAGTCAAAATATTGCTTTCATAATTTGCTATTAAACGAGCATGAGTCAAATTTGAAGAACGATTAAAGCATATATTTCA
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TAGACATCCGAAATCTTGTCCAAATAAATTTAAACTCTTGCAA

SEQ ID 3048

FPINICTIATPCLY*NI*FSQIFYP*LHS**SS*LHT*INIFGAFACSPCRKFIFF*KFFNGSI*NRISINIFLTKHFRKN*TTSGNPTFF*PINLGNHIIISLKSWSIKN*LDGNA*PS
KI*RLTRPFRPFIKTIAYPFSIFAFPRP*FIKPIKIIVVYFSCCTLLNKIP*LIHSLMVSHLLSPCRNQFLIIIMHLK*LIH*LSNS*FLIVNFSFLILIKPIFRYRDRPHRNF
SPRFDYKILLGNFSQNICPIIAIKRMSQI*RTD*SIIFILILPKYSPRMTLNALSYHQCEFMGRKPFQHPNSLFFRQSEILSKNFKILLQ

SEQ ID 3049

ATGAACGTTAACGTTATCAACCATCCGCTCGTCCGCCACAACTGACCCCTGATGAGGGAGGCGGATTGCGAGCACCTACAAATCCGTCAGCTGACCACCGAGTTGGCGCGCTGATGGCAT
ACGAGGCAAGCCGCTGATTGAAATGAAAAATACCTTATCGACGGATGCTGCGGACAGATTGAAGCGGACCGCATCAAGGCAAAACCCCTGACCGCTGCTCCCATCTGCGCGCGGCTTT
GGGTATGCTCGACGCGCTGCTCGACCTGATTCGCACTGCCAAATCAGCGTGGTGGTTGCGAGCGGACGAGGAAACGCTGAAGCCTATTTCCTATTTTGAGAAATTTGCGACAGTATG
GACGAGCGTCCGCTTTGATTATCGATCTATGCTGGCGACAGCGGTTTCGATGGTGGCCACCATCGACCTGTGAAAGAAAAAGGTTGCCCGCAACATCAAGCCTTAGTCTTGGTTGCCG
CCCCGAGGGCGTGAAGGCTGTTAATGATGCGCATCCCGATGTTACGATTTATACCGCGCGCTGGATAGCCGTTTGAACGAAACCGCTATATTTCCCGGTCTGGCGGATCGCGGCGA
CAAGATTTTCGCGACCGCG

SEQ ID 3050

MNVNINHPILVRKILTLREADCSTYKFTLTTELARLMAYEASRDFEIKYLDWGCGQIEGDRIKGTLLVVPILRAGLGMLDGLDLIPTAKISVVLQRDEETLKPIISYFEKFDVSM
DERPALIIDMPLTGGSMVATIDILKEKGCNLIKALVLVAAPBGVKA VNDAPDVITTAALDSRLNENGYIIPGLDAGDKIPGTR

SEQ ID 3051

ATGAATTTCCAAGACTATCTCGCCACATTTCTCAATCGACCATCTGGCGGTTTGGATGTTGAGGATGCCGAAGGCAAAACGTTTACCACATTTCCCGCGCTTCAGGCGAAGCTCGGTT
CGCTCAAGCTGTACAATGCCCTTGGCGGAACGTTTGTATGAAAAATGGTAAAGAGCGGCAGAACAGGTTTGTATGTTTGGCGAACATGTTGCCGACGCGCGGCCCATCCGCGGAA
GCATCCGAACATCGATTGCTGGAATAATGCTGCAAGCGGCGAAACCCCTCTGCTCAACCCGCTTGGCGGCA

SEQ ID 3052

MNPQDYLATFPIDHGLGLVDQAEKTVHPIPAVQKGLSLKLYNALAEKFDKLGKEABQGLWPAEHVADARAHGKHPNIDLLNVQSGETLLKPLAAQ

SEQ ID 3053

ATGCCGCTGAAACGAATTTAGACGGCATGCTCGAAAAATTTGCGCGGCAACGCGTTGAGCAGGAGGTTTCCGCGCTTGCACGACATTTCCAGCAAAATCGATGTTCCGATGCTCT
CCCGGATGGCGCGCGCTCGGCAACATGTTCCGCAACCATATCAAAACCTGTTCTGCGCTTCTT*TAACCAATTTCCATCAAAACGTTCCGCAAGGATGTTACAGCTTACGCGAAC
CGAGCTTGCCTGAAACGCGGGAATGTGGTGAACCGTTTGCCTTCCGCGATCTGAACATCAAAACCGCCAGATGTTGAT

SEQ ID 3054

MPSETNPRRHGRKLLRGKRFEGFAALHDIQQIDVRMLPRMGARVGNMFGKPYQTLFCRFFTPQFSIKTFQGIQVQLERTELALNGNVNRPAGFILNIQTAMVD

SEQ ID 3055

TTGATTTTGCACATAATTTTGTATAAAATCCCTTATAACAAATGAACTATAAGGATTTTATAATGTCGGCGTAACAAAAGAAATTAGACATTTTAAACAACCTTTT

SEQ ID 3056

LIPALIFDKIPYNKLYKGFYNVGRNKRIRHFKTTF

SEQ ID 3057

TTGTCGATACGGATAAACAGGCTTTTGTACTCTGTCAGCTCAAAAGAACAGGTTAAAAAGTCATTGAACCAAGAAAAAGTTACGAAGTGCCACATTTGCCAATCTACACATTTCTGCA
AAAAATGCAAGATTTGGCAACCAACGCTTTTGTGTCGTGATTGTAAAAAGCTTTTGTGAGCAGACAGGCACTATTCTCTACAACAGCAAAAAAGACATTGAAGTTTGGGAAAAATA
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GAAGTTCAGTTAGACGGCATGTCAGCTGATGAACTTATTCGACGATTTCTTACAAAGGCGACCACAAAAATTTAATCTGCCACGCTCTGCTCAACAAACGAGGAGGAGCAACGA
AACGTGGCATTTCAAAAGAACAGGTTTGTGTTCTGTGTATCAATTTAGACGGTAAATCTGTGTGATAGCAATTTAGCAATTTGGGTAAGCCATCTCAAAAAATATCAAC

SEQ ID 3058

LSDTDKQALFVSKEQVKVIEPRKVTFCPCQSTHFVKNKDCGNQRLCRDCKSFVEQTGTILYNTQKIDIEWKYIHCMIKYPRLKCAEICKINLATAFTWRHKILDALQNMN
EVELDGLVQADEFTSYI SYKGHKNFNLPRAHKGRTATKRGISKEQVCPCGINLDGKSVARISNLGKPSLKNIN

SEQ ID 3059

ATGTTGCTCTTGCCTCCAGTAATATGATTTTACGCGGAGAGCGTAAAGCCAAATTTACACCAAGCAGTGTGTTTCATGACTGATTTTCAGGATTTAATCAAAATCCCAACCTGAAACAG
GCTTAAACCGCCAAATGTTGGCTTTCTCAATCCACCTTACGCCCAATCCAAAGCGATGCCGAATTCATGAACCTTTATTTGTCAAGAAATGTTGGATATGTTGGCAGAAAGTGGCAC
AGGCATTGCCATTATTCAGTCAGTTGCGTGATGTCACCAAGCAAGCCAAAGCGAAATTTGAAATATCATCGCTTAAAGCCGCTGATGCTATGCGGAGCGAAGCTGTTTACCAGTTA
GGCAGCGTAACGTCATGTCGATTTGAAGCCCAATAACCGCAATTTTCAGACATGCTGATTGACCCGACACACAGAAGAAATCAGCACGAAAGAAAGCTGTCGCAAAACGTTGTTG
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AGGAGAACTCGGTAACAGCATTTGTAACGATAACGATGATGGTTGCCGAAGCCTATTTGGAAGCTGATTATTCAAAAATACCCGAGCAGATTTTGAGCAAGTGTGCGTGAATTTGCT
TTATTTCAACTACTGGGAGCGGAAGTAGGCCGACTGAAATTTGGATAATGAAGCTATGAAGCAGATGACAAATACGACTTCCGAGACAGTAA

SEQ ID 3060

MFALAASMTLRGDKANLHQSSCFMTDFQDLINKPKPETGLKRPVNGVLPNPPYAQSKSDAELHELYFVKEMLDMLAEGGTGIAIIPVSCVIAPSKAKSEIVYHRLKAVMSMPSLPYFV
FTVTCIVVFEAHKPHFQVVIDPDTQEEISTKKACRRTWFGYWRDDGFEKTKHLGRIDLIDYRWQGIKARWLEHYLNNEVHTGESVTAFTDNDENVAEYLETYDYSKITRADFEQVUREFA
LPQLLGAEVGPTENLDNESYEDDNDNDFGDDE

SEQ ID 3061

ATGGTTGAATTCAGAGATTTTGTATGTGAGTTACGGTTCAAAATTAGATTTGAATAAAATGAGCAGCTTCAATCCAACATCAACTTTGTAGGAGGTCAGGCAAAATATGGTGTAA
CAGCATCTGTGGATTTATGAAAAATACAAACCTTATCCAGCAGGATTTAATCACTGTTGCATTAGGTGGTCTGTTTATCTACTTTTACAAAAACAAACCTTTATATCAGCTCAAAA
TGTGCTGTTTAAATCCCAAAACAGAAATGACAGAACCAAAACCTCTTTTATGTGCTGCTATTTTGGCAATGCCTACCGTTTCTGCTTGGGTAGGGAAGCTAACCCGACGTTA
CGAACCACTGTTTGTGACATCTTGGATGAGATCCCAAGCTGGGTTGAAGCGTGAAATTTAAATCCATCTGCGGTTGAACCGAACCGAAATTAAGAAATCGCTTGTATTTGCTGTGGTTC
GACATCAAAACGACTTGAAGAAATTTTACTATTCAAAACGCGATTGCCGCAACCAATTAAGAAATTTGAACACGCGAAAGAACAGCGGTGTGCTATATCCCTCTGCCAGTACGCA
AGCAAGAACGCTACGAAGTTATATCGCTCGTATAGCGTTGATGAAAAACATATTTTCCATGCCATACGCTTTTCACTTCTACCAATGGCGAAGGTAGCCATCTATAGCTATGTTTCA
ACTTGTGAATTTGTAGCAATAGTGTGCGGCTATTAAACCCATACAGTCCGATATGCCAATAGAAGTAAAGCTGATTACGCTAAATGTATACAGCAAAACCGCTATCTGTTTCTT
ATGGACGTAAACCAAGGCGAAATTAAGAACTATTGTACCGTATTTTGACCAACAGAAAGATTTTGAATATATCTGCGGTTTCATTACACCTTCTGATTATAGTAAACATTTG

SEQ ID 3062

MVELQEIFDVSYGSKLDLNMKSMNPNTINPVRSGKNNGVTSVDLLKNTKPYPAGLLTVALGGSVLSFTLQNKPFYTAQNVAVLNPKTEMTQKLFYCAAIIFANAYRFSACGREANRL
RQLFVPSLDEIPSWVESVINLPNSAGVTEPKLESLLDPVVRQSKRLDEFTPTQNGIAATKLEKEFEQRQKDTVVYIRPASTQARTLSYLARDSVDEKHLFPCHTLPTSTNGEGSHYTSVS
TCEFVANSVDVAVLTPIQSDMPIEVKLYYAKCTANRYLFSYGRKPKGEKLSIMLPYDQQRDPDYICRFIHTLLFSNNL

SEQ ID 3063

TTGTTAAACACAGCCTTCTATTTCAGGATACGGGCAATGATGTTTCAACACACAGGACGACACATAAAGCCCGCCCTATGTTGTCGCC

SEQ ID 3064

LKHSLLFQDTGNDVSTHRTTHKAPPYVLP

SEQ ID 3065

ATGATGAAAAAATGTTCTTTCTGCGCATGCTTCTGTCGGCTGCGCCCAACCGTGTGGGCGGATACGGTATTTCTGTAAACGGACAACAACAAATACATAGAAGTTCAAAAA
TCAACCCGAATCTTTACCAATATTCGTTGCGCAGTGGCGGCAAAAAAGAAATGGCATACGCAACAGCAAGCTGACCTGTTGGGGCGTTCCGACAGGTGGCAAGGCATGGCAGCGGACG
CGGGCAACGATGAAATTCACAAACGGCGAATTTATGTACACCGTATGGACAGGCTTCGATTCGGTACTATACGGAAGCAGCGGTGTCGTTGTGGAGCGTAGGGGCAAGGAAGTCGCA
CGGTTAGGCTGTACGCCGAAACCGCGCAGCGAATTTCAACGATGACGATTTTTCGCG

SEQ ID 3066

MMKMFSLAALLLSAAQTFWADTFVFSCKTDANKYIEVQKINRNLVEYFSGSAKKELAIRNSKADLLGRSDRWQMGSGRRATMKFQNGEFHTVWTFDSVTHTESSGVVVERRGKEVA
RVGCTPKTAQANFNDDFSR

SEQ ID 3067

TTGGTGTATCTGAATGTAAAAATAACTGTGTATCCCTTTTGACTCCTCTATATTGTTGAGATTGCCTAAAAAATTTAGSAAACAGATAATTTGCATGTTGGCTATTTACGCTGTTGG
GTACCATTTTGTTCACCCCTTTGACT

SEQ ID 3068

LVILNVKITVSSLLTPLYLLRLPKFRKQIICHLAISRLGLTILFHLPT

SEQ ID 3069

ATGGATATTAAACGGTATTCGCGCTCTTTTCACGGTATGGATCTTTATCTGTTTCCTGTTAGTACTCTATATCGTCTTCAACAGGCGGAATAAGAAAACTACGATGATGCCGCAACAGCA
TTTTTCTGTAACCAAGATGCGCAAGATAAGAAAGCGAAACCGT

SEQ ID 3070

MDINGIRALFTWIFICFLVLYIVFNRRKNYDDAANSIFAENQDAQDKSENR

SEQ ID 3071

TTGTTATTTTATTTACGTTTATTTACGATATGCAATGCAACGGTTACACAAATATATTCGCGCAACCGTTTAAATTTGTTGAATTTTAT

SEQ ID 3072

LLFLPTPIYDMQMHGTYNIQAQPFNVVEFY

SEQ ID 3073

ATGGAACAGCGAAGCCCGTCATGCTGATTGTCCGCCGTCGGGCGAGGCGAAGGACGATGTGAAGTCTCCGTCGTGCCGATGGCAGGCGGAAGTGTGAGTCCGATTGAATCGAAA
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GGCGCACATTTCCGTAAGGCGAAGCGCGCGTATGCGCGCGTATGCGGCGCGTATGCGGCGCGGCGGCTTTGCACTGGAAGACGGCAACGACAGCGAGGCGGTTTTCGCCCTGCCGTTTGAAC
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TCAGACGGCATGTTCTTCCGGAACCTCAAAACCA

SEQ ID 3074

METAKPVMILVRPSGRAKDDVEVCRRAGQAEVLSPIEISTDEASLKRLPEMYARADAVFVSPAIVETAVPYLNLSDGIKAHIAVQGGRRALARYAGAGVFPAPEDGNDSEAVLRFPVNH
SLPEGARVLSVRGHGGRDLFMAALQEKGFRTVEAEVYFRHKLNFQNFQNTENIAAYITSTELVQSLFAQLPPQFSRPFKSLLYPTHHPRIAEALKREGVCSVETVPTLEALSYSSISV
SDGMVFPQTSQ

SEQ ID 3075

GTGGCGGAACCTGAAACCAATCATCCGAACCCGTACCGGAGATACAGGCATCAAAAGAAATGCCGTCTGAAACCTCTTCCCACGCAAGAAACGAAACAGAAAGTACACATTTCCCGCG
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A

SEQ ID 3076

VGEPEKSSPEVREIQASKEMPSSETSSPRKENETEVHIAAPFIVKQSGSNALAAALVLAALGLGASGLFVQGNVLNQLAFNQKIDKALGESENAALLKIDNLNRQSAIQSELDRL
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GVQARNEAVSASWQNVWEKSLGTLKGLVEIRLENNDAHLISPEQATFVRENLRILRDARTALMQRNGEVYQGLNNAEAAVRQYFDKSPATQSWLKELAEKLTLDVRMTADDGLKTS
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SEQ ID 3077

ATGAAACCGTAGTCTGGATTGTTGCTCTGTTGCCGCCCGCTCGGACTGGCGCTGCGGCTTACACCGCGGACGTGTATATGCTACTCGGACAGACCATGCTCAGAAATCAAC
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CCGCT

SEQ ID 3078

MKTVMVIVVLFAAVGLALASGIYTDGVYIVLGQMLRINLHAFVLGSLIAVVVYLFKPIIGVLNIPENMRRSGSARKGRKAALALNAGLAYFEGRPEKAELASRVLGNKRGDNR
LALMLGAHAAGQMENTELDRYLAEIAKLPEKQQLSRYLALLAESALNRDYEAERANLHAAAKMNANLTRLVRLQLRYAFDRGDAQLVLAKEKLSKAGALGKSEMYQNWAYRQWADA

ADAAALKTCLKRI PDSLKNGELSVSVAEKYERLGLYADAVKWKQHYPHNRRPELLEAFVESVRFLGEREQKADFADSWLKEQPDNALLMYLGRLAYGRKLWGRKAGYLEASTALKPS
IPARLVIAKVPDETAQSQKAEQRNLVLASVAGENRPSAETR

SEQ ID 3079

ATGACTCTTTTAAAAACGATACCTTCTCCGCCCGCTGCTAAACAGCCCGTGAATACACACCGATTGGATGATGCGCCAGCGGGCGGTATCTGCCCCGAATACAAAGCCAGCGCA
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SEQ ID 3080

MTLLKNDTFLRALLQPVETTPIMMRQAGRYLFEYKATRTKAGSFLDLCKNTGLATEVTIQLERFDLDAALFSDILTVPDAMGLGLYFABEGGPKFKRALQHSEDIKHLVPMKELQ
YVFDVTSIRKALDGRVPLIGFSGPFTLACYMVEGGSGKEFTIKTMYSRPDLTKILDNTAQAVTAYLNAQIDAGAQVQIFDITWGGVFLSDAIFKEFSLKYITQIVAGLKRSEGRV
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SEQ ID 3081

ATGATGTACCTTACGTTTTCCTAAAGCCAGACCAATCTTCAGATAGCGGACTACAGCATCCAGCTCGGATTGTTTGGCCAAAGCCTCAGGCGCTTTCGCAATTTCTCATCTACTGTAA
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GTTG

SEQ ID 3082

MLLPVVFQSQSLQIGDYSIQLGFVCSLRRFRNPLITVRSYFTQSLHVGNGCIDIDFIACKPRECRHILGRHDITGIQVDAVPFVGLAAHTCQIRTGTFGLERMVNVNRLSGNRV
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SEQ ID 3083

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SEQ ID 3084

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DFDLKGNPILIGGNVIGRLITPKLQTVVYSRTAKPNADTFWQHSKIFGDRDKSLRLLYIPFDVYFFVQLNQANLLIIGQAKNSGGNIQVLYPKNINPTRKNVLFDSINQIVGGVN
YFPLHFNEDNLSEINKILPSILKDEIQSDLYQIDIEDLFVLVDKLGRYVPPDWNKEKFIAGVEALKAQRPSFKTYVLIKTGRKLSRATGTMLESDDRKLGEKYPNDLFLTYQVVGNDKG
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SEQ ID 3085

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SEQ ID 3086

MNVFVSNIAKITEKSLNAVMDLFRSADEVIMATGYVSNDAVVELHKILELNDHIQKIDLLVGMHYLEGFSHLQYDSICLINDFLRHEKRGAVYVSPFVKHGMYSFKNYQKINGLIG
SANLTCFWDSTERTYETMLHLNGKPAQIILQADIQSTHKLKNIQEVERPSKPIRHNSHLENCLGQKIAPEQIRQLPAQTSEYHFSIPAKTEKSNLNVFFGEGRRDRKGRVFKRPWYEV
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SEQ ID 3087

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SEQ ID 3088

HLRSKQISNLNSSSNPKILSLFSGCGGLDLGFHQAGCETVWANDPSHWACESPRKNIGDVIIEGDIQINPNDPTIPDCDILILGGFPQCFDSMTWKQPGLEGERGNLYKSFRLRFVNAKKPK
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DRLSKTRGGKQ

SEQ ID 3089

[illegible]

SEQ ID 3090

LIKILVWILKVNALNATQRNATQRNATQRNATQRNATQRNATQRNSTIIFNGKVIVWDSCFVFSVIMPONNRKPPLFVS

SEQ ID 3091

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SEQ ID 3092

MAKTLKTLVQCTECGGTSPKVGQKCPHCGKWWIQLQESFAAPEPKNARQPSWAADASTVQSLASVATAAEVPRNPFGMELDRVLGGGLVDGAVILGGDPGIGKSTLILLQTIATMAQSRKVL
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SEQ ID 3093

TTGGTTTGTGGCGGATTGAAACAAGGACATACCGGCGACAGATAAGATTTCGGCGAAAGTTGCCCTGTGATATGGCAAAACGCATACGCCCGTCATCCCTGCGAAGGCGGGAATCCGGAATCGCTCCGTTTCGGCAATGATTGGAAATCACGG

SEQ ID 3094

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SEQ ID 3095

TTGCCTGTGATATGGCAAAACGCATACGCCCTGCATCCCTGCGAAGGCGGGAATCCGGAATCGTCCGTTTCGGCAATGATTGGAAATCACGGTAACCCAAACCGCTTGGAATCCCGACTTCG
GGGGAATGAGGGGCGTGCATT

SEQ ID 3096

LPVIVQAYARHPCEGGNPESVSAMIGNHGNPTAWIPDFGGMRGVC

SEQ ID 3097

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SEQ ID 3098

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SEQ ID 3099

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AAGG

SEQ ID 3100

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SEQ ID 3101

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CAACCGTT

SEQ ID 3102

MICCPSTQNKQSCNMLIYIVIFYVYLRYANARLHKYIRATV

SEQ ID 3103

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SEQ ID 3104

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SEQ ID 3105

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SEQ ID 3106

MTHTLTSKYSFDETVSRLETAISKMDIFAVIDHQEAARRNGLTMQPAKVIVFGTPKAGTPLMVKDPALQLPLRLVLTETDQKVRTAYTDTRALIVGSRISFDEVANTLANAEKLIQ
KTVGE

SEQ ID 3107

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SEQ ID 3108

VPKRLKCRVRRSGGVCSSYFLIGLFIGLRTGRHAPRIMPCRVPERRRMPSESLSFQALRHFIPIFLSRSS

SEQ ID 3109

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SEQ ID 3110

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SEQ ID 3111

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CCTGATCGAAGGCTTCGCGCAAGACAGCCGCGAAACCGTCCGCGTACCTATGCGTGTGAAAAAGACGGCATAACGATGCTCAACGCAACTGGCGCGGTGGCGGCAATGCCCGGCG
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GCCGCAAGCTGAAAAATACGGTTTTGAAGAAATATGCTGCCCGCGTTCGCAAAATGGCGAAGAGCTGCCGCAAAACGCGCTGACTGGGGCAGACGCGCTGTCGACATCCCGCGCG
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CGCAGGGCGATGGACGAAGCGCTGCGCACAGCACTATTACCTTCAGGCACTGATTACCGCGTTCGCGCGCGCTACTTCAAAGTGGCGGACACCGCGCGCGCGCTTTCCGTC
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SEQ ID 3112

LEQKSVVERVLVVTFFKAATARLRLRLRLDVLQVLESKEIAELGDDTLDGIAAYCAEHHEGDTFLPALLEQALQKESRTRLIVRLKAAIGQFDNAITYTHFGQRLRDYAFILQAP
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IDEPQDTPLOYEIPQKIFLARNRPLFLVGDPKQAIYSFRGADIYAYLQAEADARHTTTLATNYSHAALIGSIALFRLKERPFVLENIYSEVGAARASRLSPKRPVQLRWLHENDN
EKANKDVLRRRAADYCADEIARALNEASGRLNFKDRPLQSGDIIVLVRTHNEAVMISAALKKRQVQSVLLSRESVSPFAAALSALIGFWLEPRRAGTLRFVLTSIGFYDAQQLHDFN
QNESEILHWSARTALDIWQYGI PAAMQPSQTHGIESTRNNGRSLTNYQLLELLAAEDAQNRNPAALHKLWLDQISLAGNNGDNRAIRLESDEDLVKIVTHASKGLQYPLVY
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GTDTFTEDAPPPAAYRGADQAAEFAANSIPERGFPRVHTSFTALSRHTQTPDGGEDACPSLDAETSVPAMPSETPTASDGISIHDFPKGTQAGICLHEILDFKPGQAAABQSTLI
ADKLKKGFEPIWPAVAEMAEACRKTPLTGATGLSDIPGCRPENGFTLHTEDFGLKRLRDWLARDIRLPEVCRAAEFTLDFHTVNGFLNGFLDMVQDPDGNICIIDYKSNLSAYT
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SEQ ID 3113

ATGCGGCTGTAACCCCTTTTCAGACGGCATTTTCCGTTTTACCGTCCAAACCGTTTCATACACGCTATGTCGCGACCCATCCGAGCATTTCGACCGC

SEQ ID 3114

MPSETLFTAFSRFTVQPFSTYLCPPHSEHSTR

SEQ ID 3115

ATGAACACGCCCAATCCGCCATCATTCGCCACCAAGCCGCGCATCTTTATCGAAGCGGACTTCGCGCGCAACCGCTCAACGATATTAAGCGCGCTGCGCGCTTCGCTCGAGC
CGTATTCGCGCTTGAAGCGCGCTTTCGCGACGATATTTGGGTCTGACCATCGCTTCGCGCAGAAAGCTGGGCAACATTCGGACACACGCGAGCAAGGAGTGAATCAACCCCTTCCC
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AGCGCGCAACACGCTTTGATGTTTACCGCATCTGCGCGACGCTGCATATATCGAAGCGCAATTAATGAGTATGTTTCGCGCAGACGCGACGCGCAAAACCGAGCTGCTGCTCGCACCTCT
CGCGCGCGCTTCGCGCGGATACTACTACGCGCGCTCGTGAACGCTGCAAAACCTC

SEQ ID 3116

MWTPQSAIIPDHQAQIFTEADFAANRLNDIKACRASLDALSALKARFPDDILGLTIAFGSKAWATFGHTDEGSEIKPFPENGLAPSTQHDMSIHIQSFRQNAAYALAQSVLAFGDS
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SGEHLMTAYCTLHNTLEAQLLSMFGDITDKTDLRLHLSAAVSGGYIYAFSVERLQNL

SEQ ID 3117

GTGAATTCGCGCAACACAAAGAACTATTTTTATATGTTATTCAAATCGGAATGGGAAGATATGCCGAAGCGCGCGAAGCGGAATAAAGGGCGCGGAAGCGCGCGCGCGC
ACGAACCGCAAAAGCGCATCAGGTATGCAACCGCGGATTCACGACGCGCTTCGCGCAAAATCCGCTGCCGATTCCGTGCTA

SEQ ID 3118

VKLRTQRIILFLYGSSEWERYAEAGSGNKGKGGGRHETEKRHQVCKRRIHARRSGKNPPADSVL

SEQ ID 3119

GTGTTGACGGCAACATATCATCTGCGCGGAAAGTTACCGTATCGGCAACCGGACTGAAAAAGACAGCGGTGTTGCGCGATGCGGTGCACATTGTGATTCCGACT

SEQ ID 3120

VLTGNISSARKVTVSANATEKDSVFGDAHVHIVAT

SEQ ID 3121

CCCTTTCACCTCGTCCAAATCGGCAACATTAATCGTTTGTGCGTTGCGGTACACGACCATTAATCGCCAAACCGGATGGCAGATTCCGCGAGCGGCAACGGTCAATACGAAGAATACGAA
ATTGTCGCGCAGTATCGCCCAATGTTGCGAGAAGCGGATAAAGTTGAAGTTACCGCCAAAGCATCAGCTCGATGGACATCAGCAATACCAGCAGCTTTTTCGGGTTCATAAGATGC
CCATCGCGCTGATACCGAACAGGAGCGCCCAATACCAGATAATGCGTCAAGTAATCAT

SEQ ID 3122

PFQLVQIGNINRLSVAVHQHNRQTDRFGSGNGQYEEYENLSGSIAQMLREGDKVEVHRQKHQLDGHQYQHVFAVHKDAHRADTEQESAQYQIHRQSNH

SEQ ID 3123

ATGAGAGCTCTCATGGACACACAACTTACAATACAAAGTGGTGGCCAGTTCCGCATCATGACTGTAGTTTGGGGGATTGTGGGCATGTTGGTTCGGGCTTATGTCGCGCGCCAGCTTT
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CTACGTTGTCCAACGTACTTGTAAATACCGCTCTTTTCGCGGTGCGTCCGCTTAATTCGCTTTCGCGGTGCGGTAATCGTTGCGCGCGCTGCTGAGCTTCCCTATGGGTTGGACC
CAAGTAAAGAAATGCGCAACTGGAATGGCGGATGACATTCGATTCGTTTGGTGGTGGCTTACGCCATCTGATTTCTTCGTTAGGATTCGCAAAACGCAAGGTAACACATTTACG
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TCCGTCGTTCACTTTCGCGCGTGTATTTTCACTATATGTTGGCGGGTTCGCGACCATCTTCACTACATCGCGCTGCTGACTGGAAGCAATCTTTGGGTATGTTCTGCTCTGATTTGT
TGCACCCCTCTTGGCGCGGTATGATTAACGCAATATGACCTTTCGCGCGGTGGGCAAACTGCGTACAGACCGGATCTTAAATTCCTGATTGTATCTTGTCTTACGCTATGTC
TACCTTTGAAGCGCGATGATGTCGATTAACCGGTCAATGACTTACGCACTATACGCACTGGAAGCTGCGCGCATCTCATGCGGCTGCGGTGCGGTGAGGCTTTGTAAACATCGT
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TTTTATGATCTGATGCGCATGTCATTTATGCGGTACACGCTGACCGACGCGCATCGGTGTAAGCAGTTCGATGCGGAAATCCCTGCGGTTTCCCAACACAGCAGCAC

SEQ ID 3124

MEFLMIDTQTYNYKVVRQFAIMTVVWGLVGLVIVAAQLFAPALDLSNIGFWPHFGRLRPLHTNAVIFAPGCGGLIGTSYVVQRTCNTRLFQGNLPAFTFWGNQAVIVAUVSPFSGWT
QGKEYAELEWPIIDILITLVWVYAI VFGTIAKRKVKHIVANWFGGFLAVALLHVNNISIPAGLMKSYPVYSAGIDANVQWYGHNAVGFPLTAGFLGMYFPVKQAARPYSTRL

SVVHFWALIFTYMWAGPHHLHYTALPDWTQSLGMLVLSLILFAPSWGGMINGIMTLISGAWDLKLTDPILKPLIVLSLFSYFGMSTFEGPMMSIKTVNALSHTYDWTVAHVHAGALGVWGVFTIG
SVYYIMPRLPFGKQBMHSTKLVEAHFWLFIATIGVVLIAAMWAGVMQGLMWSSLNDGTLTYSFVESVKRMTMPYNTIRFAGGLLYLSGMCIMAYNVVRYTAIGKKAVDATPAVSQTQHH

SEQ ID 3125

ATGTTGAAAAATTCGACTCGGCGGCATTGCGGCATTGGTTTTGGCGGCTCGCGCGGTTCCGAAGGCGGCACGGAGCATCTTCGCGGCTGCACAAATCGCAATTTCCGGTTCTTTAA
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TGACCAGCACTACCGCGCAAAAAGCCAAAGCCGAGGTGGCGCAACTGTGCGCGTGGACGTTTGGCGGATCCCTGACCTCGATTGACCAAAAACCGCCGATGCGCAGTTGAAACGATGA
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SEQ ID 3126

MLKKPFLVGLGIALAVLAACGGSEGGSGASSAPQAQSAISGLIERINNKGTVTVTGFTGYAPPTHYDHDGKLGTYDVEVTRAVAELKGVKVEFKETQWDSMMAGLKAGRFDVVAQVGLTSFE
RQATFTDKSEFPYSWGAVLVAHNDNIIKSADIKGVKTAQSLTSNYGEKAKAAGAQLPVPDGLAQSLTLIEQKRADATLNDLAVLDYLLKKNFNAGVKIIVMSAPADERVGSGLIVNKGNDEA
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SEQ ID 3127

ATGACGATATCAGCGCGTGTTCGTCGTCATAAACGGCAGAGAGSCAAGGAATAATTGAACACTGATGTCCTTTCCGAAGAAATGTCGCCCAAGTTTTCACAGTCGCCGTCGGCTTTCAGC
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GGTTCGGAAATTTGTCAAATGTGCGCTGGCGTTTCGGGGCTGGTCAGCGCGACTTGTTGTCGCCACATCGTGAAACGTCGGCTTTCAAACCGCCGATCAGTGAATCCCATATGCGTTTCTTTAA
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AACCGTGCCTTTATTGTTGATGCGCTCGAT

SEQ ID 3128

MSISARVSVINGREARKILLNTDVFSEELFAQFFQRAVGFQLVDCRAEFHRLGLVIALVDNQGTGTDFFIIGRRGPHDFHPRIIRVFLQIVNQRFIVQRRIGAFLFNQGQRLRQTVHRRHELRTCG
FGFFFAVAGQGLRGFHAFFDVGYGFNVAVVMNRQNRTPAPVRFGFVKRLAPGAGQADLVCHHVETSGFQTRHRIPLRPFKLDFYAQFFRHGAGYFHVVTGQFAVFVVVVGKRCVSAFRADG
NRAFTVDALD

SEQ ID 3129

SEQ ID NO: 3129
ATGACGGAAACACCGCGCTGATATGCTCATCAGCGCGCTTTTGGCCCATGCTTAAAGCCGGCTTTACAGTGTCTTTGCCCTTGGCGATC8CTPCTTTTCGTTATCGGCATGATTATFTGCCGTAG
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SEQ ID 3130

MTFTADMLISAFWPMVKAGTVPLSLALAFSVIGMIIJAVAVLVRIMPSGGIPQKCLLKLVEFYISVVRGTFLLVQLVIVFYGLPSPVGIIYNIPAAIIGFSLNWGAYASETIRAAILSV
PKQWEAGFSIGMTYMQTFRRIAPQAQFRVAVPPLSNEFIGLKNKTLAAVTVTVTELFRVAQETANRITYDFLVPVYIEAALVYWCFCCKVLFLIQAQLEKRFDRIVAK

SEQ ID 3131

SEQ ID 3131
ATGGATATTTCGGGATTTTAAATCATGACAACTCCTTATTTTGGCGACATAACCGTGGAAACGTTTTTCCAAACGCGCCTGAATCAAAAACAGCACTTTACAGAAACACCAATAAACCAATGCA
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AGCTGAACCAACAGCGGCGTACCGCGAACGACGGAATAATAAAATCCACAGCTTCAACAAGCATTTTGAAGAAATACCGCGGAAGGCAATGATCTTACCAAGCAACCGGCTATCGGCA
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SEQ ID 3132

MDIADPNDHNSLFGDITVETFFQTRLNQNQHPTETPINQCSYDIDRQKVISAVCRFLCDTEKLRYRYHGGKRGVFEQADKLVAQRNGDABCLRCDDAAERLHI GHTDGETCFPLPFRHQ
NRRAYGFGSVCADIERKADDDGGGNRIDADGRQPVKHNHKLNQORRTANDGNIKFHQLQQAFLNTAGRHDSYQSGNYGNNHADNERSDRQQRHCKAGFNHGPKRADEHISACFRHQR
RGKEUHEH

SEQ ID 3133

SEQID 3133
ATGATTAAAAATCGCGAATATCCATAAGACCTTTGGCGAAAAACACCAATTTTGGCGGCATCGATTTTGGATGTGGGCAAAAGGGCAGGTGTGTCGTCATCTCTGGGCGCTTCGGCTCGGGTAAAA
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GAAAGAGGCTTTGAACTGCTGGA AAAAGTCGGCTTGGGCGATAAGTGGATTGTATCCCTACCAAGCTTTCCGGCGCTCAGCAGCGGTGTGCGTATGCCGCCACTCGCGATTTCAGC
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TTAAGCCAAATCCAATTCGCAAGATT

SEQ ID 3134

MIKIRNIHKFTILRGIDLDVCKGQVVVILGSPSGSGKTTFLRCLNALEMPEDGQIEFDNARPLRIDFSKKTSHKHIDILARRKSGMVQFYQYNNLFPHKTVLENNMEGFPVAVQKPKAAQAR
EALIKLLEKVLGDKVDVLYPYQLSGGQQQVRVGITARALAIQPELMLFDEPTSLADPELVQDVLDAKELAREGTMVVVTHEIKFTLEAVTNVVMDGGVIVEQSGPKELFDLKHETRE
LSOTOSAKI

SEQ ID 3135

SEQ ID 3135

ATGCGCAAGCATCACCCGCGACATCTTCAAAGCCTACGACATCCGTGGCATCGTTCGGCAAAACCTGACCGCAGCATGCCGCTTATTTTCATCGGCAGGGCCATCGCCGCCAAAGCGCGGAA
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CGCAAGCAATTTCCAGCCCGAACTCAACATCTCCCTGCCGAGGAGCAGCAACGGGCATCAAGTTATCGAAGAACTCGCCGCCAAGCCGAATTTGAAGGCGCAACCGAAATCATACCA
TCGACGGCTTGCCTGTGAATTTCCCGACGGCTTCGGTCTGATGCGTCTTCCAATACACGCGGATTTTGGTGTTCGCTTTGAAGCGGATACGCAAGCAGCATCGAGCGCATCAAAA
CCGATTCAGAGCCGTCATCGAAGCAATCCGCAATTAATCTGCGCTCTG

SEQ ID 3136

MASITRDIKAYDIRIGVKTITDDAAYFIGRAIAKAAEKIARIAGIRGRLSGPELMEHQRLTDSGIGLVNVMVITPMLYFAAVNBCCGSGVMITGSHNPPDYNGFKMILGGDTL
AGEAIQELLAIVEKDGFPVADRQGSVTEKDISAYHDHIVGHVVKLRPINIAIDAGNGVGGAFAGKLYKLGNEVTELPCEVDGNFPHNHPDFSKPFLQDLIAALKNGDAEIGLAFDGA
DRLGVVTKDGNITIPDRQLMLFAQDVLNRNPGAKVIPDKSTRLLAPWIKHGGBAIMEKTHSFIKSAMKKTGALVAGEMSGHVFFKERNFPGFDDGLYAGARLLEILSASDNPSEVLNLI
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SEQ ID 3137

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GTCGGGTTGACGAAATCGAAGCCCGCATACGCTGCAATCGCGTCAACCGCGCGGCGCGGACACGCTGTTCTGTTGTCGCGCAAGACGCGGAAGGACGAATCTTGGGCTTG
GGCGCAATCAGGCAATATGGTATCCATCCGCTTGAACCTGCGGACATGACGCTACTTCTGGCGCTCAAGCTGATTTGGCGGCAAGCGCTGCTTGTCCCGCGCGAAGGCG
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SEQ ID 3138

MTLEPWLAEARHIGLKEIPGAKHNPTIVQWLKETGFPGAASWYFEDETFWCGLFVGYCLGKSGRAVIRDWYRAKAWSMGLTKLEAPAYGCIKVPFRGGGHVFFVVGKDAEGRILGL
GGNQGNMVSIIFFDPADIDGYFWPSKLIIGKAVPSSPAEGRYRLSDVAATKQGAGEA

SEQ ID 3139

TGCTTTGCCCTCCCTTCCGCTTGGAGCCGCTGAAACTTCGCTTCTTCCGCGAGATTCGACTTGGGTTTGAACGCTTCCATTTTACCAGACGATACGGCCTTGATCGCGCGTACT
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CGGTATAAATACGGCTGCCAAATCCCGGATATTTGTTAATCGCGCGGAATGCTTTTCATCAGACCAATCGCGCCAGGTGCGTTTTCGGGTTGACGAGAATCAGGATCAGGCAACCGC
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TAAACCAACCAACCGCTACGCGCCAAACCTCCGCTGATCAGCATCAAAATCATCGCGCTCAACGAGAGGTGAGCACCAGATGCAAGCGCGCATGGACAGGTTTTCGGCGGTAAACG
TACGAACCGCACTACAAACAGATGGCGCAAGGATATAGAACAAGATCACGGAACAAAGTCAAT

SEQ ID 3140

CFALPFRLEAV*NAFFPGRFLRDRFHFHQTHTALIGAYFNLVGHITFRIGGFVAVNQCNRGHHAQQOYRQPKRQVVGINTAAQLADIVVIGRNVFHQTKCGQVGFVVDQNDQGR
QQRDHTYGNRRVFPETGAHFLVDIQLHDEDEQEHYHGDVNHHRHAQKRLRHQHPNRAHABGQHMQSGMDRVFGNGTNRVTQNDGKDLBQNHGKSH

SEQ ID 3141

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SEQ ID 3142

MFLKCSLTYINKVPQKGIKNKNSGRRVVIYNNMIYH

SEQ ID 3143

ATGCGTAGTATGGTTGCTCTGTGGGCTTATGCTGTACTGATGTAACCATCGACCTAAACAACAAGACCGCTCTGAAAGAAATATTTTCAGACGACCTTGAAGTTTGTGTTTACAGACACAA
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TCTTAAATCTTCGCTTCAAGAGCTGTACGGCAAAACCGCTGCTCAAGATGCGGCTATGCGGTATTCGGTAAAGTCGTTGACGGTTTGTGCGATGCCATCGAAAGCGTATCCAC
CAAACGCGACGCTACACGACGATGTCCGACCGAACCTGTATCATCATTAAGACCGAAGCAGTA

SEQ ID 3144

MRSIGCSVLCTDYNHRPKQDRLKEYFSDDLVECRSDTICRIIQRILLTKGKPMILHTNKGDIIKIELDFDKAPVTAKNFBQYVKDGFYDGVIFHRVIRKPMIQGGMDENMNEKETRD
PIQNEASNLPRNDKYTIAMARTSDPHSAGAQFFINTADNAFLNFRSKELYGKTVVQDWGYAVFGKVVDFDVDDATESVSTRKHGYHDDVTEPVIILKAEAV

SEQ ID 3145

ATGAATCCCCGTGATGATCTCTGTTTTCCTTACATATCAATCCCATCTCTATAAACAACCGACAAATCGTTTACAATATATTTACATACACCGAATTACAAATATATCTGAAAGCGG
TTGCGAAGCGAGCGTTTCGCAACCGTTTCGGATTGACAGATACAAAAGAAAACCGATTTTGTGCTTAAAGGAGCATTCATGAACCTGCATGCAAGGACAAAACCGAGCATCCCGA
AAACGTGAGCTGCTAGTGGCGAGAGCGGATACCGACTTAAAGGTTTGTGACCAACCATTTTCCGCGCTGCTGTTTCCGCAATTTACACATCTGCTTACAGCCCGATGCC
AATAAAGGATTCGCGCTGCTGATTTTCGTTGCCGCACTTTGGTTACCGAGGCGCTCCACATCAGGTAACCGCATTAATGTGTCGATTCGCGCTGCTACTCGGTTTCCCGACATGG
ACATCAAAAGGCGATGGCTGATTTTCCAAACCGATTTATCATATTTTTCGGCGCTTCGCGCTTCGACCGCCCTGCATATGACGCGGCTGGACCGTAAATCGCGCTCAGCTGCTG
CGGCTGTGCGCGGCAATATGAAAGTGGCGTTTGTATGTTGCTCTGCTTCTGTCATGTCGCTTCTGTCATGTCGATCAGCAACACCGCCACCGCGGATGATGCTGCTCTAGCAATGGGT
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TATGCTAGTATTTGTTGCTCTGTTGGCTTATGCTGCTACTGATG

SEQ ID 3146

MNPPDASCFSPIYISPHKQNRQIVYNITLHRTNILEVAEPTVSQTVSDCTIQKNRFPCLKGAFFMNLHAKDKTQHPENVLLSAQKPTTDFKLLITIIISAVVCFGIYHILPYSIDA
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MLSHLDREKHKTYVFLLLGIAYCASIGLGLTVGSPNLIARALNLDVFGVNMKLGFLMMLLILPLALLSLVILKPNLNERVEIKAESIPWFLHREVIALLIPLATAAAWIFGSKIRTA
GISNPDVIALSAVAVVVGVAQWKEVARNTDVGVLMLFGGGLSLTLLKTSASEALGQQAATFSGAPAFVLILVAAFIITFLTEPTSNITASALIVPISGIANQMLGPEQVLFVVI
GTAASCAFMPLVATPPNAIVFGTLIKQREMMNVGILLNLCVVLVALWAYAVLM

SEQ ID 3147

TTGCGGACGCGCGCGCAATTCCTGCGCTGTCCAAAATCTGCCAAACGTGGCTGGACGAGGAGGCGGCGATGAAGCTGCCGCGCAACCGCTTCAGCTGCTTCCGCTTGTGTTTGGC
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TCAAAACCGGAAACTTCCCATCCCTACCGCAGCTGATTGCGTTCGCTCTGTTTTCGCGTCGGCAGCGAATCGCGCAGGCATGGTTTACCGCAACGCGAACCGGACGTTTGGGCGA
TGTCTTTCGCGACCTGACCGGGCGGACCCCTTCCCTCTTTCGCGCGCTTCTGCTGCGCCGCGACTAAATCGGTTTATTTCTCCAAACAGAGATGAATCCCCC

SEQ ID 3148

LPHAAANSACPKSAKRGWTRRRHEAAQPLQAPFRIVVCRRLFAALQSCRHRAAAVSTFRQSTPCCVFRTNLASGQSIQNRKTSHEPLQPDVRLIFCRRQMRAGMVRNANRQFGR
CPCRPDGRSPCLRAFCLPPLNRFISPKQDESP

SEQ ID 3149

ATGACCGAACTCAAGCAGCTTATCCAAACCAATCCATCCCGTCATCGAAGAAACCTCGATTCTGCTGTACGAATGACGATCGACGACGACCGCTCCGCGAAGAGTGGCACAAT
GGCGGACATATCTGCGCAGCGCGGCAAAATCTGCGCTGTCCAAAATCTGCCAAACGTGGCTGGACGAGGAGGCGCA

SEQ ID 3150

MTFLKQLIQTESIPVIEETLDFLLYECSIDDAPSAAEVAQWRDILAARGGKFLRLSKICQWLDDEAA

SEQ ID 3151

GTGGCTGGACGAGGAGGCGCATGAAGCTGCGCGCAACCGCTTCAGCTGCTTTCGCGATGTTGGTTTCGCGCGGCATCTATTGCTGCTCTTCAAAGCTGCCGACACCGCGCGCGC
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CTTCTGTTTTCGCGTGGCAGCGAATGCGCGCAGGCATGGTTTACCGCAACCGCAACCGGAGTTTGGCGATGTCTTGGCGACCTGACGGGCGACGCTTTCGCTCTTTCGCGCGCT
TCTGCTGCGCGCGGAC

SEQ ID 3152

VAGRGGGKLPFRNRSLLSALWFAAGIYSLLFKAADTAPPPFFHFDKAAHLALFFAQILLLLAKAFKTKGLPIPYRSLIAFAFCFVAGSECAQAWFATRTGSLGDLADLTGAALALFAAR
SACRPD

SEQ ID 3153

TTGGATAAGCTGCTGAGTTTCGCTCATGACTGTTTCGATACGGAATCGGGAAATGCGGCTGTAAGGGCTTCAGACGCGATTGGATTATTGCTGTGTCAGGAAGCGCGTTGCTCTTCC
CATTTGCGCGGAATGATGTCGGGTACGGCTTCAGGAGATTTCGGCAGCGCATGCTGATTTCGCGCGGTGTTCCGCGCTCGGTTGTTCAAGACGTCAGCCGACGACGAGGTTGCGGTTCG
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TCTGTTGCTATTCTTTCGCGCGGTTCGCGAAGCGCAACCATTTTGAATGTTGTT

SEQ ID 3154

LDKLLRFHDCSDTEIGKMPSEASDGIGLFAVQEARCLPFFAGNDVGYGLQFGDGLVDLPVFRFRFQDVADDEVAVAGVADAQAVIVCAEFCINVFQAVVSAAAEFFDFPSA
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SEQ ID 3155

ATGTCAAACACAAATCAAATGGTTGTCGGCTTGGGCAACCGCGGCAAGAATACGAACAGACCGCGCAATGCGGGCTTTTGGTTCTTCGACGAACTGGCGTGGAAATGGAAGGCTTCGT
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ACAGTCTACAAATCAAACCGGAAGAAATCTCGCTGCTGCAGCAGCAATCGACATCCCTTCGCGACGAGTCAAATTCAAACTCGCGCGCGGCAACCGCGGACACAAACGCTTGAAGAC
ATTGAGCAAAACTCGGACGCGAGATATTACCGCTGCGCTCGGATCGGCGACCGCGGCGGCAACCGCGGCGGCAACCGCGGCGGCAACCGCGGCGGCAACCGCGGCGGCAACCGCGGCGG
AAATCGACGATCGCTGCGCAATCCCTGACGCGGTACCGGACATCATTTCCGCGCAATGGGAAGAGGCAACCGGCTTCTGCAAGCAAA

SEQ ID 3156

MSNTIKMUVGLNPGKEYEQTRHNAGFWPLDELAWKWAASFKEKFFGEVARAALPDGDVWLKPKATFMNRSQAVAAALQFYKIKPEETLVVHDELDPGRIKPKLGGNGGHHGLKD
IQAKLGTADTYRLRLGIGHPGDRNLVVGIVLNKPSAEHRRQIDDAVAKSLQAVPDIISGKWEATRFLHSK

SEQ ID 3157

ATGCTTGAATTTGAGATTGTGACGCTGCTGCCGACCGACAGGTTTGAAGAACATGACGCTTGGCGAGGGAACAACCGTCCGACCGCGCGCTGCAAGCGGTTTGGACGGCATATTG
AAAAATTAACCTGCATTTCGCGCTTTTGGCGATTTCGCGCAAGCGCTCAAGAGACGACGCGCTGCGCGACGCGGACCGCATGAGGTGATCCGCGCGCTGTTGATCGACCCCAAGA
AGCGCGCGCAACCGCTTCAAATCAAGAAGAA

SEQ ID 3158

MLEIEIVGLPDRQVLKTNQLAEGTIVRTAALQSLDGIFFENLNLHSAPIGIFGRAVKDDTFLRDGRIEIVYRPLIDPKEARRKRVQNEE

SEQ ID 3159

TTGATAGTTATGATTATTATAAAATAGCCCCCTCCCTCTAGACCATGAATGGACATCTCTGTAATTCACACAAGATAATGATTTTCTATAGAAATAAGCCTTCGGAATTTGGGTGC
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CGCGGAGTGGCAATCCGCTACACCGTATATGCAATTCGATTGTCGCTGCGGATTTCTTCTGACGACGAGAACCGGTTTTCGACGCGATCTGCTGTTTGAAGTTCGAAGGAACG
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SEQ ID 3160

LIVMTHYKIAPFLDHEWHLLKFTQDNDPPIEISLPNVPGSYLIRDFSRHITSIHACNGTSMPLQIAKNRWHATAVRGEWQIRYTVYAFDLVSRGSFLITERRGFFDGSCLFLKVBGT
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LADRHSLLPYGHTDADDAATTLGLFSHEYFHAWNKSIPKPAFAPYDLKKNYEQWAFEGITSTYDDLFARSRTISPEFYINLLAQGITRQQTRGRRLQTLAESSTAWNKFYKP
DENSPNAIVSYQKALALCLDLIIRNRSNGRSLDVTMDKLYREWRDTHSGIPEKHQIRCBETGLDLTDFPQALYSTEDLPLAELCATTTGVLFTFLPLRQHGGSYAEHIFPIPT
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SEQ ID 3161

ATGATTGGGGCTTTGCTGAAAAATTTGAAGCCGCTGCTTATTTTGTCCGCAATCGCGTTCTTCGCGCTTCTTGGCAGCTGGACAGGGCGGGCAATACCGTTCGGGATACGGTTCGGCGG
TGTTCGAGGTTTTCGAACGCCCTCAAGGCCGCGCGGTGGAACACGCCGCAACACGCCGCAATCGTCCGCCGCTATCAGGCGCAAAAGCGCGCGCGAGGAAAAAGAAAGGTTGCGCTA
TGTGCAACCGCTTAAATCATTTGAAAAACCTGTGTACCGCAATGCTGTTTGTATGCTGACGGGTGCGGCAACTCAACCGCGCTTACGACGGCGGT

SEQ ID 3162

MTGALLKRWKPLLLLSAIAFFAVSNQLDRAAQYRRGYGAUVSEVSESLKAAAVEHAHARKSSAAYQAQKAAREKERVRYVQTLKIIEKPVYRNACFDADGVRELNAAVDDGG

SEQ ID 3163

GCGGTACGGCGCGTTCAGCGCTTTGCGTTTGGCGATTTCGGCTTCGTATTTGTCCGCGATTGCCAAGAGGATGGGCTTGGTCATATGCAAGTCGCTTTTTCGCGCGTGGTATTCAAAA
ATATGGGTTTCACAATCGCATCGGTTCGGCGAGGCTCTTCGCAAGAACCGCAGAGATGCACTTGGTCAGGTGATGTCGTAACGCTTGGTCGGCGGGTGCCTTCGCGCTTCGCG
ATTGATGTTGATCGCCATTCGGGACACACCGCTTCGCACAATTTACACGCGATGACGCGTTCTCTCCGTTCCGATAACGGCGTTCGCGGTGACAGCGCGGAAACGACGCGATTGCGG
CGTTTCTCTTCGCGGAAAAATAATTGTGCTTTTTCGCGGCAAAAAAGTTTTTGAGCGTTACGCCATGCTTTTACCAGTTTCGCAAGCAGAAAGGTTTTTACTAAGTTAGCCATATTATGT
TCCCTCAA

SEQ ID 3164

AVRRVSGFAFGDFGVFVADCCQEDLGHMVAFLLAVVFKRMGFHNRIGRAGLFAETAEDALGQVVDVVLGAAGAVFAFRFDVDRHCRTHRLAQFTRDAFLSVRTALRVQTAETHGLR
RFLFGKINCVFAGKRVFERAHAFDQFAKQKGYFVSHIMPPQ

SEQ ID 3165

GTGATGCCCGTGAIAAAAGTTGAAAAAACATCTTGGTCTGCACGGCGCGGCAAAATGTCGAGCTGGTCGACAAGGTTGAGGATTACCCGCACTTTCTGCGCGTGGTACAGCAAGACCG
AGGTATCGGGCGGTAGCGGCAACGAAGTGAAGGCGCGCTGTTTATGAGATTATATGCGCGTTCGCCAATCGTTGCCACGCACAACCGCAACATCCCGCGCAGGAAATCCGTATGGAAT
GCTCGAAGGCCGCTTCAAAACCTTACGTGGAACGTGGAATTTATCGATTTCGGCGCAGATATGTCGCAAAATCGAATTCATTTGGAATACGATTTTCCCATGCCGTTTTCGCGCTTA
ATTTCCCGCGCTTCAACACCTTTCCGCCACGCTGGTCGAGCGTTCGTCGAAAGGCGAGCGCGCTTATGCT

SEQ ID 3166

VMPVKVKNILVLHGADKMFELVDKVEDYPHLPWYSKTEVIGRSNELKARLFMDYMRVRSFATHNRNIPGREIRHELLBGPFTLRGTWKFIDLDDMKIEPNLEYDFSNAVLSAL
ISPVFNHLSATLVEAFVKEADRYA

SEQ ID 3167

GTGGGAACACCTTTAAATCAATCCTTGTCTGGGTGCGCTTGGGTATCGGCTGATGGCTGCGCTTCAACGCTTTGGACGGCAAAAAAGAGCAACCGGCAAAATCGAATATTCTCAGTTCA
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TGACAACTGATTCAAAACCTTTTGAACAAAACGTCGCGTAAAGTAACGCCGGAAGAAAAACCGAGCGCGCTGACTGCGCTGTTTTACAGCGCTGCTGCCGCTCTGCTGCTGATTGGC
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CGGAAACGAAGGCGAAGTCTTTTGGGCGCGACGCTAACCGCTTCGCAAAACATTTCCGAGAAAACCCAGCAGGACATCGACGCGGAAATCCGCGGATTTTGGACGAGCAGTATCAGGT
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SEQ ID 3168

VGNTPFSLVWVALGIGLMAAFNALDGKKEDNGQIEYSQFIQVNNGEVSGVNIIEGVSVSYGLIKERTDKSTFTTNPALDDNLIQTLLKNVVRVKTPEEKPSALTALFYSLPVLILLIG
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FSGADIANLVNEAALFAGRRNKVKVDQSDPEDAKDKIYMGPERRSMVHDEKRAYHESHAIVAESLPPTDPVHKVTIMPRGALGLTWQLPERDRI SMYDKQLSLSILFGGRIAE
DIPVGRISTGASNDFERATQMARENVTRYGMSDKMGVMVYAEENGEVFLGRSVTSQNISEKTDQIDAEIRRIIDBQYQVAYKILDENRDKMETMCKALMEWETIDRDQVLEIMAGKQPS
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SEQ ID 3169

ATGGCTGTACGTTCCAAATCCTCAAAAGCGTGGCTGCACGAACACATCAACGACAGTACGTCATATGGCGCAAAAGAGCGGTACGCGCGCGCTGCGGCATACAACTTTTGGAAATCA
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CAAAATAAACGC

SEQ ID 3170

MAVRSKSSKANLHEHINDQYVHMAQKDGYSRARAAYKLEINEKDIIKPGTVLADLGSAPGSWSQVAALITGTSAGVAFDILPNEAIGGVSFIOGDFRENDVLAQFETLLDNRPDLIVIC
DMAFNMSGNVSDQARSFYLCLEALDFASQHLKTGGSFLVKVFGAGYQYEMAMREIFGTQTRKPEASRNRSSEIYLLGKNKR

SEQ ID 3171

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GTGTGAGGCGTTGACGCGCAACCTGTTCCGCATATCGGAAACTTTTGGTATTTGCGGTAAAGATATCAGGCGC

SEQ ID 3172

MLHYFFYSNRKMDTKLNTKEILELKARAHLEHPVMVGQQLTDAVIKSTDAALTAHELKIVRVFGDDRAERIEICNTLCEAVDAQFVRHIGKLLVLRKNTIEA

SEQ ID 3173

GTGGTGTGTTTCTATTGTTCTTCAATGGCGCGCAGCTGTCTTCGCGCGCGCAATTCGCGGTGCGGAAACCTTTCCGGTGAACAGGATTTTGATTACCGCTCGATGCGGTCTGCAA
GTTCCGCGCGCTTCGCTATGATT

SEQ ID 3174

VVLLLLFPQWAARCPSARHFGVPKPFPVKTDYRSMPASACGGFRMI

SEQ ID 3175

TTGCAATAAGCCCTCCAATCATCTGTGTAACAAATTCAAATCATACGGAAGCCGCCGCAACTTCAGACGGCATCGAGCGGTAATCAAATCCGTTTTCACCGGAAAGGGTTTCGGCACGCCG
AAATGCCGCCGCCGAAGGACAGCGTGCGCCCATGGAAGAACA

SEQ ID 3176

LHKPSNHFPVNNNSNHTZAAATCRRHRAVIKIRFHRKGFRHAEMPRRRTACRPLKEQ

SEQ ID 3177

SEQ ID 3177

ATGATTTGAGGGGCTTATGCAATTTCTTACCCCAATGTTCCGGCTTCGCGTATGCGCGGTATGCGCAGGAGTATTTTTCACGCCCGCTGATGCGCGAGCATATGCTGACCGCGGATGATT
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SEQ ID 3178

SEQ ID 3178

MTGGMLQFPYRNVPSASRRMRRRDDPSRRLAREHMLTADDLIYPTVFLVLEGAAREEDVPSMPGVKQSRDLRLFTAAEEAVKLGIPLMLALFPVVTANKTGRAQEAENPGLVPSTVRLRERF
SELGIMTDVALDPPYTHVQDGLDENGIVMNDETVEVLVKALCHAEAGTQVVPSPDMDGRIAGIREALEDAGIHTRINAYSAKYASAFYGPPEADVGSSGNLQKADKKTYYQMDPANTD
PALHEVALDIOEGADMMVMVKPGLPYLDVVRVRKDEPGVPTTAYQVSGEYAMLQAAVANGWLDGGKVLESLLAPKRAAGADGLTYATEAARMKLR

SEQ ID 3179

SEQ ID 3179
TTGCGCGCCGCAATCGGGGAAGTGTGGCAATCCCCCGAATTTTACATATCGGGCGGACCGGCAAAATTTTGCCTTTTGTTTGCGCGAAGGGGGCGTTATACAAAATTTATCAGCGCG
ACCAA

SEQ ID 3180

LAASGEVSAFPPIFYISGGRGKFLPFCLREGGVICQNYQAHQ

SEQ ID 3181

SEQ ID 3181
ATGTTTAACATACACCCCTTCAGGGAACCTCTTATCAAAACAAAAGCCGCAAGCGCGCAATAACCACGAAAGAAACAGGCCACCAAACTG

SEQ ID 3182

MFNIHP SGNSYQNKSRKRGNNHERNRRPNL

SEQ ID 3183

SEQ ID 13183
GTGTCGGTCCGGCTACGACTTTCGGCGCGTGGAGGATAGCGGCAGATTATGCCCGTTACAGAAAGTGAACGCAATAAATATTCCTGTGAACATAAAAGAGTTGGGAAGAAAGGATGTTACCT
CTTCTAGCGCGCGCTATCTTAAACATACAAACCCGAAAGACGGAATAATCAGGAAAAACGGTACGTTCCACGCGCTTCTCTCTCGGCTGTGTCAACCGTTTACGATTTCAGAGCCACAGATAA
ATTCAAACCCCTATATTCGGCGTGCCTGCTGCGCTACGGACACGTCAGACATCAGGTTTCATTCAATGAAAAGAAAGAACCCAGCTGTTTACCATTATCCCAAGCGACGGTAGTGCAGAAACTTCT
GTTCCATCAGAAATATGCCCCCAAACCTGCTATACAGAAAAACCGACAGCCGCGCTTGGGCTTCCGGCGCGTATGGCGGCTGGGCATAGACGCGCCGCTGCACCTTGGACGCGG
CTTACCGTCAGAACTATTGGGACCGCTGGAAATCAACCCCGCTTCAAAGCCAGCCGAAGCTTCAATTGGCATGCGCTACCGCTTC

SEQ ID 3184

SEQ ID 3184
VSVGYDFGGWRILAADYARYRKWNNDKYSVNIKELGRKDGTSSSGRYLNIQTKTENQENGTFHAVSSGLSLTVYDFRANDKPKPIYIGRVAYGHRVHQVHSMKEKETT'TV'TPYSDDGSAKTS
VPSEMPKPKPAYHENRSSRRLGFGAMAGVGIDVAPGLTLDAGTRYHYWGRLNTRFKTHEASLGMRYRF

SEQ ID 3185

SEQ ID 3185

TTGGGCGTAGAAAAGGTATGTTGCTGCACAGGTTGGACAAGCAGGCGGAGGCATATTGCTGTTTGCCCTTAATTCCTCCAAAGTGCCGCTGTTCTTGCCGCACAGTTTGCCGAAAGGAAAA
TGAAGAAAAGCTATTGCGCTTTGTCGACCGCCAAACCGTCCAAAAACAAGGATGATATAAAGGCGGCATGAAAAATCCAGGCGCGGGTGTGGAAGCTGACGGCCAAATATGAAAAATAT
TGCCGCTTACCCGCTTTTTCAGTATCCGCATCAGTGAAAAAATGCGCGTGTTTCATCTTGAGCCACATACGGGTAAAGACACATCAGTTGAGGGTGGTAATGAAGAGCTTGGGCACGCTCTATA
TTTGGGGACAGCCTGTATAGAGGAACAGAATCCGAAACTATGTTCTCTGTATGCG

SEQ ID 3186

SEQ ID 3186

LGVEKWVLLHRLDKQAGGILLFALNSQSAVLAQAQFAERKMKSYLALS DRPKSKKGWIKGGMKESRRGAWKLTNNMENIAVTRFPFSIRISEKRWLFLEPHGTGKTHQLRVVMSLSGSSI
FGDSLRYRGTESEIMFLYA

SEQ ID 3187

GTGTATTGTATTGGCAGGCAGATGCCGCTCTGAAAAAACGCTGTGCGCCGCGCTGCCTGCAAAATGCGAGATTATATCACTTGCTTTTGGCGGCGCATTGATTGTTTCTATTTTTCGGGATAGTGT
ATAAAATCCCGCATTTATCCATATCTTACAGAGCGAGAAACAGATGAAATTCCCGACCCGTACCATTCCATTCGCGGTACGATTTCGCGAGCAACACACACCCGCGCGTGTATCGCCGCGGATTTATCA
AACACGATGTTTTCGCGTCGACGAAATTCGGCGAAATGTGCCTTACCGTTATTTCGCGCTGAGCAACCCGACCCGTCAGATTTCGGAAGACACCGTTGCGCGATTTCGGAACACGCGTCGGGCA
GGTTTTCGCGTTTTCACGCGGTATGGCGGGGATTGATGCCGTGTGGCGTACCTTCTTCGCGCCCGGGCGATACCATTGTCGCGGTCGCGGATATTTCACGCGGCGCATATGACTTTATTGGTGTG
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GCTTTTACGCTTGGTAGACATCAAAGCCCTTCGACGCGAAAGCCAAAGCAGCCGACGCGCTGGTCGGCATCGACAACACCTTTGCCACGCGCGATTCTCGCACGCGATTTGGATATTGGGTTTC
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CGCGGATTTCGAGGTCGACGCGACTCGTGGCTGGTTTCGCGGCAATCAAAACGCTTGCCTTCGCTATGGAGCGACATCGCAAAAACGCGCACTCGAAATTCGCGGCGCGTTTGAAGGCCCATTC
TGCCATTGAAAAGTGTTTCCATCTCCGCGCTCGGCTCTACGAAACATTACGCATCTCGCGGCGCAAAATGACCTCCAGCCTCGGCGGCGTGAAGAGTCTGGTCAACCATTTGCTATTCCCAATCTCACAGCGGCGTCCGCGCATATG
GAACCGGCGAAACAGCGTGATTAAAAACATGAACATGCTGCTCAAAAATGACCTCCAGCCTCGGCGGCGTGAAGAGTCTGGTCAACCATTTGCTATTCCCAATCTCACAGCGGCGTCCGCGCATATG
TGAAGATTGGAATATGGGCATCAGGTCGGAATCCTCGCTTCTCCATTCGCTATTGAAGACGTAGATGATATTTCGGAACGATATTTCCGCGCGCATCGATACAACTTTG

SEQ ID 3188

SEQ ID 3188
 VYCHAGRCRLKKRCPPACKCEIISLAFPGCICDYPFRSDKIPITYPYLTRQKQMKPPTTIHSGYDCDEHNRLMPPIYQNSMFLHEIGENVPTRYSLSNPTQTQILEDTVADLEHGA
 GFAPSSGMAGIDAVNRTFLRPGDTIVAVADIYGGAYDLLVDVYQKQNGVNVFADLNGPDNLDELKAKHNKVLVWLEMPSPILLRLVDIKALAKAKAADALVGDNTFATPYLQOPLDMGC
 DPAFHSATKYLCHSDVLNGIVVARTKELAQPLHDMVHTGALAGPTDCWLVLRGIRKTLALRMEAHCKNALETARRLEAHPAIEKVHFHGPLPSHERYALAAQAKPMQIGGVVTVYLNDR
 EAANSVTKNMLKVQKFTSSLGGVESLVNHCYSQSHSGVPHNVKMGIRVGLLRPSIGIEDVDDIWNDISAALDTTL

SEQ ID 3189

SEQ ID 3189
TTGCAGGCAGCGCGGACACGCGTTTTTCAGACGGCATCTGCCTGCCATACAATACACATCTCAATAATTATCTGAATATTAAAGGACAAACACGCATGAACGCCATTGCAGACGTGC
AATCCACGACGAGATCTTTCGCAACCTGCCGATCAATCAGGTTCGGCATTAAAGACCTGCGCTTCGCCGATTACCTTGAAAACCCCGGAAGGAACACAATCCACGCTGTCTGCGCTGACGATGAC
GCTTTATCTGACCGCCGAGCAGAAAGGACGATATGTCTGCGCTTTGTGCGATTGATGGAGCAACATACCGAAGTCTTGGATTTCGCACAATTGCATTAGGCTGACTGCCGAAATGCTGCG

CTTTTGGATTCCCGCGCGGCAAAATCAGCGTTCTTTTCGGTTTTCCGCAAGAAAACCGCGCGGTATCCGGTATCCGGTCTTACTGGATTATGATGTACGCTCAGGGTGAAATGA
AAGACGGGCAATACGGCCACAGTATGAAAGGTATGATTCGGTAACCTCGCTTTGCGCGGTTCCTCAAGAAATTTCCCAATATGGCGCGCATATACAGCGTTCGACGTTACCGTCAGCCT
GACTTCCGATGCCGAAGTCGGTATCGAGGAAGTTATCGATTATGTGGAACCGAGCGAGCTGCCAACTCTACGCGCTGCTCAAACGCCCGATGAAATAACGTTACCGAAGAGCCTAC
GAAACCCGAAATTCGTGAAGATATGGTCCGCGATGTCGCTACTTCGCTGATTGCCGACAAACGCATCAAGAGTTTCGTCGTGAGAGCGAGAAATTCGAGTCTATCCAAACCATTCGG
CTTATGCTATATCGCTACCCG

SEQ ID 3190

LQAGGRQFRFRLPAIQYTHLNNYLNKDKQRMNAIDVQSSRLRLNLPINQVGLKDLRFPITLKTAEQTSTVARLTMTVYLPABQKQTHMSRFVAINBQHTVLDFAQLHRLTAENVA
LDSRAGKISVSFPFPRKKTAPVSGIRSLLDYDVSITGEMKDGAYGHSKVMHPIVTSILCPCSKELSYGAHNQSHVTVSLTSDAEVGIREVLDYVETQASQLYGLLRPDERKYVTEKAY
ENPKFVEDMVRDVATSLIADKRIKSFVVESENFEINHSAYIAYP

SEQ ID 3191

ATGGTTGTGGATAGACTCGAAATTCCTGCTCTCGACGACGAACTCTTGATGCGTTTGTGGCAATCAGCGAAGTAGCGACATCGCGCACCATATCTCCACGAATTCGGGTTTCGTAG
GCCTTTTCGGTAACGTATTTTTCATCGGGCGTTTGAGCAGGCGGTAGAGTTGGCAGCTTCGCGTTCGCTTCCACATAATCGATAACTTCCTCGATACCGACTTCGGCATCGGAAGTCAGGC
TGACGGTAACGTGCGAAGCGTGATTATCGCGCCATATTGGGAAATTTCTTTGGAACACGGGCAAGCGAGGTTACGGGAATCATGACCTTCATCTGTCGGCGTATGCCCGCTTCCTCAT
TTCACCCGTGAGGCTGACATCATATCCAG

SEQ ID 3192

MVDRLEILALDDETLDAFVGNQRSSDIAHHIFHEFRVFGVLPNVPFIFGAFBQAVELARLRPHIIDNPLDTPFGIGSQADGNVRLIMRAILGNFPGRTRAKRGYGNHDLHTVAVCPVPH
FTREADIIQ

SEQ ID 3193

ATGACAGTATTAAAGCAAAGAGCAGGTTCTATCCGCAATTTAAAAACGCAATCTGTCGCGGCATACGATGCGGCACGTAATAATCAGTCCGAGGATTTTCAGTTATTTTAGAACTCGGGC
GTTTGTGCGCCAGTTTCGGTTCGGTTCGGAGCTTGGCAGTTTGTGTGGTTCAAAACCCGAAATCCGACAGGCAATCAAGCTGTTTCTTGGGGTATGCGCGGATGCTTTGGATACCGCCAG
TCATTTGGTGGTGTTTTGGCGAAGAAAATGCCGCTTCGACAGCCGTTTATGTTGGAAGTCTCAAAACGCGCGCGCGTTACCGAACCAGGATGCGGTAGAAAATCTTTGGCGAGGTAT
CAGGCGTTTCAAGCTGACGACATCAAGATTTTGGACGATTGCGCGCCCTTGTGACTGCTGCGCGCAGACTATATCGCGTTAGCCAACATGATGACGGTTCGGCGATGCGCGGTA
TCGATCTTCGCGCGGTGGAAGGTTTCAACTATGCCGATATGGAACGCGTATTTCGCGGCGAGTTTCGCTTGTTCGATGCGGCAGAAATGGGCGGTTCGCGTTCGCGGACATTCGGTACCG
GTTTCAGGAAATCGTCACGAAAGCGCGCAGGCCCTTGAAGAACGTTATTTGGCA

SEQ ID 3194

MTVLSKEQVLSAFKNRKSCHRYDAARKISAEDPQFLELGRISFSSVSGEPWQFVVVQNPBIRQAIKLSWGMADALDTASHLVVFLAKKNARFDSFPHLESKRKRGVTEPDAVEKSLARY
QAFQADDIKLILDDSRALFDWCCRQTYIALANMNTGAAMAGIDSCPVBGFVYADMERVLSSQPLGLDAAEWGVSVAATFGYRVQEIIVTKARPLEEFTVINA

SEQ ID 3195

ATGAATTCAAAATTTCTCCGACCATACAGAAGATACCATACGCTCTCCAAACGATATGGCACAACCTGGGCTTTGTTGCGCGCGGAAGCCGACGCGCATATCGAACAGGGCTGGGTAA
CGGTCAACGGCAAAACCGCGTACTCGGTAGAAAGTTTACCAGGAGACCGGTATCGAACTGAACAGAAAGCCACGACAGCAGCGCGCACGCAATACCATCTGCTGAACAAACCGGT
CGGCTATGTCAGCGCACAAGCGGAAAAGGCTATAAATCCGCCCGCGAACTGATTACCCCTGAAATTTGCTGGGAAGCGACACAGCGCATCAGTTTCGATCCGAAACACAAAATCGGT
CTTCCCGCCCGCGGAGGCTCGATATCGATTACGTCGATTTGCTGTTGACGCAAGACGGCGGTATCGCCCAAGCAGCTTATCGCGGAAACAGCGGAGTGAAGAAATATTTGGTTC
CGGTGCGCGCGCAATTTGGACGAAAAGGACTTGCCTTACTGAATCAGCGATTGAGTTTGGACGGTGATAAACTGCGTCCCGCCAAAGTAGAATGGCAAAATGAAGACCAACTGCGCTTCGT
GTTGAAACAGGGTAAAGCGGCAATCCGCCGTATGTGCGAACTGGTCGGACTGCGCGTTCGCGGTGAAACGCATCCGATGGGCAAGGTCAAACCTGCGCAGGCTGCGCGCGGCAAA
TGGCGTTATCTCGCTCCCGCGAATCGTTT

SEQ ID 3196

MNSKISSDHTFEDTIRLSKRMALGLCSRREADGHI BQGWTVNGKTA VLQKVPADRIELNKAHQQAARTITLLNKPVGYSQAEGYKSAELITPENCWEGDTSRISFDPKHIG
LNPAGRLIDISVGLVLVTDGRILAKQLIGENSGSEKEYLVVRGKLDERGLALNHLGLSDGDLKLRPAKVEWQNEQLRFLVKQKKRQIRRMCEIIVGLRVVGLRIRMRGKVLGRILPFGK
WRYLAPGESF

SEQ ID 3197

ATGAACAGCCCTTTTCAACATCGGTATCGTAACCGCCCAACACGCGCGACATCCAGATACCGCACACAGCTGATTACCTTTTGAAGCAGCAGCGCTTACCGCTTATCTCGAGC
AAGTCGGCGTAAGGGAATGCTGCATCTATACCAAGACACGAGCGCTGCCATATCGTCAACAGAACCGAATCGGGCAATACCTGCGACCTGGTTCGCGCTTCTAGGCGGAGACGCGACCTT
TCTCTTCGCGCGCCGGAATACACCCCGCGCGCTTCCGATTATCGGCATCAACCAAGGTCAATTTGGCTTTCTTACCCAAATTTCCCGCGAATATATGACGAGCAAGCTATTGCGCGTT
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GACAGATGATTGAATTTGAAGTCTCTGCTCAATCAGGAATTCGCTATACACAACTTTCGGAAGCGGCTGATTGTCTCCACCCCAACCGGATCGAGCCGCTATTTCGCTTTCGCGCGCGCGCGG
AATCATGACGAGGAGTATACAGCCCTTACGCTCGTCCCATCTGCCCGCAATCTATGACTAACCGCCCATCGCCATTCCAGACAGCTCCGAAATCGAAATCTCGTTACCCAAAGCGGC
GACGCGCGGTCAATTTGACGCGCAATCTTCATCGAGCTGCAAAACCTGACCGCATCATCTCGCGCTACCAACATCCCTTACGCACTCTACACCCGACGAGTACCAATATTTC
AAACCTGCGCCAAAACCTGCACTGGGCGAGCAATAGT

SEQ ID 3198

MNSPFFHIGIVTRPNTPIQDTHLITFLKQHGFTVYLDVGVRECCIYTDQDGHIVNKTELQYCDLVAVLGDDGTFLSAAREITPRAVPIIGINQGLHFIATQIPREYHDKLLPV
LEGKYLAEERILIEAALIREGKTAERALALNDVLSRGGAGMIEFEVFPVQEFVYQTSDELIVSTPTGSTAYSLAAGGPIMQAGLHAPTLVPICPQSMTRPIALPDTSEIKLVTGG
DARVHPDQSGIDVQNLDRILIRRYHNPLRILHPTDYQYFKTLRQKLHQBGLV

SEQ ID 3199

ATGTCGCGCTCTCCCATCATCAACCGCTGATTCTGCAAGCCCGGACAGCGCTCGGAACCTACCTCTTTGACAGGCAAAACACTGACCTGAACATTGCCGGGCTGAACTGGCGG
GACGATFACAGAAGACGTTTGTCTCTCGCGGGAACCGCTTTCAGACAGCGAAATTAACCTTCGCAACAGCGCGATACGGAAATCTCCAAAGCGGCGAAGCCCGGCTGGGACAT
CAGGCTCGAAGCGCACTCATCTCGGATCGCGTACTGCTCGCGGAGCTGCTTCGCGGCAATTCGCGGCAATTTGCGGACGATCGGAGCAATTCGCGGATCGGAGCAATTCGCGGATCGG
GCCACCGCATCGGACAGGCAATCAACAAATCGGCAAGCATCGCGCAACAAATCGCGGATTTTCGCGCAAGCCGAGTCCGCAACACCGGCAACAGGCGCTTCGCGGATCGGCTCG
ACGAAATAGCAGACTGCGCGAGCGGCTGGAACGCTCAACGAAGCGCTCGACAGGCTCGAAGCGCATTTGGATAGAC

SEQ ID 3200

MSALLPIINRLILQSPDSRSELTSPFAGKTLFLNIAGLKLGRITFEDGLISAGNFADEITFFRNSAIRKILQGGEPGAGDIRLBDLILGLAVLSLGLSLRSASDELARIPTQAGIGSR
ATDIGHGKIQIGRNABQIGGFSREPESANTGNEALADCLDLSRLRDGVERLNERLDRLEIDIWD

SEQ ID 3201

ATGCGCGCAGTCCCCCGCCCATATCTCCATCACAGGCTAGGTTACTCGGCTGCCCTGGCACAAGGTTTACCGACACGCGAGCGCGCTCGCGCCATAAAACGAGCCTGACTT
CGGACGACATCAACCTGCCATACCTCGACACCTTCGACCTCAACCGTACCGATGCTTTTCAGACGGCATTTGGCGGCGATCAGCGGCAAAACCGCTGCTGCTTCTGCTGCGCGC
CTCCTTTTGGCGCATTACCGCGACACCGTCAACAAATGGGAGAGCTTCCCGCGGCTGCAACGTCGAACACCTGATTTTCAAGCAGCACAAGCGTTTACCGGATTAAGCGCGAGAA
TCCGAGCAACCGCGCACCGCATCCGCAACCGAGTCCGCGCGCAAAATCTTCCCGCGCAACACACCTGCTCGCAACCGCGTTCGGAACATCGACATCTCGCGCTGGCGGGCTTT
ATTGCGCGAAGCCCATCCCGTACGCGGCTCTGCAAAAGCAAAACATCAAGCGGCAACCGGCTGCTCAATATCGTCCACCGGACATCGCGCTGAAACCTGTTTCAGACGGCAT

CAACCCCGCGCAGCGGCTGAAACATTATCGAACCGGCCACCGACCGCGAATTTATACGGAAGCCGCCAACTCGGCTGCGCGCGGATTTCACCGCAGAC
AGCGTGGCAAAATCATCCGTACCGTTTCGATAACGGCTTAAGCCTG

SEQ ID 3202

MRAVPPHISITGLIGLPLAQKPYRHSRVAIKRSLTSDINLPIHLOTDFLNRTDAPQALWRHDKPVMFFLLPSPFLAHYADTVKQNAELARACNVQHLIFTSSSVYDKARE
CDETAAPDPQTESARQILAAEQHLLDNGVFNIDILRLGLLYCAERHPVSRVLQKQNIQGNRPVNIVRDIAVENLFTASNPGRRLKNIIEPRHPTREFFTEAAKILGLPAPDFSPDD
SVGKIIRTVCDNGLSL

SEQ ID 3203

ATGCGCTCTGAACACCAACCGCAAAGCAAAGGAAACAAATGGCGATTCTCAAACCTTGACGAACATCTCTACATCTCCCCGCACTGACCAAAGCGGATCGGGAACAAATCGCGCAACTTG
GCATCAAACCGGTCACTCTGCAACCGCCCGGACCGCGAAGAAGAAATCGCAACCGGACTTCGCCCAATCAACAGCTGGCTGGAACAAGCGGCTTACCGGATTTCATCAACCAACCGGTTAC
CGCACGCGACATCCAAAACACGATGTCGAAACCTTCGCCCACTCATCGGACAAGCGGAATATCCCATCTCTGCTTATGCGGACCGGTACCGCTGCTCCCTCTGTGGGCTTCGCG
CGGCGCGCAGAAGGTATGCGGTTGACGAAATCATCCGCGCGCCCAAGCGGAGGTGTAATCTGGAACAACTTCAGAGAGCGGTGGAACAACCGCGCGTC

SEQ ID 3204

MPSEHPQSGKGNMALLKLDHLYISPOLTKADAEQIAQLGKTVICNRPDREESQPDFAQIKMLEQAGVTGFHQPVTARDIQKHVETFRQLIGQAEYPIIAYCRGTGRCSLNMGFR
RAABGMPVDEIRRAQAAGVNLNLENFERLDNAEV

SEQ ID 3205

TTTCCACAAATTCAGCGGTGAATCATCCACGCCCAAAACACGATGAGGCGAAGCGGATCGGAATCAGCACTTTCCAGCCCAACGCATGATTTGGTCTGAGCGGTAGCGTGGGAAG
GTTCACGAATCCACAGATACAGTACAGCACCGCCCGCAATTTTACGAACATCCGAATCGGAAGCGTACCGACAAATGCCCGACTTTGCGGGAACGAGACAACAGCGCCCGGAGGA
ACATCAGCGATGTCAGCGCGGCAATCAGAATCATGAAATGTATTCGCAAGGAAGAACAGCGGAAATGCAAGACCGGAGTATTCGACGTGTGTGTCGCGCAACGATTTCAGACTCGCCCTC
TGCCACGTCAAACGTTGCGGTTGGTTTTCGCAACCGCGGAAATCAGATAGACGATGAAGATTGGGAACAGCGCGACGCAATTCACGAGAACAACAGACCGCCCGGATGCTTTTGCC
TGCCGGCAACGATGTCGGAAGATTATGCTGCGCGATACCATCAACGCAACAGCGCGGCAATCATGCAATCTCGTAGGAATGCTTTGCGGGAAGCAGCAATTCACACCAAGA
ACGAATATTGAGATTGGAAGCCAGCCCGGATAATCAGCGGTAAACCGCAGCGAGGTAAATCATCAGATGTACAAAGGCGGATATTTGATTTGGTCAGCAACCAATCTTCGTTAA
CGGAATCACCGCCACCGCCGAAAGACGGGCGGAGCAGCATAATCGCGCGGATGTAGAAATAGGCTTTGTTGACAGCTTCGAGCGGTTACCTCTTTAAACAGAGTTTGAACACGTCG
GCAACGCGCTGAATCAGACCCCGCGGCGCGTTACGTTGCGGCGCAGCGGAAGCTGCATAAAGCGGATGACTTTACGTTGCAATACGTCAGGTAGGCAACGCTCAGATCAGCGGAATCA
GGATAATCAGCAATTTGACGATGACGATACCAACAGGCTACGCTGATGCCAAATCGCCAGCGAGCGTTGCGGCAAGAGGTTTGGAAACCATCTCGCATATCA

SEQ ID 3206

FPQIQR*NHPAQNHVDGEADRNQHPAQTHDLVVAWEGCTNPQIPVQHRHFHEHPECGRRITDAPALRERRQPAEEHQRCQRGNQNHENVFGEQRECKAGVFDVVSNDRLAL
CHVRCVAVFGNGENQIDDEDWEQRQPVPREHRTARDAPCLRGNDVGEVHAARYHNAHQRTGHNVLGNALRGSTHCTQERIFGVGSPARDNHAVNRQGNHQDVQKADIDIGQHPFVK
RNHRPRRERRGRNRADVE*GFV*QLRTGYLFKQEPHEVGRKLNQTPRAGYVRADAKLHRAADDPTFEIRQVNGNQNRQNDHDFDDGYHQATGDAQIAQTERCCGEVLEPFLHNG

SEQ ID 3207

GTGCGGCATCGGTTGTTGTCGCGGATCGGTACGGCATTTTCATTTCCGCCCATTAATTTGGTGCCTGATAATTTGTATACGCCCCCTTCGCGCAACAAACCGGCAAAATTTGCGCGT
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TACCAGCGCGCGTGCAGCGCGCTGCAGTCTTATACATACCGCGCGCTTCAGGCGCCACCGCAGCAGCTCCGCGCGGTTGCTTCCCTCAAGGTGCGGCAATTTCCGGGCGAGGCGCGCACC
AAATCGCGCGCGGCTTAAACCGCGTCTCAACCGCGCGCTTGAGTTGCGCGACCGCTCAGCATCAAAACAGGCAATTCGCGTACACAGTTTTCATGATTTTAAAGCGTTTGCACATAG
CGCACCTTTCTTTTCTTCGCGCGCGCGCTTTTCGCGCTGATACCGCGCGGAGATTTCGCGCGGTTGCGCGGTTGCGACCGCGCGCTTTGAGCGGTTCCGAAACCTCCGACACCG
CGCACCGTATCCGCGCGGATTTGCGCGCGCTTTCAGCTGCCAAGAAACCGGCAAGAACCGGATTCGCGCAAAATTAAGCAGCGGCTTCCAATTTTCAGCAAGCCCCAATCATTTA
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ATGTCGCGAGGTCAAACGGGATGATGATACCATATTCGCGCTGATTGCGCGCAAGCCCAAGATTCGCTTCCGCGCTTTGCGGACACGAAAGACAGCTGTCGCGCGCGCGCGCGGCG
GTTTACCGCGATGACCGGTATGCGGGGCTTCGAGTTTTCGCAACCGGACAT

SEQ ID 3208

VRHRLSGSVRHFFRPLLVRLIILYNAPFAQTKRKFAASARYVKNRGECHPFRGCGPTGDSVANFRLITQSAFNARTSAPCRALQSLYIPAFRAHGSTSAPVPSRCGSPGQRT
KSAGGLTAVVNGVEFAHVAISIKTGIARHFFNDFKRLHIAHPTFLARRLLRLIRGGRFAGVGFVDRGGFEAFNRLRHRRTVSATVLRPPVQLFRINGEERDCGQKRLPIFQSPNHL
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SEQ ID 3209

TTGGCTGCCCACTTCGTTACGCTGTAAATCCAAGGATATGCGCGTACCGCGCATTCGAAACCAATFACTTACACCGCATCATCGACCGCAGCTTCGCGCTTTTCAACGAGGAAGCG
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CTGTTGCGCATACCTGAATGAAGCGGTGTTGCCCTCTGATGTGGAAGACTTATCAACTATATGCGAGGCAATTCAGATGTCATGTGGAATACCGCTTCTCTTTAGCGAGCTAAACACC
CTACTTGGCGCAGTCCGCAATTTGTTGGCGAACAATACCTTTACCAAGCCAAAGCTTCGCGCTTCTAGTCAAATGCTGACCCAGCTCAACGGGCTGAACGTCATCAACCGCGAC
AAACCGCTATGAACGACCTTCGCGTCAATATGTTGATGTTACGAAATCTGGTTGCACTTCGACAGCTCCCTGCGCGCGCTTACCAAGCTGACCGAAGACTCCAAGACACCGCGCGCTCG
TCGTACTTAAAGCTCTTCGCGCTATCTTTTCCCGAACACCGCGGGAATACAGCCGCAAAATCGGCAACCGCAACCGG

SEQ ID 3210

LAAHPVQVNPVPRMPTRIAKNTYTRIIDASLALFNEEGERNISTNHHAAHLGISPNGLYHFRNKDEIIVQLFKRYSEALLAYLINEAVLPSDVEDSINYMAGIYDVMWEYRFLPSDVNT
LLARSABLGEHMTTQAKVSPLLVLLTQNLGNLVINADQTAANDLAVNMVNTKYNFDFSSLRGRITKLTFDSKARGVRRTLISLIRPYLLPEHRAEYDRKIGNGP

SEQ ID 3211

TTGCTCGCTCACCATCGCAGCGCTGCGCTTGGTGGTCTTGGAATAACAGATGAGGTTGGTCAATCACAAGGCGCTGTGAAACCGCAGCACTTCAATTCAAATACAGTTA
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CGTCCGACTGCGCGAGTTCGACCGGATACCTGTTTATGCTGGCGCGCGGAGCAACATCTTTTATGTCAGGATTACGACGCGTGGTCTCATATGGAACAAAGGCAATACGCGAG
ATTGCGCGCTCAGACGCGATGTTCTGATTGAAGCGCAGCGCGGAAATTTGGCAGGATTTCGTTGTCACACCGTTCGCGTGGTTGAGCGGTTTGAACAACTTGAGCTGATTCGCG
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GATCGACCAATGCGCTTGAAGGCTTCCAAATCGCGCGTTCGCGGTACACGATTAACAGGCAATGCTTTGTTAAACAAACAAACCGCTCGGCAACGATGTCGCGAGTTGGCGCAA
CAGATCAAATTTACAGATTTTGTCTCGGTTTACGTTAGAAATACACCGCAACCAATTTGCTGCCCACTTCGTTTACGCTG

SEQ ID 3212

LPRSPQSPWCGANKNTVNSNSNHRPSENAHFNSTVKAQTMPIRYRTDLTPYNTFLHAQARAFIALKHADELRTDVLRLPEFDRDTVLWLGGSNILLMDYDGLVVMENKIGRE
IARSDGMVLEAQAQELIWHDFVLHTVALGLSLENLSLIPGTGASPVQNTIGAYVEAKDVHSVRCFLDLETFTLSNADCRFAYESILFKQEGKGRYIVSVVFAKTHFVNLGYD
LAAKVLELSAGREATAKDVSDAVSAIRNSKLPDPKVLGNVGSFFKNPVVSAEKAATLLQRHDFMPTYPQDGSVKLAAGWLIDQRLKGFQIGGAHVHDKQALVLVKNKNASANDVRQLAQ
HIKFTVPARFQVELHAEFNWLTSPSL

SEQ ID 3213

ATGCTGTGGCGCAGGTCCGCGAGGTGGCATCGGTTTCGTGATACCGTGATGGCGGGCGGTGGGGCAAGGAAGATTGGCGCGGTGGCTTTGGGCAGCAGCGGTTGGCCACGGTTT
ATATTACCTTTATGGGCATTATGGCGGGCTGAACCCGATGATGCGCCAGCTTTACGGCGCGGTAAAACCGGTGAAGCAGCGGAAACGGGGCGCAGGGGATTGGTTGGCGTGAITTT
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TACAAAGTACCAAGGTGCCGATGTTTATCCACCGCGCGCTTCTGGGGCTGGCGCTGCTGGCGGCTATCTGCTCGCTACCGTTTCGATATGGCATTTACGGCTTCTGGAAGCGCAT
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SEQ ID 3214

MLLAQVAVGIGFVDTVMAGGAGKEDLAVALGSSAFATVYITPMGMAALNPMIAQLYAGGTGEAGETGRQGIWFLILGIPGIMLWAAITPFRNHLFLSDYVEGTHAQYMLFTSLAM
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VFLIAPFEDYVLAQQVQVIGLSGLLYMIQSVGSAGTVIRIYFSLGRREP SRARYISGVSLSVGVLAIVITVLSVLFRSPLASMYNDPAVLSTASTVLLFAGLPQADFTQCIASIALRG
YKVTXVPMFIHAAAFWGCGLLPGLLYLRYFDMGIYGFWTALIASLTLAAVALVWLEKYSMELVKSHKAV

SEQ ID 3215

ATGTGCACCATTTATTTCTCATCACTTCCCGCTGCCGTTTTTTTTGTGTTTCAGACGGCATTTTTTATTGACTGAACACTTATGCTGCTCGACCTCGACCGCTTTCTCTTTCCGCTCTTC

SEQ ID 3216

KCTIISHFPLPFFLPQTAPLITLHLCSTSTAFPPFS

SEQ ID 3217

GTGATGAGAAATAATGGTGCACATTATATAGTAAAAATACCGTCCGTCAGACGGCGGATACGGGGTATATAAGTATATTAGATTGTGTGATTTTATGGTAAAGTTGGTTTAAAG
ACTTGACGGCATTTGAGCCGTCGGACAGGGCTGTTCCGATTCTGAATCGGAAGGAAGCATCGCGGTTT

SEQ ID 3218

VHRRNGAHYIVKNTVPSDGGYGVYKVSVCVYFHVKFGFNDLIALSRRTGAVRILNRKEASP

SEQ ID 3219

TGTGTAATCCGCTATACCCGCTGTAATAACGGAGAGACAGAGGACGGCAGTAAGGTTTGGCGTCTCTTTTTCAAGTTGCGGTGGAATGCCGCT

SEQ ID 3220

LLIRYTRCKNGEGQRTAVRFAVLFFKLRHNA

SEQ ID 3221

ATGAGAATCTGCCTTCTGTTTATCTCTGTAACACAAAAGACTGCCCGATCCGCAATCAGACGGCATCTTTGCCGCAACGCATACCGCGCTGTCAAACGGCGATGCTTCTTCCGATTC
AGAATCCGAACAGCCCTGTCCGACGGCTCAATGCCGTCAAGTCCGTTAAACCAAACTTTACCATAAAATACACACAATC

SEQ ID 3222

MRICLLFYVWTKDCPIRNTASLPQRITPLSKRRCLPTIQNPNSFPCPAQCRQVVKTKLYHKIHTI

SEQ ID 3223

ATGPTCCGGAAGCTGCCATGTCTGCATGAGAAATCTGCCCTCTGTTTATCTCTGTAACACAAAAGACTGCCCGATCCGCAATCAGACGGCATCTTTGCCGCAACGCATCAGCGCGCTGTCA
AAACGGCGATGCTTCTTCCGATTCAGAAATCCGAACAGCCCTGTCCGACGGCTCAATGCCGTCAAGTCCGTC

SEQ ID 3224

MFRKLPLCHENLPSVLSCKHRLPDPQSDGIFAATHAAVKTAMLPSDSEBQPLSDGSMPSRR

SEQ ID 3225

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SEQ ID 3226

MYTWQLPEHIADVLPTNARQLESARBQLLALFRVHYELVQPLMEYASHLTHIDAGLSLRTILVTDRLSGRQLGIRADITPQVARIDAHLLSANQGINRLCYAGFVLHAQPDGLPMRE
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LDELQAVCDAPDNEIHLIDSELVDNYHTGLLYAAYAADFDAVARGGRYDLGGYFGRARPATGFSFDLRSFIRLPAVERQPAVLVDAEDAEAREAVEALRBQGCQVVIDYGIHNV
SEELAGRLKTKTDGVWQVVKR

SEQ ID 3227

GTGTCCGATACCGTAGTCAATCAGACACACTGCCCTTGTTCACGCAAGGCTTCGACCGCTTCGCGCGCGCTTCTGCATCTTCCGATCGACCAACAGCGGGCTGCCGTTTCGACGGCG
GGCAACCGCGGATAAAGCTGCG

SEQ ID 3228

VSDTVVNHDTLPLFTQGFDRFARRFCIFRIDQHGGLPFDGGTPDFKAA

SEQ ID 3229

ATGGCTATGGCTAAAAATGTTGTAGTAATCGGCGCAGTGGGCGCAGGGGTAAGGTAAATCTTTGACTGGCTGGCGGAAGAGCGCGCGGCTGTCGCTTCCAAGCGCGCCACA
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SEQ ID 3230

HAMAKNVVVVIGAGWDEGKGKIVDWLAEEAGGVVRFQGGHNAGHTLVVGGKKTILRLIPSGILHEGLDCFIGSGVVVSFEALLGEIDELNAAGVKNVEGRLLKTAPTCPLILPYHIALDQAR
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 TSSNCLAGASAAGVGPQMLDYVLGIVKAYTTTVGSGPFPTELDFEVGAGLAERGHEPGSVTGRARRCGWFAAALKRSIQINGISGMCITKLDVMDGVETINICVGYELPGGGKTOLL
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SEQ ID 3231

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TGCCAGCCTGATTGTGCTATGTGGTTACGCGCCCAACGCGAATACCGCGCAGCGCGGCGCGGCGAAACATGTCGTGGCGCACGGAATATTTCCGCTATGTTCCGCTCGCAAGTCTTAAAGCGCAACCG
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SEQ ID 3232

VKRIPLPLATNIAVLVWINIVLAVLGINSRGGAGSLLAYSAVVGPTGSIISLLMSKFIKQSVGAEVDTPTREEAWLLIATVEAQARQWNLKTPEVAIYHSPEPNAFATGASRNSSLIAV
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SEQ ID 3233

TTGCAAGCAAATGTTTTCATACCTTTGCCGAGCCTGATATTCACAAGGCGGCAACTTTTGGGACAATCCCCAAATTTCAAACATCACACCCTACCAAAAAGGAACATCCG

SEQ ID 3234

LQANVLHTFAEPDIHKAATFWDNPQNFKTSHPTKKEHP

SEQ ID 3235

GTGATCCTTTTAAATGTGTTTATTGGAATCAACAGATGGTTTACGATTCTACACGGCTTGGCGCAATAGTTCAA AAAACCAACTGCACAACTGCCATTTCGAAGCAAAATGTTTTCGATAC
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SEQ ID 3236

VILLNVPIGKQMVYDSRLGAIVQKPTAQTAICKQMFCIPLPSLIFFTRRQLFGTIPKISKHHTLPKRNIRETHFSVFGYQYRCFGRNQHCFCGSGSQHPGRRGQPVGVFRRRRLHWFDFYF
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SEQ ID 3237

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SEQ ID 3238

MKALLLGASPGAGKGTQAFITAAFGPIQISTGMLRAAIKAGTPLGLEAKKIIDEGGVLRDDIIIGHVKERIAQDDCKNGFLDGFPPPTLAQAEAMVEAGVGLDAWVEIDVSDSVIVDRMS
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SEQ ID 3239

ATGTTTGAAAAATAAAAGAAAAATCAGATGCTTGATTCCCGCCTGCGCAGAAATGGAGACGGTGCTCTGTCGTCCTCATTTTGTGTTTAATCAACTATATATAAAGTAT

SEQ ID 3240

MFENKRKIRCLYSRLRRNGDGALSSHFCEFNOLYITD

SEQ ID 3241

ATGAAATATCCCGTACCGATCCGGACAAACCGATGCGCGACCCGCGGGCAGGCTTGCACACTCTGAAAGGTCAGGCGGCATTTTTATTTGGAAGGCTTTTTTTTGTCAACCGCCTTACACA
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SEQ ID 3242

MKMPPYRSQQQMPHPAGRLRTLKSGGGIFIGRLFFATALHKAVFCVRTAIIAACHROGRMLPKFQPRERSVIMCDFRGYZEPDMVKRPPVVVIARNRHNKLVTVVPLSSTEPVLADCH
 HKMSNPDPKHPIQCRAKCDMTAVGLARLDKRYKPKGRDRCPIIISEEDFOAVKTAVAKAFELY

SEQ ID 3243

AGCTCCCGCCAGTTCATAATGCCCATCAACGCCACCCAGCGCGGCATTTTCGGTATGCAGCGGCAGATGCACCAACGCTTTTCAGGCAAAACGGGCATCGCTTTGACGGCAACCGGATACGCTTGCACCGTTTGTGTTGGCGACAGCGGTTTGTTCGGTCTTGCAGCGCCCAAGCGTGCCAAATGTGTTCGGATTTCACAGCGCGCGCAGGCACGGCGGCATGCGTGGTTTCTTGCAACGGTGGCGGAACGGCCAGCAGATAGACATCATGATAAATACCGACGGCGTACGAGGACGAGGCGGTTTGAGCGCGCTTGAGCGCCCTCCCTTGCCCATATGCTGTGGGTGTGTCAGTTTGACCGGGACACTTTCGGCATCAGCAACGGCGCTTTCAGAAATCGACGGCTTCGTGGTATTCAAACCGTTTCAGGTCAAACAGGTTGCCCAATACCGGCACACCTTTCCCACTCGGACGTTGAATCGCCGAGGCTTGTACCACGCGCGTGAAAGATTGCAGACGGCCTTCCATATTGATGAAGCTGCCGTGATGTTTCGGTAAACGGCGCAATCGGCAGCACTTCGCAACAGCTTCGACAGCTTTCGCTGTGACAT

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SEQ ID 3244

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SEQ ID 3245

TTGATAAACAGCGCTGTTGCAACCGAAAAATAATCATTCGCGCTCATTCGCGCGCAGGCGGGAATCCATTTCTGAATTTGGGCAATCGCTGTTAAATCTGATGAACAGGTTTATCAATG
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SEQ ID 3246

LINSVLQPKNNHSAFPRRRRESISEFGQSLFKSDELSFINGFPFAPRE

SEQ ID 3247

ATGACGCGCTGATGTACCGGTTCAAATTTATCCGAACAGTTTGTGCGGGGCTTGAGTCCGCGTAGGTCGGACATCAATGCCCGGCTACGGTT

SEQ ID 3248

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SEQ ID 3249

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SEQ ID 3250

LNRYISRHSRAGGNPLIKLSSDLNSDCPNSEMSRLRGNDAB

SEQ ID 3251

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CAAGAAGCCCGCGCTCGCGCGGAAATTTGGACGCGGATTTGTCTTGGTTACACCGGCTATCCGCTTGGACGCTTCCGCGCAACACGACGACCAACCGCGCATATGACACCCCGCGAAG
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SEQ ID 3252

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SEQ ID 3253

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GCACCATGCCGAAGCATGTACCTTGCCAATATCTCGCGCGGCTGTCGTCGCGGAACTCGGTACGCGCGTTGCTCTGTTGACAGATTGCTTGAAGCACTGACGCGGCA

SEQ ID 3254

MPAKPQQTSLKSRFAQKVLVVGDMVLDVRYWFGDVSRISPEAPVPVAKIGRIDQRAGGAANVARNIASLGGAGLLSVTGDDEAAALDALMVQDGVASVLMRQIATTVKLVRVARNQ
LIRLDFEHPNREVLQIKRYREILPEYDAIIFSDYKGGSLSHSDMIDWAKHVGTVLIDPKGDDYKYVGTATLITPNCALKEVVGWSWKNESDLTZAQNLRRHLDITAVLLTRSEB
MTLFSGEPIYQPTRAQEVYDVSGADFTVLGMLGLAAGCTMPEANYLANTAAGVVAKLGTAVCSFAELVEALDQ

SEQ ID 3255

ATGACCATCAATGCGCTGAAACCTCAAAACAAAGGAAACCGAATATGACCATCATCTGTAACAGGCGCGCGCGCTTTATCGCGCAGCAACCTCGTCAAAGCCCTCAACCAACCGCGCA
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TTTACCTTATCAAAACATCGAGACCGCTTTTCAATCAAGCGCGGTGTTCCGATACGATGAACACGACGCGTTTGTATATGATGGAACCAACTACCACTACACGCTGGAATTTGTGGACTGG
TGTACGAGCAACGATCCCTTCTTTATGCTTCAAGTTCGCGCGGTTTACGCGCAAGGCGAATTTTCGCGAAGAGCGGAACTCGAAGAAACCGCTTAATGTGATACGCGTACTCCAAAT
TCTGTTTGAACCAAGTATTCGCGCGCGCATGAAGAAGGCTCACCGCCCAAGTCGTGCGCTTCGCTACTTCAACGTTTACGCGCAACACGAAACACAAAGCGCGCATGCGATCGGT

CGCCTCCACCACTTCCACCAATACCGCGAACACGGTTACGTCAACCTGTTCGGCAGCAACGACGGCTACGGCAACGCGAACAAACCGCGACTTGTGACGGTGAAGACGTCGCCAA
ATCAACCTCTACTCTCTTCGACCAATCCCGAATTTTCGGCATCTACAACTCGGCACCGCGCAGCAACAGTTCAACGAACCTCGCGCGCGCGCTCAACCGCTGCCCGCGCGGAG
GCAAACTCGAATTGAGCTTGAAGAAGTTGGTAGAAGAAGAACTTATCCGCTATATCCCTTTCCCGCAGCGCTCAAGGCAATACAGGGCTTCACCAAGCGGACATCAACAAATTCGG
CGAAGCCGATATAAGGAAGAAATTTTCGATGTCAAAGCAGGTGTCAACCGCTACGTCAAATGGATGTGGAAAATTTGGCT

SEQ ID 3256

MTIQCRKPKSKQRKPNMTIIVTGAAGFIGSNIVKALNQRTDIIIVADNLTGKEFKFNLABCEIAHYLDKHEFIRQVREHILPYQNIETAVFHHQACSDTMNHDGLYMMENNYQYTLDLLD
CQDERIPFLYASSAAVYKGEIPREERELEKPLNVYGYSKFLFDQVLRMRKKGTLTAQVVGFRYFNVYQHEQHKGRMASVAFHFFHQYREHGYVNLFGSNDGYNGEDYTRDFVSVEDVAK
INLYFDHPELSEGLYINLGTGRSQFNLAAAANVACRAAEGKSELKELVEERLEIRYIPFDALRGKYQGFTQADITKLREAGYKEEFPDVKAGVRYVKNLENLA

SEQ ID 3257

GTGCACTTGGCGCGTGTGTGCATTTCCGTCATCATCGAAATCCATATATAAAGTTAAACAAATCAAANTCGCCTGATATTTTCAGACGATTTTTCACGGCATTCAAAT

SEQ ID 3258

VQLGALLHFGHHRNFTIKLNKSKSPDIFRRFFYGHSH

SEQ ID 3259

ATGCAACACGCGCCCACTGCACCGCCAAATTTGGAAAATCGCCGACGAAGTACGCGCGCGGTGGATGGCTGGGACTTTAAACAAATACGTTCTCGGCACACTTTTCTACCGCTTTATCA
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CAAGGCATCAAGGCTTGTGTTCGACGACTTCGACACCACAGCAGCGCGCTCGGCAGCACCGTTGCGGACAAAAACAAACGCTTGCAGCGCTCTTAAAGCGGTGGCGAATTCGATTTG
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CCAACTCAAAGACAGCAAAACCTTTGATGCGCTGCTTCAATCGCCCTATTCATCGACTGGATAGGCGAGCAGACCCACCTTGATCAACGACGCGCTTTGCCCGCGAGCGGT
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GCCGAAATCAGCGAAACCGTTCGCAAAATCGAACGCGTTCGCGCTGAAATTCGCAAGGTGATTGACAGATTTGAAAC

SEQ ID 3260

MQQRALHRLQIWKIADVEVRGAVDGFQYVLGTLFYRFISENFTDVMQAGDSSIDYAMPDSIITPEIKDDAVKVGYYFYPGQLFCHIAAEAHQNEELNWKLEIFTAIESSASYPSSE
QGIKGLFDDFTTSSRLGSTVADKNKRLAAVLKGVARELDFGNFEDHRIIDLFGDAYETLISNYANAGKSGGEFFTPQSVSKLIARLAVHGGQEVKNKYDPACGSGSLILQAKQFDEHIE
BQFPQGEINHTTYNLARMNMLHNVNKNFHELGDTLTNPKLKDSPFDVAVSNPPYSIDWIGSDPTLINDRFPAGVLAPEKSKADFAFILHALNVLSSRGRAIIVSPGIFRYGGAB
QKIRQYLVENGVETVIALAPNLFYGTCLAVNLVLVSKHNDTDIPIASGFFKKTNNVLTTEEHLAEIVKLFADKADVPVHIAQNAAQQTVDKNGYNLAVSSVVEADTREVVIDIRQLN
AEISETVAKIERLRREIDEVIAEIEF

SEQ ID 3261

TTGATAAATAATTTTATGGAGATCGTCTGAAAAATGGGCTTCAGACGGCTTTTGTAGTTTCATTGACAATCAATCTGTTTAAAAACGTTTACTGCCACTTTCGCGCTATTCGCCACAG
GCGGGAATCCATTTTGAATTTTCGGCACTGCTTTTCAAAATATCGGCTTCTG

SEQ ID 3262

LNNFLWRSEKWSADGLLSFINDQYCLKRLPPCRHSRTGNNPFFRQLLFKYRL

SEQ ID 3263

ATGGGACGCGCGCAGCGGCGACAGCGGATGACAAGCGCTCCGTGCTGTGATGGGCGCGGAATGCGCCCTTGTGCTATCTGCAAAACGCTTACAAATCCCAATCATCCCTTCAA

SEQ ID 3264

MGRARATGDDKPSVRVMGRMRPLSYLTPTNPQSLQ

SEQ ID 3265

ATGACAACGAAAAATAACGCTTTTGAACACGCCAACACATCGACGAACAGGCAATGAATATGTCGGCGCGCACCTTGCAGCAAACTCTTGAATATTTCCGAATATTCGCAATTTCCAAAC
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ACCGGCTGCCAATCTGTTTCGCGCCACGCAACCGAGAGAAAACTACGCGCGCAAAACATCAGGCAAAACACAGGCAAAACCGGCTGCAATTCGAAGTCGGAACAAAAGTGGCCAAAC
ATTGAAGAACTGGCGGCGCATGCTTGAACACGCGCTACCGGAGAAAAGCATCAACAGCTTGAAGAACGAGAACAGAAAAGGCTTGCAGCAACCGGAGCATCAACACGCAAA
AA

SEQ ID 3266

MTTENNAPENAKHIDETGNEYWSARTLQOILEYSEWRNFQRAIDKAITACETSGNDKNHVFETNMKIALGKGQREVADYRLSRYACYLIVQNGDPSKSVIAAGQTYFAVQARRQELQDE
AARSLGEDKQRLRLRLREHNTDLAAAADAGVEKPEYAVFQNHGYRGLYGLDQKGIHSRKLKKSQRIIDHMANSEPAANLFRATQTEELRRKNIQKGTQANRVHFEVQKVRQT
IEELGGIMPENQVPPEKSLQLENEBQKRLAATBQHONGKX

SEQ ID 3267

GTGAGCCGAAACCCCGCGCAACCGCCCACTCCCGCGCAGCGGAGGAAACGGAACCAACCATGGATATGCAAGCAAGCGAAAAATTTGAT

SEQ ID 3268

VSRNPPRNPTSRSGKETENNHYAKQSEKID

SEQ ID 3269

ATGCAAAAGCAAGCGAAAAATTTGATTGAGATGATTCAGACGCGACCGGTGGAGTGAAGCCATTGGGGGAGGTTTGTAGTTTCGTACAAAGGAATTAAGATACTGCTGGACAAATGAAG
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CAAGAAAATTTTTCGTAATATCGGATCAAAAAATGCAAAATGCCCAAAATAGCAACACAGATACAGATAAATATAAAATCCCATCCCATCATTTGGAACCCCAAAAAATTTGAAAAA
TACTTGACAAATTCACCGAGCTGGAAGCTACGCTGGAAGCTACGCTGGAAGCGGAATTAGCCCTCGCGCAACGCCAATAACCGGTATTACCGGACTTACTTTTAGATTTCGACAAATCAAT
CGGGGGGATAGC

SEQ ID 3270

MQSKARKLIEHQIAPVWVKPLGEVLVTRKTKITAGQMKEMHKDAPLKIFAGGKTFALVDFDVPDKDIHREPSIIVKSRGIIIEFYDYKPSHKNEMSYHSVKNHITIKYVYVFLKT
QENYFRNIGSKMQPIATPDTDNYKIPIPSLETQKIVKILDKPTELEATLEATLEALALRRRQYRYRDLLDFDQIGGS

SEQ ID 3271

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SEQ ID 3272

LPIKSGGIDAGYQCRILKNVWMTLGEVAEYSKNRISCDKLEHNYVGVNLLQNRREGKLSGYVPSEGRMTETVNDILIGNIRPYLKKIWDQADCTGGTNGDVLVIRVTEKVNPKYLYQV
LADDKFFAFNMKHAAGKMPRGSKAALIMQYKIPPLPEQEKIVAILKGFDTLTHSVSEGLPHIELLRKKQYEVYREQLLAFPKAA

SEQ ID 3273

TAACATCTATTATTATATTTTAAATGACTTAAATAACTCTTTAACAGCAGCTCATTTGCTTCTCATCTGTAGGCTCAAACCTTTTCACACCAATTAATTAATTTACATCGCCATGCAATATC
CTACTGCATCGCAA

SEQ ID 3274

*LIYYIFK*LK*LFHSTLIVFICRLKLPDPNYIYIAMQYPTASQ

SEQ ID 3275

ATGGCAATTGGTTTCGATGAATTCACGCGACGATCTCCGATGTCGACATCAACGTTACGCGTTGGTGGAGCTGATGCTGGTGTGCTGATTGTTTATGATTACTATGCCGGTCTGA
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TTCTGCAAGCAAGTGGAAATCGGGGAAGTGGAAAGCGCTCTGAAAGCGCGCAAGGAGCAGAAATGAAACGCTGATTGTCGCTGATTGCGGCAGCAAGCGGTGGAATACGATTATGTAAC
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SEQ ID 3276

MAFGSMNSDDSPMSDINVTPLVDMVLVLLIVPMITMPVLTHSIPLELPTASEQANKQDKQPKDRLRLTDANGYVVGDSASKEVEGESRLKAAEQENNVIVAIAADKAVENDYVW
KALEARQAGITKIGFVETRAQ

SEQ ID 3277

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SEQ ID 3278

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YEEYMGNTDSQTEARRGYLDVAKELHERFPDPDKIETEKDKDPFAKLFGEYLRARLVQNYDEFAALRELQNVDADEDAKPAQEKYYLSEDEVDQEMRKVPMPSEARVQDYSAYNDI
RDWLRQKAGEQREQSKIDWDVVFVDLLKSQRINLDYILQVFEHKKIKGKAEVBETIRIRASIGHRAKBLIVDFINDTDLKVPDVPALLETFTYTAQEVMRHEAAGLIAEGL
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SEQ ID 3279

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CTCTCGCA

SEQ ID 3280

SEQ ID 3280
LSRRFMILAPELEQILQQLYREARKAHYFISLEHLLLVLTIEDRAVPNVILKLGADLKAVSEQLAASVAENPTPLIDHLLDVTETPTLGLFQVRIQAMVHTQSAGKGLAEPLDVLVAIN
SETDSHAVYPLGLQSVTRFEVLRCAIHGSPDEDEDGNYPSDGMDDDENRTPKGPKNLSAITYTNVLAENAVKAGRIDPLGRKHMERLVQILCRRRKNPNLLVGEAGVGKTALADGLAHQI
VNDIDIPDALKEAEVYALDMGSLLAGTKYRGDFEARVKSVLKQLEKIPHALIFPDIETHIIGAGSTGGTMDASNLLKPALAKGSLRCIGATTYDEYRTIFDKDHLSRRFQKIDVVEPTVA
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VKMSRSGLGLPDKPIGSLFSGPTGVGKTEVAKQLAYSIMGVFLQRFDMSEYMERHAVSRILGAPPGYVGFPEQGLLFEAVNKPQCIVLLDDETEKAHPDIFNVLLQVMDAGKLTDNNGKSA
DFRNVLLIMTINAGAESLSRPSLGFTAKRREGDEMQINKLTFEPRNRLDAIIPPAFLSEPTIIVKVVDFKFLQLQLEHRLDKKKVEAEFTPALRKYLEAGKGFDPQHGARPMHRLIQEKIRK
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SEQ ID 3281

SEQ ID 3281

TTGTTAAGACAAACGTC AAGCTATGTTTCAA AAAAGTGGGAAAATAGGCGAAAGTACCGAAAAATACA CA AAAAATCCGCTGTAACGCGGCTTTCAAATGGGACACGCTATGACCGCGC
AACACCAATCCGACACGCTTTTG CACCGCCTGAACACCCCTGCGCGCAAAACGCTACGGCGTATTTTATTGAACGACGATTACACACGATGGAATTTGTCGTTGAAATCCTGACCGAAAT
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CGGGCAAAAGCCGAAGGACATCCGCTGCAATGTATTGTGCGAGGAGATT

SEQ ID 3282

SEQ ID 3282
LLRQNVKLCFQSGKIGESTENTKMPSEKFGMCHAMTAQHQSDTLLHRLNVLPPKRYGVFLINDYTTNEFVVEILTEIFMLGQEQAVAVMLSVHHEGKGLCGTYTRDIAQTKQQQVMQ
RAKAEGHPLOCTVERI

SEQ ID 3283

SEQ ID 3283
TTGCTGATTTTGTAAATTTTAAGTATAGGAAGTTTCTAATGGCAACCGGTATCGTAAATGGTTTAAACGACGCTAAAGGTTTGGTTTCATCACTCCTGACGAAGCGCGGAAGATTTGT
TCGCACACTTCTCAGCGATCAATATGGAAGGTTTCAAAACCCCTGAAAGAAGGCCAACGCGCTCTCTTTGACGTAACACCGGCCCTAAAGGCAAAACAGCCGCCCAACTTCAGGCAGCT

SEQ ID 3284

SEQ ID 3284
 LLILLIFKYRKPLMATGIVKWFNDKRGFGFITPDEGGEDLFAHPSAINMEGFKTLKEGQRVSPDVTTPGKKGQAANIQA

SEQ ID 3285

SEQ ID 3285
TTGCACATTTTTTTCATCAGCACTGATTTTCCCTTATCCGTCAAAATACTAAGCCACTTGCCCAACAACAGGGTACACACAAGTTCAGGATAAGGCGGGCGGGGATTGGGGACATTTTCCGCC
ATCGCGCAAAACGGCAGACAAAACGGCGGGACATTGCCCTGTCCCGCCGTTTTCAAATATACATTTGACCGGTACATCAGGAATTAAGCTGCCTGAATGTTGGCGGCCCTGTTTGCCTT

SEQ ID 3286

SEQ ID 3286
LHIFPISITDFPISVKILSHLPTTGYTQVQDKAGGDWGLFHRHONGRQRRDIACPAVFKYTFDRTSGIKLPECNRPVCL

SEQ ID 3287

SEQ ID 3287
ATGCCGCTCTGAAGACGAAGGCGGCGCGTTTGGCCCCGTGCCCTGCCCGTTTGCCGTTTATGCCGCACCGCCCTTTTACCGGCACATTGCACATTTTTCATCAGCAC

SEQ ID 3288

SEQ ID 3288
MPSEDEGGAFPCPVPARLPFYAAPFTGDLAHFFHQH

SEQ ID 3289

[illegible]

TACTTACTT
SEC ID 3200

SEQ ID 3290
LHRNYPVSLFCONKITIMRIKFV*ISPNIIVITIR*IKTNPLFLMIKYCNKI*AVSISFKKD*KFRKPTNLIKRIECLTLFVGCTV*KNKNSFPHYHPPH

SEQ ID 3291

SEQ ID 3291

GTGCGCGATAAACCGCAACCGGGCAGGCACGGGCAAAACGCCGCCCTTCGTCTTCAGACGGCATCGGCAGGGCGTTACGCTTCGCGCAACCGTCATCCCGCAATCAGAAATCGAACCG
ATTTTGTGTGGACGAACGCCGCAAAAGCGTATCTCGCCACCGCGCAGATGTCGCGGTACATATCTCGCAAGCGTCCGCGAACGGTAATCTCTGTGGACGGGTGAGCAATCA CGCCGTTTTCGA
CCCAAAACCGCGCGCGCGCGGAATAGTCGCGGTAAATGGTGTTCGACCCGTGCCCAATCTCGGTATACCAACAATCCGTCGCGCATTTCTTTACGAGGTCGGATTGCGTTTCTGT
CGTATGGTTCAAAATCAGGTTGTGCGCGCCGCCCGGTGTGCCCGTGTCTGATCTCCAGTTTTCGCGCGCGTGTAACTCCCGAGGAAATAGCCTTCGACAAATGCCGTTTGAATCACGAAG
CGCGCGCGGTGGTGCACACTTTCCGATCAAAATAGCTGCTGTGCGGAAAGAGCGGGGATGTGCGGTTCTTCGCGCAGGTTGAGGAAATCGCGCAGGACTTTTTCGCCATGCTGTGATCA
GGAACCTGCTTTTGGCGGTAGAGCGCGCGCGGAGAGTGTGCCGACGAGGTGTCCGATCAGCCCGCCGAAACGGTGTATCGAAGAGGACGGGGTAGCTGCCGTGTCGGGATGTGCGCGCT
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GGGTCGCGCAAGTCGCGCAACCGCTTTCGCGCGTGTGGCGGCGATGTGCGCGCGCGCGCGGACGCGTGTGCGCGAGGCTTTGTTCGAGAAGTCGCGCGTTCGCGCGCGCGCTTTGCGT
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GTGCGCGCGCTGCTTTTGTCCAAGTCAGCGTGTGCGCGCGCAGAGTTCGAGGAGTTCGGAACCGGTGTGGTTGAACAGCATAAACAATCTTCTTGTGTGAGCGCTTGTGCGCATTT

SEQ ID 3292

SEQ ID 3292
VRHKTANGQARCKTRRLRLQTASAGRSASGNRHPRNQNRTPQSVTRHADDVAVHIQLASGNGNLVDGVCNHA VHPKPTRRAARTIVAGNGVRLTSHQFGYQOSRAHFFQOVGLRFV
RMVQIQVVRAGVARGHLHSEPARAVATAEELAPDNAVLNHEARRGNVTRFKIAAAEAGDVRFFAQVEEIQGDDFPADAVDQETALAAVERAAGECADEVSDQPARNGSTEEDGVAACRDA
AESQAAGGQITDGFAGVHIRMAGAGVTPVVALSHVPGVGGNDAGNAVVRALPVCCKTGVGAVNVVLVSGLHRRAPGVFDAAVRVQRCLFALPCQADGGFRQIQIPFVVKVGVADVLRHQL
GVKSGATVTPGGVAGDVGGGADGVAQGLFGVEVGGAAGAFAPADVNGNVQRFLLELDLDFQAQAHADLSEFRAEVFGGGGRARCFQVERAAAEVEEFGSGVVEQHNLNLSWVSVA

SEQ ID 3293

ATGCTGTTCAACACACCGCTTCCGAACCTCTGACCTTGCCTGCGCGCAGCTCGACTTGGCAAAAGCAGCGGCGCGACCGCGCCGAAGCCGACTTCAGCGAATCGCTCGGACAAAGCG
TCAGCGTGGCGTTGGCGCAAAATCGAACAATCGAGTTCCAGCAGGACAAATCGCTGGACATTACCGTTTACGTCGGCAAAAGCAGCGGCGCGCGCGCGCGCTTCTCCGAACAAGC
CCTGCGCGACACCGCTCCGCGCGCGCGCGACATCGCCCGCACACCGCGGAGACGGTTGCGCGGACTTGGCGACCCCGAGTTGATGGCGCAACACATCGCGCGCGCGCGCTTTACAC
GAATGGGATTGGATACGGAAGCGCGCTCGGCTTGGCAAAACATGCGAACAGGCGAGCTTGGACACGGAACCGCGCATCGAAACCTCGAAGCGCGCGCGCTGCAAAACCGGACATACC
AATACGTTTACGCGCAACCCACCGCTTTTCCGCGCACCGCGCAAGCAGCACCACAGCATTTCTGCGAGCGCTGCTGCGCGCGCGCAAAACCGGAATGCGAGCGCGACTACTGCTACGATTC
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ACCAACGCTTTCGGCGCGGCTGATCGGACACCTCGTGGCACACATCTCGCGCGCGCGCTCTACCGCAAGCAGTTTCTGATCGACAGCATCGCAAAAGCTCTGCGCGGATTTCTCA
ACCTGCGCGGAAGAACCGCACATCCCGCGCTCTTCCGCGAGCAGTATTTGATCGCGGAAGGTTGCGCACCGCGCGCGCTTCTGATTCAAACCGGCAATTTGCGAAGCGCTATTTCTCGG
CAGTTACAGCGCGCGCAAACTCGGAATGCGACACCGCGCAAGCGCGCGCGCGCACAACTGTATTTGAACCATACGCGAAGCGCAATCGGACTGCTGAAAGAAATGGCGACGGGA
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SEQ ID 3294

MLFNHTASELLDLRRTYDLAKAAGATAAEADFSLSLQSVSVRLGIEIEQIEFQDKSLDITVYVGRKRGAGTADFSQALRDTVRAAADIAHRTAEDGAGLADPELMAQIHGIDPDLYH
ENDLDTAAVGLAKQCEAALDTSRIENSEGAAYQTHGYVYVGNTHGFAHRQSTHHSISCVVAADENGMQRDYYWDSACRHPDMSPETIGTQTAARRTLRLGSRISPTGSYFVLPD
TTVSGGLIGHLVGLSGGALYRQSSFLIDISIGKVLDPDLNLRREPHIPRSFRSSYFDEAGVATAPRFVQINGIVEGYFLGYSARKLGMQTTGNAGGAHMLYLNHHTHTQSDLLKKEGTG
LLVTELMGQGANITGDIYSRGAAGFWVENGVIAPVHEITVAGRLQDMYRDIVGVADDLRRSSNKIGSILIAHGTAVGS

SEQ ID 3295

TTGCGAGGCGTGGGTGCAAAAGCCGCTGGAACGCGCGCGCATCTGTTAAATACGCTATTGGAATAATTCGAGAATCAAGATGTTTGAACAAGAACGAGTGGATCAGCAAAACCC
AAATGAAAGAGCAGATGAACGCTTTCAGGATTTGGGTATGGAATGACAGGCTCTCAAACGACACCGCTGAAAAAATCGGTTTGGATGAAGATTGTACGAGGCGCTGCTTACCTATATA
AAAAATTACGTGCAACGCGCGCTCAAACGTCAGCGCGCAATTTATCGGACGCTGATCGCGGATACCGATCCCGCGCCATCGAGGCGCTCTCTGCGCAAGCTGCGCGCGGACGATCGCGCG
CACAAACGCTTTTTCGAACGCTGGAACAGCGCGCTGACGCTGTTGCGAGCAGAGGCGCGCTGACGCGCTTATGTCGATTTTCCAAACGCGCGCGCGCGGAGGCTGAGGACGCTCG
TCCGCAACACCAAAAGAACAGGAACAGGACAAACCGCGGAAAACTTCCGCGCTGTTTCAAGAAATGAAAAACCGTGATGGAAGAACGGGCGCGGAAAT

SEQ ID 3296

LQGVRCCKPSEGGILLKYAIGKNSRIKMFQDEWISKTQMKQMNGLQDLGMLFRLSNDTLKKIGLDEDLAEAVVYKITYSNGALKRQAFIGRLMRDTPAPTEAFIAKLRGDDAA
HNAFLQRVEQARVRLLADEGALTPQMSDFPNAGAGRLRLVRNTKKEBQDKPKPNFRALPQLKTVNMENGGAET

SEQ ID 3297

TTGTCGAACCCGCGCTTCAAAAGCCGCGTTCAGCTTCCGCGAATCTCGGGATGACGGGAACAGTATTTCCCGCCCATCATCAGGCTGCCCTTTTCAATTTGGGCGATTGCTTTCGG
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CAAAACGCGCGCGCTGTTTACGGAACAACATTTTATCTTCCAACTAAATAACGCGGATGCGCGCTGAAAAATATGCCATAAATTTCCGCGCGCCCGCTTTTCCATCAGGTTTTCATATC
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AGCGCGCGCTGCTGTCGCAACACCGTACACGCGCTGTTCCAGCGCTGCAAAAGCGCTGTCGCGCGCATGCTGCGCGCGCAGCTTGGCAAGAACGCGCTGATGGGCGCGGATCGG
TATCGCGCATCAGACGCTCCGATAAATTCGCGCTGACGTTTGAAGCGCGCTGTCAGCTAATTTTATATAGGTAAACGCGCGCTGTCATAAATCTTCAATCAACCGATTTTTCACGCT
GTCGCT

SEQ ID 3298

LSNPAPKRPVSFAESSGLTANQYFPPIITRLPFSNWLSSATTFKARIWSLSTCLRVIWVLTGLPIPRNIIVQFFSIKVAATAAVVLRNNILSSNLNNGGCRKIKICLNFRAPVPHHGPFQ
LKQGAEVFRFRVFLFFFFGVADERPQPARAGVWKIHKLRQALVQPPYTRLFHALQKGVVRRIVAALQKRLDGRIGIAHQTSKDLRLFFERAVGRNFFIGNDGLVQIFIQTDFFQR
VW

SEQ ID 3299

TTGGAAGATAAATGTTGTTCCGTAAACGACCGCGCGCTTTTGGCGGCAACCTTGATACTGAACGCGCTGTACGATGATGTTGCGGGGATGAACAACCCGCTCAGCCAAACATCACCC
GCAACACGCTTGACAAGACCAATCCGCGCTTCCGCTGCTGTTGCGGAAGCAATGCCAATTTGGAAGGGCAGCTTGTGATGATGGCGGGAATACCTGCTCGCGCTCAATCCCGA
AGATTGCGCGAGCTGACGCGCTTTTGAAGCGCGGTTGGACAAGCCCTTCCAAATAGTTGAGGATACCCCGAGCTATGCGCGCCCAAGACCGCTGCGGCTCAAAATCGAAGCGCGCGC
AGCCAGAATTTCACTACCGGAGGCTTTGCGCTGCGCTATGATACCGGACAGCTGACGACATCGCAAGCTGAACAGCTTGAAGTGAAGCGGCTCAAACTCGAACAATCGGACCAATTACA
CGCGCTGCTGATCCGCAAGGCAATACTACGCGACCGCGCAAAATCGAAGCGGATGATATCATTTTGAAGCAAGGTGTCGCGCGCGATATTTATATACGCTTACGTAATAACCGGATCGG
CAAAATCAAGCTTTTGAATAATCTTATATACGCGCGCTTGTGATATTGATGATGCGCGCGCGGCTGCTGCTGCTGCTGATGTCAGCGCGGAATTCCTCAGACAAA

SEQ ID 3300

LEDKMLFRKTTAAVLAATLILNGCTMMLRGMNPNVSPQITRKHVDKQIRAFQVVAEDNAQLEKGLVMGKGYWFAVNPEDSAKILGLLAKAGLDKFPQIVEDTFSYARHQALPVKFEAPG
SQNFTGGLCLRYDTRPDDIAKLQLEFAVKLDNRITTYTRCVSARGKYATPQKLNADYHFEQSVFADIIYTVTEKHTDKSLFGNIIYTPPLLILDAAAAVLVLPMALIAANSSDK

SEQ ID 3301

ATGTCAGTCAAAATCAAAACCCCGCTCAATACGACGTTTCAATCATTTGCTGCGCGCGCGCGCGGATCTTTAATCGCCCGCTTTGTCGCTCGCGCGGTGTCGAAGTCTGCGC
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TGATGCGGACGCGCGACCGCGTGTGCGCTGCTGTTGGACGCTTTGGCGGCGATGGCGCGCAAGTGAATTTCTCTGTCGCAACCGCTTTGACGACGCTACGCTTACGCGCGGAACTC
GCCGAATTCGCGCGCGCAAGCGTGGATTGCTGATTACGCTGGATAACGCGATTCGCGATTTGCGAGCGTGGCGCGCGCGAGGCTCTGCGGTTGGATGTCATCGTTACCGACCAACC
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TGGGGGACGCGCTTTCGCGCGCGGAGCTTTACCGAGGATTCACGCTGCTTCCGACGAGCTTTGGCGCGGGAAGGCAACCAAAAGCGCTGCTTGCAGAAAGCGCTTGAAGTGA
AAGCGATGCTTGGCGCTGCGAGGAGACATTCGCGAATACATCCGACGCTGACCGCGCGCTTGCACCAAGATGGCGCAACCACTCGAATTCAGCTTTATATGCACTACTGGGAAGC
GGCG

SEQ ID 3302

MSVKIQTFRPWNITVFNHLLAAGADPLIARLCASRGVQSPAELDDKLSALLPYQSLTNCEAAAGRLADAVRKEKILIVADYDADGATACAVGLDGLAAMGAKVDFLVNRFERHGYLFPFL
ARIAAAGQVLDLLITVDNGIASIAGVARAQAAGLGLDVIITDHLHPADTFVPCITVNPQKCGCFPSKSLAGVGVIFVYVLTALRAELRRRNYFSDGIKEPNLGLLLDLVALGTVDVVPDLHNN
RILVDSQGLKRMRSKMRPGIRALFEVARRDWRKAQPPDMGFPALGRINAAGRLDDMSVGIACLLARDDEAQLAARLNNLNIERRIEBQSLMDALNAFFPETLPSGQTLVAYRDDTHQG

VVGIVASRLKDRFYRPTIVFAPADNGEVRSGRSIPNLHLRDLALVSKRHPDLILKPGGHAMAAGLSLEHNTIPAFQAFEEAVRENVCEDDLSTQYITIDGSLPACDITILEQAQNLACHV
WQGFAPPPSFTDEPHVVRQPLGABGKHKKAWLQKDCFEFAMFWRCSEDIPEYITRVYRPVANEWRRNLEQLYIDYWEAA

SEQ ID 3303

GTGTTACAGACTGCATCAGGCGGTACGATTCCACAAGATGCCGAAAACATAAGCAAAAGCGGTAGAAACTACGCCGTCCGAATCAGCCGCCCTCGCGGGCGCAACGCGTCATTATAACAG
ATTGCCCTTTAAAAATCAGACCCCTGCTTTTGTGGCGAGTCTGAAATTTGATGCACCTTATATATTGCGTCCC

SEQ ID 3304

VFRLEQAVRPHKMPKITSKRRRNYAVRITPPSRQRVITDCLKNQTLILWBSLKFDAFYILEP

SEQ ID 3305

CCACCCCTCCCACTTATGCTCTTTTCATCGGCCCGCGGTTCGATGTAATGCCAACTCATCAGGAAATGCTTGTAAAGCTGCGGACAGGGAAGCGCGGCATCGGCAAGGCGCAG
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GGGTGCATTGGCCGAGGATTCGTCTAGTAGAATAGCTTAAGCGTTCGAGGGCTTTGACCATGCACACGTCTTCGTCCATCAGATAATCGCGCCGGAACCGAGCATCGAGCGGCTTT
GGAATTCGAGTCATAGTCCATATTGGTCTGCATCATAATGTCGCGAGCAATACGGGGCGGAGCAACCGCGGGAATAACGGCTTTGAGTTTTTACCGCCGCGCATACCGCCGCCATT
TTCAAGACTTCGCAAAACGCGGTGCCAACGGCACTTCATAGTTGCCCGGACGCTCGACATGCGCGGAAATACAAAATAATTTGGTACCGCTGCATTCGGAATACCTTTATCGGCAACG
CTGTCCCGCTCAGCGATAATAACCGGACGAGGAGAACGTTTCGGTATTGTTGATGTTGCGTTTGCCTGACAGCGCAACGAGGCGGGAACGCGGTTTGAAGCGCGGCTGGCC
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CTGCGGCAACGCGCTGCTCCAAAGCGGTTCAAAGCGTTGATAACCTTCGAAAATTTGCGCGTGGATATAGTTGTAGCGGCTTTCGCGCCCATCGCGTAACCGCAATGATCATGCTT
CAATCAGGCGCATGAGGATTAACATGATGATGTCGCGGTTTAAATGTAACCGGCTGCGCTTCGTGCGTTTGCAAAACCATATTTTTCGCGCGGAAAGAACGGGCGCATAAAGCTCCA
TTTCAACCGGTCGGGAAGCCGCGACCGCGCGCGCGCAAGCGGAGGTTTGTACTTCGTCAATCATATCGGTTTTCGAGAGATGTTTTCGAGCAGGATTTTACGACGCGGATAGCCG
CGCGTTTGAGCATATTCGTCATGTCAGCAATCGGATGCGGCTATCCACTTGGTCAAAAATCAGCGCTGATTTGTAATAGCCAT

SEQ ID 3306

PPSPMLFHRPAVDVVRKLIEMLGKAADREDGGIGKADGAACHLVADRIQIQVPHAFAPYDAADDAVKPAGTFAAGGALAAGFVVVEIA*AFEGPDHAFVHVHDNRAGTEHRAGF
GNRVIVHIGLHNVRQYGGGRTAGNNGFEPTAAHTARHFQDFGKRRARHFIVARTLDMAGNTK*FGTACIRNTFIGKRLSAVTDNKRDDGGERFIVDGGRFVQAEGRGERRFEARLA
FPAPQRFKQCGFFAANICAVAVVGEFEFKIRTQNTIFQKACGTRLLQSGFKALITPENFVAVDVIWAGFAHRVGTGNDHAFNQGMRIEHDVAVFKCTRLAFVGVANHIFPARERTGHKAP
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SEQ ID 3307

TTGCGGCAGCTTGGATGTTGATGGTTTTTTCAGTGTGGAATCATATGAATTTGAAATTAGTGTGTTGAATCGGCGATCCCGTCTGATCGGTGTGTTTGTGTTGATGCTGTTGATGA
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AGTGGCGCGCTCGATGCGCTTTGTCCAACTCGGCGCAAGAGGCAATTCAGCTTACCGCAACTACCGCGCAACGAGCGTCCGAACTGGCGAGGCTTTGCGGTGAACGAGTATTG
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TTTACCACGCGCTGATCAATATCGGCAAGCGGCGAGATGATGTCGCGGTTTGCAGCGCGGATGCGGAGGCACTGTTGCGGCGAGCGCGCGGTTTGTTCGCGGATTCGCGCGG
GTTGCGATACACTTCCATCAATCGCGGCAAAAATACTGACCCAGGATTTGGATGCGATGCGCGCAGATTTGCATGTCGCGCTGCTTAATCAAAAGGATAGC

SEQ ID 3308

LRQLGCLIGPFSVGIIMNLKLVFESGDPVLIGVFLMLIMSTVTWCLVLRICKLYRARKGNAAVKRHRMDTSLNDAVEKVRVADAPLSKLAQALQSYNRYRNEASELAQALPLNEYL
VIQIRNSMAQIMRRFDYGMTALASIGATAPFIFLGTWNGIYHALINIGSGQMSIAAVAGPIGEALVATAAGLFAVPAVLAVNPLNRGTKILITQDLAMADHLVRLINQKDS

SEQ ID 3309

GTGTATGTTAAACATACACCTTGTGTAAGGCAACGCGCGGACTTTCGGACATCTCCGGATGTGCTGTTTCCACGAGCAGTCGACCAACCTGAAACGTCGCGCTACCTCTCTTGTGT
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SEQ ID 3310

VYVHTPLIKKPTGGLSGHLRMCCFHEQSTNLKRPTSSWSKRGFTFVELKQNTLSVSPKSKQNVRTQILGAEPWFLGDVAEILQIQNARQLPLKQDGIQKSSVATKKGQELLFINE
PNLYRVIPRSRKABAVKPDWIFEEVLPQIRKQGYQITPKTTADRTGLRRAVALVGRKIRGYSSAYSMIHQRFNVEAVEGIPADKLPEAVAYVHALFLHTGLAGEVDPDRPLPAPQPA
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SEQ ID 3311

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GCCGAAACAGGTGCACAAACTCTCCGCGCGAGCGCATCATCGGACGGCTTTTCAGATTTGTCATGATGAACGGTTCGCGGAGATTATCGAAGTAACGACGTTTCGCGCGGTCGGAAG
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CGTTTCAGACGCGCATCGCGGAAACGCGGAGCGAAATGACAAAAACGAGCGCGCGCGCGCAAGAAAAACGAAAGCAGGCGGAAAAACCGCGCGTTCGAGCGGCAACCAAGCC
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SEQ ID 3312

MLKKWLNLKMLPSGRSSKABSKFVI PAERHNSAEMLSFAAENVIRRLKAGFQAYVVGAVRDLGLIEPKDFDVATDATPEQVHLFRSRRIIGRRPQIVHVMNGARIIIVTTFRRGAK
VHQNAGRKIMKDWYGSIEEDAMRRDFTCNALYYDPEKERILDPHNGIADVAARLLVMIGNAERYQEDPVRIILRAIRLSGLFELSEETAAPRIASICRLKHPEVARFLFDEIMKLLFSG
HARECLRLNGFDIPDIHPLNLALVSDGIAGKMTALALKMTDERLRADKSVSVGFLAALMPELDRHWKSNLQQLKPTPALSDAINTMRETVERGWGVQRFPSATMREITMFPQPFEN
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SEQ ID 3313

ATGCCGCTGAAACGCCCTCCACCACTCGGCAAGTGCAGCGTCCGCAATTCGCGGTTTCGGCGCGCAAGAGCAGGAAATCATAGCGCGCACGAAACGCCCTGTCGAAACAGTTTGTGCGG
ACGTGCGCTTTTGGCGTTTCAAACTGCGCTGGAACATCCAAATTTACGCACTGTCGGCGGAAAGCGTTTCGCGTACGCCCAACCGCGTTTCGACGTTTCGCGCATCGSTAT

SEQ ID 3314

MPSETPSTTRQVRGPHCRFRRARAGNRRHGNAPVQTVCAADVRLCGFQTAAGTSKPHASWRKSVAVRPNRVRFRASY

SEQ ID 3315

ATGCCCAAAATACATTTTTCATCAATTTTCTTGTGCTTGAAACCTGCCACCCGACATCTTTTCCGGCGCGCAGGGTCAGACTTATTTGCAGGGATGAAGCCCCTTACAAATC
AGAATAATACA

SEQ ID 3316

MPKIHFFINPSLLEPCPPGHPFSGRQGTFLFAGHKPLTNQNT

SEQ ID 3317

ATGAAAAATGTATTTTGGGCATTTTGACCGCGTGTGCCCATGCCGTGCAATTTGCCGACAGAATCAGCGATTGGAAGCAGTCTGGCGCAGTTGGAACACCGTGTGCGCGTATTTGAA
CGCGCGCAATACCGTCAAAATCGACCTTTTCGGTTCAAATTCACCATGTATGTATGACGCGTTACCGCTTTTTCAGAAAGCGTTTGAGGCAAGCGATCGGAATGAAGCGGTGGCGCGCA
GAAAGTGGTTCAGCGGTCAACCCCGAAACTTCGGCAATGTTTTCGGGAGTAGGCAATCGATGCAGAAAAATTCGAT

SEQ ID 3318

MKRCILGILTACAAMPAPADRISDLERLAQLEHRVAVLESGNTVKIDLFSGNSMTYVCSVTTPQKTFEASDRNEGVARQKVRQACNRETSAFPCGDEAIRCRKFD

SEQ ID 3319

ATGACCCATACCGTCCACCTGCACCTTGAAGAAACCGACAACCCGACGCTGCAACGCCCTGTGCGGTTCTTTGACAGCAACCTCGATTTCGCTCGCCAAAGCACTCGACATCCATATCAGCC
GCCGTTTCGAGCATTTTACCTTCAACGCTGCATTTGCACACGCCCGCAACCGCCACTGCTCAAACTCTTGGAAACGGCGCAGACGGCGGACCTTAAACGACAGCATCATCCGCTTGGCGC
CGTCGAAACCCAAACCGAAGATGCCGGCATCAGGAAAAAATCACGAACACGCCCTATTATTTCGAAACCAAGCGCGGACGATAGCGCGGAGAACGCCACGGCAGAACGCCCTATATCCGC
GCCCTGCTCGACCAACGACATCGATTTCGGCTTCGGGCCCGGAGGTACGGGCAAACTTATCTTCCGCTCGCGCGCGCGCTCGATGCGATGGAAGAACACCAAGTCGAACGCATCATTTAG
TTCGGCTGCGCGTCAAGCGCGTGAGAACTGGCTTCTGCGCGGAGACCTGACCCAAAAGTCGACCCCTACCTCCGCTCGCTTTATGATGCCCTCTATGACCTGATGGGCTTTGACCG
TGTAAACCAAGCTGATTGAAAAAGCGCTGATTGAAATCGCCCCGCTCGCCTATATGCGCGGAGGACGCTCAACGGCGCATATCATATCTCGACGAAGCGCAAAACACACCGCCCGAACAA
ATGAAAAATGTTCTGACCCGATCGGCTTCGGCGCGAAGCGCTCATTTACCGCGACACAGCCAAATCGACCTGCCCAAAACATCAATCGGGATTGAAGAGCGCAGCTGAGAAATGTC
ACGGCGTGGCAGGACTGTATTTCCATACCTTACCGCGCAAGACGTTGTCCGCACTCTCTGTGCAAAAAATCGTCGAAGCTTACGAATCGGCAAGAACCGAC

SEQ ID 3320

MHTVHLHLEFDNPTLQRLCGSPDSNLDLAKALDIHSRRFEHFTFNGAFAHAGKRALKLLETAQTRDINDSIIRLAAVETQTEDAGHQEKNHEHAYYFTRKRSIGGRTPRQNGYIR
ALLDHDIVFGLGPAGTKTYLAVAAVDANEKHQVERIILVRPAVEAGEKLGFLPGDITQVDFYLRPLYDALYDLGDFRVTKLIEKGLIEIAPLAYHRGRTLNGAYIILDEAQTTPPEQ
MKMFLTRIGFGAKAVITGDTSQIDLPRNIKSLGDKAREKLHGVAAGLYPHFTTGEDVVRHPLVQKIVEAYESAED

SEQ ID 3321

TGTGATGATCTCGACCACTTGCCTGTCTGCCCTCATTTCCGCGCAGGCGGGAATCCATCTCAATGGTAAGCAATGTCTTATTAATTCAGAAACCGAATCTTACCGGTGGAATCCCGCCT
CGCGGGAATGACGGCATTTTCAGTATTTTCAGTAGGCGGATCTT

SEQ ID 3322

MLDLHLVCRHSRAGGNPSSMVSNVLLNSETESYRWIPACAGTAPFYFSRADS

SEQ ID 3323

TTGGCAATGCCCGCAACTGCGCTGAACATCGCGCGCAGCGGACAGGAAGAACAGCGGCTGAAACAGCAGGCGGACACTTGGGCATCGCCCATGCCCTTACATTTTTCAGCGCACTGC
AACCCGAAACCAATCTTGGATTGATGAGGAACAGCGACGCTTCACTCTCGCCAGCGCGCAGCGAAACCTTTCGGCGTGGCTATATFCGAAGCCCTCTCGCAAGGCTTGGCGCTCATCGCCAT
ACATTCGCGCGCGCGGAATCCATCGTTTCAGACGCGCAACGGATACCTCGTTTCCGTTGACGATGCGCATGTCTTACGCTTCTCAAATAATATGAACACCATCGCGATTTCGCGCGAA
CAGCTCAGAACCGACTGCTTCGCAACATTGCGCGAAGATGCGTTATCGCGAGACTGATTGCCGTATTCGCTAGCGCGCGGGAACAGCGCGGAAACCGCGGAAATAGATTAAAA

SEQ ID 3324

LAQCPQLRNLNIGSGQEBQLKQQAADLGAHAVTFLGALQPEAILDLMRNSDAFILASRTETFGVYIEALSQGLPVIAIHCGGARSTVSDNGYLVSDADVLLALKIYEHADFSAE
QLRTDCLATFGEDAVIGRLIAVFRQAARNTARKRPKNRLK

SEQ ID 3325

ATGTCGAAACCGTTGCACGCTCTGTCATCCCTTATGGTATCCAGATCCGAACAGGATGTGGACGGAATATTTTCCAAATCAAGCACAGACCTCCAACGCAAGGCATCAAAACCG
CCATCTCGCCCCCATGTTCCGTTATCTGCGGAAAGAAACAGCAAGCATCTGACCGTCTTACGTTTTCGCCGATACCGGCAAGCGGTTTGACATCTACGCATGCGCGCAGCATGTA
TTCTTCCCGCTTTTCGTTTATCGACATCGACCGATCCGCTGGGTGCGCGCGGTT

SEQ ID 3326

MSEPLHLVLPIMWYRSEQDVGIFPQNAQTQKRGIKTALAPMFRYLKETAAILTGPVGPARYRQSGLDIYAWRSMTYPPAPRLSTSTASAGCAPV

SEQ ID 3327

GTGCGCGCGGTTTGAAGCCTTCAAACTACATCCGCGAAACGGACTGCCGACCTGATTACGCCCACTGATGAATATGAGGCATATCTGCCCAAAAAATTTCCGAAAAATAG
GCATTCCTACGTTTAAACGAAACACAGCAGCACCATCAGCGCGGTCTGATCCGTCACCACTAATGGCAGCGGATGGAAGAACAGCGCGCGCGCTCCGACGCTCTCGCGTCAGCGG
CCATTTCCGACACGCTCTGCAACACAAATACGGCTGCGAATGGCAGTACCTCCCAACATACCGGGTGAATATTCAAGCAAACTTTGAA

SEQ ID 3328

VRAGLKPKHYIRENGLPDLIHAHCNMYAGILAQKISEKYGIPVLTESSTITRGLIRHMQPHEKAAAPASARLAVSRHPAHLVQHKYGCENQYLPNIPGGIFKQTFE

SEQ ID 3329

TTGCGCGTTTTCAGTAAGGATACGGATATGCTGCGTCTATTTTGGCGGCTTCCCTGCTGGCGGATCTTTTCCGCGCGCGGCTGAGGCATTGAATTACAATATTGTGCAATTTTCG
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GAGGGCAGGGAATTTGATGCTTTAAACCGTTTATGCTGATGTTTCAGACGATGCTTCGCTTGAAGATACCGAATTCAGCGGTGTGCGCGAACCGCGAAACGAGGTATCATGAGGTCA
GCAAGGATGCGGTTTTCGCTTCAAGCGCGTGCAGAAAACTGCGCGGCTTCTGGGTGCGTCCGTTTAAATTCGTCAAAATGAATTTTGGGCAAAATCGGACGCATATTTGCGGCGCA
TGGGCTGTTCCGCGCAAAATGCTGCGCGGATCCGATGCGCGCAAGCTCAATATGAAGGTACGAGTTTCAGCCGACCGGCTGTGGAGGAATTCAGCATCAGCATCAATGGACGTT
CAGTTT

SEQ ID 3330

LAVFQVIRIRICCVLFWRLPCWRYLFPAAABALNYNIVEFSESAGIEVAQDTMSARFQVAAEGRDKNAVNAEFVKFNFTRKSKNGSPKTELVSRSAMPRIYQYTNRRRIQTGWEEARBFKA
EGRDFDALNRFIADVQTDASLED/DFSVSRERREVIDQVSKDAVLRFKAREKLAGVLGASGYIKVILNFPQIGSHIAGDAVRANKLRAMPMAASVNMKGTDSAAFVERISISINGTV
QF

SEQ ID 3331

ATGAGCATCAAGTCCGACAAATGGATACGCCGAATGAGCGAAGATTTCGGCATGATTGATCCCTTCGAGCCGAACCAATCAAAGAAGCCGACGCGCATCATCTCTACGGTACGT
CCAGCTACGGCTACGATATCCGCTGCGCCAATGAATTTAAATTTTACCAACATCAACAGCACCATCGTCGATCCAAAACTTCGACCCGAAAAATTCGTTACCGTCGAAGACGACTG
CTGCATCATCCGCCCAATTCCTTCGCACTGGCCGCGCAGGTGCAATATTCGCCATTCGCGCAACGTCCTGACCGTCGTTTGGGCAAAATCCACTACGCCGCTGCGGCATCATCGTC
AACGTTACCCCGTTCGAGCCGAATGGGAAGGCTACGTTACCCCTCGAGTTTCCAAACACCAACCCCTGCCCCCAAAATCTACGAGCGGAAGCGTGGCGCAAGTCTCTCTTCGAGA
CGCAGCAAGTGTGTGAAACTTCATACAAAGACCGCAACGGCAAAATACATGGGACAAACCGCGTAACCTTGCCCAAGCC

SEQ ID 3332

MSIKSDKWRIRMSSEFPMIDPFEPNQIKADQRIISYGTSSYGYDIRCANEFKIPININSTIIVDPKNFDPKNFVTVEDDCIIPNSPALARTVEYFRIPRNVLTVCLGKSTYARCGIIV
NVTPEPEWEGYVTLFESNTTPLPAKIYAGEGVAQVLFESDEVCEISYKDRNGKYMGTGVTLLPKA

SEQ ID 3333

CTCCAACCTCCGCCAGTTTCTTCTCAATCGCCTCTTCGGTCATAAAGCTGCACATGCTGTGGTTGTGACAGCATAACGGGGCATCGCCGACGCGCCCATGCATTGCGCTTCGACAAAG
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ATTTCGCGACAGGCTCAAGGTCGTATATTTGTAGAAAGTGGCGACTTCATATGCTGCGCGCGGTGATGCCGATGTAGTCGCGCAACAAAGCGATGTTTCGGGGCGGAGCGACGCTTT
TTCGGTTTGGCGGATACGCAACGCGCCATGATGGCGGAACGGCGTGGTGGCGGATATTTCGCCAATCAATGTCGATTGTGTTTAAAGATTTCGGGATAACAT

SEQ ID 3334

LQLRQFLNRLFGHKAHAHVVDQHNGLIAARAHAFAFDKGFVAVGRGFAVADTEFLFEVFAGRHTAAQSAGQVGTNGQFVFPADRLKVHVHVESGDFICLRRRDADVGNKSDGFGGEPAP
FGLGDTQRAHDGDTALVGGIFRQLNVDLF*GFCG*H

SEQ ID 3335

ATGATAAAGAAATTTTAAACCCCGCAGTCGTGTTTTCGTCGCACTGCTGCATTGGAATAAGTGCCATTGCTCTGCGAGCGCACAAGCTGCCGTGATAGAGTCAGGAATGTTA
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GCCGTTTGAAGCCGCGGTTCACAAAAGCGGATGCGGATATTGACCAACCTAAGGAAAGAGCCGAACCCGAAGAAAACCTAAGCCGAACCCGAACCGGAAGCGGAGCCGTGCGCG
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AAAGTGTGAAAAGCAGCGGTTTTCGCGTTTGGACAATGCGGCACGCAAGCGCGCAAAACGGGCATTTTCAAGCCAATGCTGACGCGAGTTTAAAGTCCCGCTCAAGTTTGAATTGA
AT

SEQ ID 3336

MDKERILTPAVVFSVALLHLAIVALLWQAHKLPVIESGNVIEFVDLDFGGGGGAPGAGAPAAPEPQAPDPKPKPVEPPKPVLPKPAVTKKADADIQPKPKPKPEPKPEPEAKPAP
KPAEKPAEKPSKPAEHSNNAKAGSBQNGEGKGTGKGDGTGRBGSKGSAGKRGHEGAGGSGGGTGVGSSKGNPLRANGSIPRPAYPALSMENDBQGMVVLVSVLSPGHHVESV
KVVSSGFSRLDNAARKAAQNGHFQANAWTEFKVPVFKELM

SEQ ID 3337

ATGATTTTAAATCGAGTAAATGTATCTACGATTATTTTCAACAGGGGGAAGATGAACCCAAACCAATCCAAAAAGCTACGAATCTAAGCGCGTTTAAAGCAGCGTTTCAATTTA
ACACTGAAAAAGAGCTAATTTATTGGAATTTTCCAATAATTTAGACTTCTCCAATGGGTAAAGAAAGCTGAAACATGAACCTGAATTAGAAAACTGAAAAA

SEQ ID 3338

MILNRVKCIYDYFQQGGRMNPTKQSKSYESKRVLKHVSFNTKEANLLEFSNNLDFSKWVKEKLKHELEKLLK

SEQ ID 3339

ATGCTTAAACATCTCGCATTCTACTGCCCCCATGATGTGCGCCCTCCCGCCGACAGCCGCGTCTAAGCCCTATCAGGAACCGGCTGCACCTACGAAGCGGGATCGGAAAAGAGC
GGCTTCTTCAGGCAAGGCATATGCGGTTCGCCGGATGGCGCGGTATACCGGTTCAATCAAAAACCGCAAAATTCGACGGGCAAGCGGTTATACGGTTGCCCGCGCGCGCAAGTATT
TCTCGAGCCGTTCAATTCGACAGTACCAAAATCCGCAATATGCGATTGTCGGGACGTTCAAAACAGGCTTGGCACACGCGAGGTTCCCGCCTCGCAAAACCGCGGAAACCCCTTTTAT
TATGAAATGCGAACACGCGCATGAT

SEQ ID 3340

MLKHLAFLPAMFALPAQTAVLSPYQETGCTYEGGIGKDLGSLGKGIWRCRDGRGYTSFKNGKFDGQGVYVAAGREVFLFPPNSDSTKFRNMALSGTFKQGLAHGRFAASQNGETLFPY
YEMRTRED

SEQ ID 3341

ATGTGGTCAAGCAGATTAGTTTTTATCCGCTCAACAAAGAAAGCTGCTGAGGCGGACGTACTTGGCGCAAACTTCTGAAGCTGAATTTACCAATTGCCAAGGTTTGGAGTGGTTCA
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TTTGAAGAGAAGGTAGCGGAAATCCAAACAAATGAAGCCCGCAATGTCGGTCGCAAGAAAAACAAGAGCTTAAAGAGCAAAATACAGACGACCTGCTGCCCGGAGCGTTTACCCGCGAGC
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CGTGGCGAATACCAACAAATCGCCCTCTTCCCTGATGACCGGCTGGCTGTTGCAAGGCGATTCGCAAGGCGGTTTGAATTAGACAGCGATTGCGAAGCTCAAAGGTACGGGCGATATTGT
TCCGCTGCTCAAAGTATCCAAACAGACTTAACCGCGGACGAAAGTGTTTCAACAGCTCAAAAACCGTAAACCGTTACCCGCTCGGTTTGTGTTGGCGGCAACAAATCGCCCTTATCCTC
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TCAGCACCATTGGAAGAGCTGTTTCTTATTTGGCGGCTGGCAAGAT

SEQ ID 3342

MWFRQISFYPLNKEKLPEADVLADKLAEAFTHCQGLDWFSEGTAPVVSFPELVFPADFLRLVALKKEEKVLPAGVIRDILEEKVAEIQNNEARNVGRKEKQELKEQITDILLPAPRTSR
SRTRAVFNTRHGYLLVNNAASAKAENILTKLREALGGLASLPNTKQSPSSLMTGWLLQGHCEGGFELSDCELKGTGDIVFVVKVSKQDLTADEVVQHVKNKGTVTTRLGLVWRQIAPIL
TQDFTLKRIQYLDVLQBEAESNGDDAAGLAFASQILMAESVSTMLEELVSYLGGWQD

SEQ ID 3343

GTGTTACGTTTACCGAACCGCACTTGACACAGAAAGACCAATCATGAAACCAACATCGCGCTTATCGGCGCGCCCAACGTCGGCAAAATCTACCTTGTTCACCGTTTGAAGCGCACCA
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CGGCAATTTGCGACGAAATGCGCAAAACCACTTCAGGCTGTCGATGAAGCCGATGCGGTTGTGTTTGTGTTGAGCGCGCTACCGGTTTAAACACCGCAAGCAAGATTATTGCCGACCGT
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CGCACGCGCAGCGCGTGTATTACCTGATTGAAGAAATTTAGAAAATTCCTCCGAGCTGGAAGCCGAAGAAGCCGATGCAAAAACATCCCGTTTTCGCTTATCGGTGCTCCGAAACGCTCGG
CAAACTACGCTGGTTTAAAGCCATTCTCGCGGAAAACCGGTCATCGCTTCGATATGCGAGGACACAACCGCGCAGCATCCACATCGATTTCGAGCGCGAAGGCAACCGTTTACCATC
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ATACATCTGTTTCGGAACCCGCTATGAAATTCGGGAAGACAAACCGAAGAAAAACCGCTCGCCGCTCAGCCTGAGCAACCGTATTGAGAAACCGGAAGGCCGAAGAGAGAAAAAC
CGCTTCAAGAAGAAACCAAGTCAGTGTGAAAAACAATTACGAAA

SEQ ID 3344

EQID 10 3344
 VFSSERHRLTQKDPIMPKTIALIGRPNVGKSTLFNRLTRTKDALVHDLPLGLTRDRHYGHGKVGSKPYFVIDTGGFEPFVVDSGILHEMAKQTLQAVDEADAVFVLVDGRGTGLTPQDKRIADR
 LRQSPRPVYLAVNKGEGGDRAVLAAEFYELALGEPHVISGAHGQGVYLLIEELLENFPEPEAEAEADAKHPVFAVIGRPNVGKSTLVNAILGSKRVIAFDMAGTTRDSIHTDFERBKGPFPTI
 IDTAGVRRRGKVDEAVEKFSVITAMQAVEAANAVVLVLDAQDQADQATAGFALEAGRALVAVVNKWDGISEERREQVKRDISRKLYFLDFAKPHFISALKRFGIDGLFESTIQAAYNAA
 MTKMPTFKITRVLQTAVERQQPPRAGLVRPKMYAHQGGMNPPVIVHGNLSHAI SDSSTRYLTQFFRKAFLNQLCTPLRIQYNVSENPYENAEADKPKKKPLRSLNSRLEKREKREKIN
 RPKKIKTSVSVKKQTSK

SEQ ID 3345

SEQ ID 3345
 ATGGCAGCCGCACTCTCGAAGAACCAACAGAGCTTAGACAACATTTAAATATTTTTTGCGAAAACCAACGGGCAAATGGCTGTTTGCCTCTGCTGAFTTTTGGCGGCACTCGGCTACTTTGGGATACACGG
 TTTACCAAAAACCGTGGCGGCTTCCCAAAATCAGGAAGCGGCGGGGTGCTGGCAACAATCTGTGGAAAAGCGGCAAAACAAAGCCCGCAAGAGCGAAATCAATGCGGAACTGTCCAAACTCCA
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 AATGAACTCGATTCTCGTGAAA

SEQ ID 3346

SEQ ID 3346
MAAHLBEQOELDNFKYFWKTKTGWLPALLILAAALGYLGYTVYQNRAAASQNEAAAVLANIYVEKAQNKAPOSEKINAELSKLQOSYPHSISAAQATIHAATEFDAQRYDWAEGHLKWLVSQ
KNSLIGALAAORIGYVLLLOKKYDAAALALDTPVEADPAILMETTKGDDVYAAOKEQBALKNYGOALEKMPQDSVSGRELLQMKLDSLK

SEQ ID 3347

SEQ ID 3347

ATGAACGACGATCTTGCCTGTGCGGGCAAAAGATTTCAAACTCAGCGCTGTGTTTGGCAGCGCTTTGAGGATACGGTAAACCGTTGGACGCGAGCTTACGGTTATCAGCAAAATCCGTACGC
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AGATTGCGGCTCTGTGTCGCGTGCCTGGTGCAGACACAACCTTCTGTACAACAGCCCCAAAGCTGTGGTATATGGGGCCGATGTTCCGCCCGGAGCGTCCGCAAAAAGACGCTACCGC
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SEQ ID 3348

SEQ ID 3348

MDNLLFVPGQKDFLTAUVFQAPEDTVNRWTRAYGYYQIIRTPIVEQTGLFVRSIGEEBTVVGKEMYTFSDSNDLSLSLRPEGTASCLRAVEHNLLYNSPQKLWYMGPMFRFRPQKGRYR
QFHQVGI EALGPEGPDI DAETIAMSADLWEKLGIREYLFLEINSLNGREERAARALVEYLTRYEAQLDEDSKRRLKTNPLRLVLDTKNPDLOEICNAAPRLVDYLGEASQNHYARFKAML
DGLGIQYIENSRRVRLGDLYNQTFVFWTTDKLGAQATVCGGGRYDGLIEELGGKPAPSIGFAMGIBRLILLVSEYGSLEVNAAPOVYAMHQEGADLQVMKYAQALRAQGFNVIOHSGYQS
LKAONKKADNSGARFALIVAODELADGTVTTLKDMNGAHGQQTVSATDLTDTLQWKNMA

SEQ ID 3349

SEQ ID 3349
GTGAGGATGGAGATGCTTTGCGGGCGGTAAAAATGCCGTCTGAACAGCTTTTCAGACGGCAATTGACTTACTCTGCGCGCCCTTGCTGATTGTGTCGACTGCAAACTCCGTCTGCCGCT
TGGGA

SEQ ID 3350

SEQ ID 3350
VRMEHVCGRVKMPSETVFRRLTYSARPCLICPTANSVCRIG

SEQ ID 3351

SEQ ID 3351

TTGCCGCTTGTGCTGTCAAGCGTTTCGGGGTCGACACCACATCTGTCAAAGGAAACCATGTTTCAAATTTTGACTTGGCGGTGTTTCTGCTGTGCTGCTGCCCGTGTCTCGCCA
TTACCGCTACGGAGGTGGCGCGCGGTATACGGCGCGCTACTGGGGAGACAACACTGCCGAACAATACGGCAGGCTGCACACTGAACCCCTGCCCATATCGATTGTGTGGCGGCAACAATCAT
CGTACCGCTGTCTACTTTGATGTTCACGCCCTTCTGTTCGGCTGGGGCGGCTCGCATTCCTATCGATTTCGCGCAACTTCGCGCAACCCGCCGCTTCGATGTGGCGGTTCGATTTCGCGT
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GATTATCTCGTCTGCTATCGTCAACCGGGGTTTGGGTGCGCTTATTGCAACCGATTGTGCGGCTGGTGATTGCGTCTGTGTCAGATGTTGCTC

SEQ ID 3352

SEQ ID 3352
LPLSVSRSLGLHTTSVQRKTFMFQFDLGVFFLLAVLPVLLAITTVREVARGYTARYWGDNTAEGYGRLLTNLPLPHIDLVTGTLIVPLLTLMTFPPFLFGNARPIPIDSRNFRNPRLAWRCIAASG
PI.SNLAMAVILMGVVVLVLTPTPYAGGAYCMPLAOMANYGILLNAILPALNIIPILPWDDGIFIDTFLPAKYSQAPRKIEPYGTWITLLMLTGVLGAFTIPIVRLVIAFVQHFV

SEQ ID 3353

SEQ ID 3353
TTGAATTATATTTATAAAAAAGGTGCAAAATAAGGTGCAAAATAAAATTAGTTTTTCCCAATGGGTTAAAGAACAATCCGAAAAGAGTTCT

SEQ ID 3354

SEQ ID 3354
I-NYTYKKGANKVOIKLVFPNGLKNKSEKSS

SEQ ID 3355

SEQ ID 3355
TTGAGATTCCGCTTACCAATGGCTGACAAACGCTTCCAAATCGGTATTCTTGGGCTTATGCATCTTCCTCTGTGCGGCGTGCCGACCATCATCAGCCGATGATTTTATCCTTATCCTCGCAA
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SEQ ID 3356

SEQ ID 33356
LRFPLPMADKRFQYGILGLMHPLCRRAHDHQPDDFILILATESLPQQWAVDPHPRNPDIVESLSRCRQLQIRRTTRRQHLLPFRFLRIHAIVHRHKRYPDDHRRHIAHFPFLFHRIVAEIQ
FNNRLLOHIAKATLOSYLALNHNKGTGAHVAVIGNLGRLOYLFQLRRIGGGVLOLFGRSVAVRQ

SEQ ID 3357

SEQ ID 3357
ATGAATTTACCTTTTCGGGCAATGGTCTCTGATTTAGGTGGCACACTTTTAACACCTGAACATTTAGTGGGTGATCTTAOCATTGATACTCTGAGAGTTATTAGAGCAAAAAGCGGTAGATA
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SEQ ID 3358

MNLPFRANVSDLGSTLLTPEHLVGLTIDTLRLVLEBQKVDIILATGRNHTDMSSILGKI GAERAVMITSNGARVRDLQGNLLYSNLSPEHLVLELYKTSYVGNLIQTFRFCRHQ

SEQ ID 3359

ATGCCGCTCGAAAATGTTTCAGACGGCATTTTACCCGCCGCCGCAACCATCTCCATCTCACAAGCCCTTAAAAATCCGCTATAATCGCCGCCAATTTGATTTTCAGCACCCCTTTTGA
AATGGCACA AAAAATCCAATCCGTCAGGCA

SEQ ID 3360

MPSENCFRHFYPPANHLHPKPLKIRYNRPQDFSTPFLKWHKSNPSEA

SEQ ID 3361

TTGTGCACTATCCGATTAATAAGCAAAACAAAGGCTGCTTGAAATTTTCAGGCAGCCTTTTCAGGAGGATTTTGATGGAACAAAAAGCGGCTTCCGCTTCCCTGCTCTCGCCGCC
CCCTGCCGCTTTGTGCACATTTCTTTCCCTTTGCGGAAGAAAACCCATAGCCTACGCCAAAGTCAAAATACAAAGCTGGAAGCGCGCGGATTTCAATATTTGTAAGCAGGATTTGGA
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TCTCGTATTTCGCGCATAGCGGCAATACGGTTTGTCTTGGCGACCGCTCGCGGGTCTGTTTCGATGAGCAGAGCGCAGTTTTCGAGGCTTGGCAAAACCGGTGAGGAAATTTGGC
AGGCAAAATTTTGGCGGCTGTCGCGAAAACGCGAGGCGATTTCAAATAAATGTTTTTCACACATCATCCCAAGCGGCAGACGGAGTTTGCAGTTCGACAAATCAGGCAAGGCGCGCA
GAG

SEQ ID 3362

LSHYPIKQTKRLLGNFRQFFRIILMBQKRRFAASLLLAALPLCAHSFPFAENPIAYGKVKIQSWKARRDFNIVKQDLDFSCGAASVATLLNNFYGTLTTEEVLKLGKBMRASFE
MRRIMPDLGEAKGYALSFEQLAQLKIPVIVLYKRRDHPVLRIGIGNTVLLADPSPHVSMRAQFLEAWQTRGNLAGKILAVVPKAEALSNKLFTHHPKQTEFAVGQIRQGRA
E

SEQ ID 3363

ATGATGAAGAACAAATATATTTTAATAAAGCAGCAATCGGCATAACCGCATATCCATATTTATCTCTGACTCAAGGAAGCATCGGCAAACTGAAGAACCATCATATTTCTTGATGT
TCATGTTTCTCAACTCGCTTTGGTTTGAAGAAAATAAACAGTTATGCTGCCGTTACGGCAATGATTCGCCCCACTTTATATTTGTGCGCATATCCGAT

SEQ ID 3364

MMKNKYILIKAAIGITAISIFYLLTQSGIKTEPSYFLMFMLNSLMFENKTVMAAVTAMIAAHFIFVALSD

SEQ ID 3365

ATGCCGTACCGGTTAAATTTAATCCACTATATATTTATCCGATATATCAACATCTCTCTATCTTATTCGAAATTTTATGTTGAAACTTGCATTA AAAACCATACAAGATGATGAAGAAC
AAATATATTTTAATAAAGCAGCAATCGGCATAACCGCATATCCATATTTATCTCTGACTCAAGGAAGCATCGGCAAAAC

SEQ ID 3366

MPYRPFKNPLYYIPIYQHSILFRIILLKLALKTIQDDEEQIYNKSSNRHNRHILSSDSRKHQW

SEQ ID 3367

TTGTTTTTTGATGAATTAATAATGAATATATGTTAAACGTTACAACGGAAGCCTTAGCCTCCCGATTGCAGTATTTCAATTTCCAAGATGGATGCCGCA

SEQ ID 3368

LEFFDEIKIMYMNVTTEALASRLQYFNSKMDAA

SEQ ID 3369

TTGGAATTTGAATATGCAATCGGAGGCTAAGGCTTCCGTTGTAACGTTTACCATATATTTCAATATTTAATTTTCATCAAAAACAAATTCAGATTATACATACCGCCCAATCGTTTC
TTGATTTGTTTGT

SEQ ID 3370

LELKYCNREKASVWFTTYPIIILSSKNKIQDVTYRQSFDCPV

SEQ ID 3371

ATGAAGATTTATTTTATTTTCATGTTCTGTTGTTTATTATCTATTCTTATTATTGATTGCAGAAACCATTCGAAAAACAAATCAATAAGATTAAA

SEQ ID 3372

MKDLFLFSCSVCLLFYFLILLIAETIGKTINKIK

SEQ ID 3373

TTGCAANTCCAGCAATTTGAATATTGTCAATGTTCCGTCGAAAAGGAATCTTTATTGATGTTGTTGTTACTGGGTTTCAGCTTGGCTTTT

SEQ ID 3374

LQIQQFEYCHCSVKESLLMCCVLGFSLAF

SEQ ID 3375

TTGGAAGTGAAGAGGAGGTAAGGTAGTGTTCGCTGTTATTTCTTTTCGACATTGGGCTGTATTTTACGATGGAATAAGAGATATTCCTAAAAATAAAATCAAAAAAATTTTGGCAAGATCCT
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TTGACAGTATTGATGATGTTCTTGTGAAAAGATTATCTAAAAAGCCAAGC

SEQ ID 3376

LEVRGKVVFAVIFSTLGCILAWIRDIPKIKSKILARSLYIIGIINVLISYVLKNIILSVSDGGGKIYVAIYLSNLFPTVLMYVLVKRLSKKPS

SEQ ID 3377

TTGTTCTTATCTTACATCTTCTGCTTGTCAATCAAAATAAGACAGAGCATATACAAAACTGACCGACATCTGAAAAATACCTATCCCTTCCATGCAATCTCCGCACCATTTGACC
CAATAGATCAGACTGAGAAACAAAGCCACAGTATAAATCAACGTAAAAAATATAGCGTAAGCGCAATAAAGGGAACCTTTATCTACGGTTGTTTATAATATATTCAGCAACTT
GATTTCCGATATACC

SEQ ID 3378

LFLLLTSSCLVNIKTEDYTKDRHTENTYPLPCNLRTIDPIDQTEKQSHSINQRKKYSVKRNKNFYLTVVFFYNIFSNLISEYT

SEQ ID 3379

ATGGATGATCTAATACTATATTTTATCAGGTATATTCGGAATCAAGTTGCTGAATATATATAAAAAACAAACCGTGAGATAAAAGTTCCCTTTATTGCGCTTTAGCGTATATTTTATA
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TCTTTATTGATTGACAAGCCAGGAAGATGAAGGATAAGAAACAA

SEQ ID 3380

MDLLIYFLSGIFGNQVAEYIILKNREIKVPIIALYALPFTLIYTVALLFLSLIYVWNGAEIAWKIGIFSMSVSFCIVFLYLIDKAGRCKDKKQ

SEQ ID 3381

TTGTTAATCCACTATAGTTTAAACAACCTTATTTTGTATTTATCCCAAGTATAAACCTGACAATCGTATTTAAAGCCGGATCTACGCC

SEQ ID 3382

LLIHYSLNFIIDFIPISINLTIVFKSRIYA

SEQ ID 3383

TTGATGGGGGGCAATATAGTCTCTTAGAAAAATTTGCTTTATCCGCTACTAAGGGAAAAATTTAAACAATACCTGTTCCAGTGATGAAAAATTTATGATTATTAATGATTTTTTATCAG
GTTTCTTGTAGTTTGTAGCTGAGACAGGGGAACCTGTCGGGGAGACGCTTAAATTTAGCAAAATGATTGATTCTTTTATGTC

SEQ ID 3384

LMGGQYSSLENFALSVLREKIINNVTSSDEKILLINDFLSGFLFDPPTGEPVGETLKEIQMIDFFLV

SEQ ID 3385

ATGAAACGTATCTTTTTCGCCGCTTGCCGCCATCTGCTTTATCCGCTTATGCGCACTGACGACCTGACGATGAAGACATAATGACCGACAAGGAAAAATGAAACTGGAACTTCCC
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TATGCTCGCCGCGCAGCTCGGTTTTCGCTACGACTGACCGCAATACCGACATTTACGCGAGCGGCACTATCTGTGGCAGCAAGAACGCAAACTCGACGCGCAACGCAAAACCGCGCAAC
AAACGGATGTCCGACATATCCGCGCGCATCAGCCACACCTTCTTAAAGACGCGCAAAACCCCGCCCTAATCAGCTTCTTGAAGCAGCGTTTACGAAAAATCGCGCAACAAAGCCTCGT
TAATCAAAAAAGGGGCTTTGCCCTTTTATACTTAAGGATAAATTAATGAATAT

SEQ ID 3386

MKRIFLPALPAIPLSAYADLPITIEDINTDKGWKLETSIYILNSENRAALAPVYIQTGATSFIPITPEIQENGSENTDLAGTLGLRYGLTGNITDIYSGSYLWHEERKLDGNGKTRN
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SEQ ID 3387

ATGAAAAACGCAATAATCTCTTCCGCTGTGAACGGTGTCAAACCCAGTTATTTGGTGTGCGCGCATGAAAGCAGTTTACGGGCTGCCGCTGCTGCATTTCTGTGCATCCGCTTTC
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ACCGGCAAGAAACACCGATTACGCGTGCATATGATGGTTTGGGTATGCCGCTGTGAATGACGCGCTTATCCCGTCCGCTGTAAGCGGTAGCGAGGATTATCGGAAACCTTTGAAGC
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SEQ ID 3388

MKRRNPLPILNGVKPSYLVLPHEKQFYGLPLHLFICIRPFLGADWRRRLNSGFVVGSDGAALDEHSLFEPGKTMFYRETGCESEPRIPFEKILFVDEHLIVVDKPHFLPVIPOGRF
LRETLRLRLRLRLEPQLHNLNVEDITPILRLDKDTAGVMLSHNPATRGAYQTMFQNTVWKTLYEALAPKRTDLFPYPLDVVSRVLRGKFPFTTQEAEGVFNATHTTVELIENRGEFSLYRLITPH
TGKHLQRLRVHMMGLMPLINDALYPVPSAEGSEDRKPLKLAKKIAFADPLSGRERVFCSGFL

SEQ ID 3389

TGGGTCAACCTCCCCGAATACGATGCTGCTGACGATGATGCAACAGCAGCTGCGGAGCATATGGGCTTTTGCCATTTCGTCATGCTTTCAGSTGGGCGAAGCCGGGTGCGCGGATT
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TGAAATGGTGAATCAGGTCTTCCATACCTGTTTTCATTTTCGTTACGTTTGGCGGAGCGCAATTTGTGGTTTTCGGTAATGACCGGGCGGATGACGCGCAACAGCTGCGCGCATTTGTTT
GATGATCGGTACCGATTGCGCGCTTCTTCCATACGCGAGAGGTAACGGTCTGATGACGCTCGCGTTGACCGCGGAGCGGATGTCGAAATTCATTTTCTGCTACACTTCGTAGGCGCTGTGTC
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SEQ ID 3390

SVNLPEDVLRITDDGNDVGEHMAFCHPVALQVGEACADPQAVGFVCAV*NDVNAELAFRVDSVGLALGNVHTLGKEFEMVNVQVPHCTHFGTFRSEFVVCNGDRIDIAQFVGLF
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KPAALVFGHAG*VAVNAAGTEVGGVHTCAGHGFVQVHQLFAVAEGVEDGHRADVEGVRTDAHQVIEDARYFGEHADVLAGDRHIDTGKFFYRQIRLLVDHBNVQVTHIGQGLQIG
FGFRQFGFAPVQEDMRIGTDDLFAVQLQNHQ

SEQ ID 3391

ATCGGTGCGGTATACAGAAAACGGTAGGTGCAAAAGTGGATGCTGTCGGAAGCCGGCAGGAAACCTCGCGCAAAATCGACGGCGGGTTGTGCTGTTTACTCGGTGTAACGCATAGCG
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GCAATTTACGCTTTATGCGCGAGCGGCAAGCGCGCGCGGCTTCGTTTTCGCAAGCGCGCGCGGAGCAAGCGCGCAACGCTTTACCTGCGAAGCGCGGAGCTGTGTACGCGGACAGCGG
ATTATGTCGAAACAGGGCGTTTCCGACGCATATGTCAGGTGCTGCTGCAACGACGGCGGTAACCATATGCTGAGACTCTTTCATGACGCGGATTTCCCAAAAATGAAGGTTGTTTC
CGAT

SEQ ID 3392

MRAVIQTVGAKVDVVSEAGTETCGKIDGGFVVLGVTHSDTEKDARYIADKIAHLRVFEDEAGKILNLSLKDVGGAIVLVSQFTLYADAASGRRPSPSQAPAEQAQRLYLRTAEILLRHHG
IHVETGRFRTMNVSLNDGFPVILLDSFMTLISPKMKVVPD

SEQ ID 3393

ATGCTGAAACCCGAAACCATACATACCCGCGCTGCGGCAATTTAGAAACCATCCATATCCCGTCCGAACAGTACCGGACGCGGTGTGCGGTATCAATCATCCCAACCCCTCC
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CGGACGCGGCAAGCAAGACTGCTGCGGTATGATGCTGCGCGGCAACATCTGCGGACGCGGCAAGCTTTCCTTTCGCGCGGTATGTCGCGGCAATTTGCGG
GCACAGTGAACATACCCGATTTATGCTGCTCATCGCGCGGCAAGTCTGCCACTATACGACGCGCGGAGCGGCTTCCCAAGCTTGCACAAACGCTGATGATACGCGCGG
AAGACGAAGTCTGAAATCGAAAAGCCCTGAAATGGGCAGAACCGCAAGATTGCGCGTTCATACCATGCGCGGTTCGACGCACTTCTTTCACGCAAACTCATGCTGCTGCGGACAC
CATCTCGGCTTCGCAACCGTATGCTGACGGA

SEQ ID 3394

MLKPEITIHIPGAGILETHIPSEQVARGVAVINHPNPLQGGTNTNKVIQTAALKSLGFHCYLPNLRGVGGSETHDYGRGETDCLAVIDIYARAHPEAPEFALSFGFSGVATFA
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SEQ ID 3395

ATGGCAAGACATCCCTACCGCGCTGCGCTCTGCAAAATCCGGCTTTCCGAGTGGTATTTCCGAAGAGGCAATATCCGTTGCGTTTCACTTGGGACGCGACCGTTCAAAGCTCGA
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TGCACGCTGGACAGACCTTACCTGCGCGACACGCGCAAAACCGCGGTGACATCAATCTCAGGTATCGCATTTGCCGCAACCTGTTTGAAGTTCGCTTTCGAGGCGGAAAAATTTGAA
ATTATCGAAGCAGACGCTGCGGAATACATCAAAGTCTTCGCGCAACACCGATATCATCTTGTGGACGGATTTCGACGCGCAAAATCATCGATAGCTGTTGAAGAACCCTTTTCA
GAGACTGCGCAACGCACTCTCTTACAGCGCATATTCGTTACCAACTGGTGGAGCGCGGACAAACGCTATCAACGCTTCATCGAACGTTGTTGAGCGTTTTGAAGGCGCGTATTTGGA

ACTTCTGCCGAAAGCCACGGCAATGTCGGGTATGGCTTCCAAAGCAGCCCCAAAGAGCAAAACATAGACAACTCAAAAAACGTGCCGACAACTGAGCAACGCATACGGATTGGAC
TTCACCCGCATGCTCCGCGGCTGAAAGCGTCAACCCCAACACGGCAAGCATTTCCACCTT

SEQ ID 3396

MARHPYRRLRPAKSGFFVEVGI SEEGNIRSLHLSGSDTVQSSMNLDRPSELVLSYRRAMGWLIFAEIRLPQHTTQIGLGGGSFARWDTTLPDTRQTAVDINPQVIAIARNLFLFFEGGKFE
IIEADGAEYIKVFRHNTDILVDGFDGEQIILDTLVEBPFFRDCRNALSSDGIFVTNWSGDKRYQRFIERLLSVFBGRVLELPAESHGNVAVMAFQSPKBEQNDIKLKRADKLSNAYGLD
FHRMLAGLKSANPNNGKHFL

SEQ ID 3397

ATGCAAAACAGCCGACTGTTTACACAATCGGGCTGTCAATCTGGTGCCGCAACCAAGAGTGAAGTCCGGACCCCTGATTACAAGTCAGGTGCTTACCAACTGAGCTATACCGGCA
AAGAAGCCGAATTATGACAGCAACTTCACACTTTGGCAAGAAATTTGTTCGACCCCTCATAAAAATACAC

SEQ ID 3398

MQNSPTVLHNRRAVKSAGTKSRTRDPLITSQVLYQLSYTKEGELCRQLHTLARNLFDPLIKIH

SEQ ID 3399

ATGATTACTGTGAACACACTGCAAAAAATGAAGCGCGCGGCGAGAAAAATCGTTATGCTGACCGCTTACGAATCCAGTTTTCGCGCGCTGATGGACGATCGCGCGTGGAGTGTCTGTTGG
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CGATTTCGCGCTTTGGTGATATCAGCAGAGTAAGAGCAGCGCTTTGCCGCCGCCCGCAACTGATGGCTGCCGCGGCATATGTCTCAAACTCGAAGCGCGCTGTGGATGGCGGAAACG
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SEQ ID 3400

MTVTNTLQKMAAGEKIVMLTAYESSFAALMODAGVDVLLVGLDGLMAVQGRSTLPVSLRDMCYHTCARGAKNAMIVSDLPFGAYQSKQAFAAAAELMAAGAHNVKLEGGVWMAET
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SEQ ID 3401

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CAGACCGATGTGGGCACAGACCGGAATTCGCGCATTTGCAAGAAATTCAGTCGTTTCCGCCATCCACACGCGCGCTTCGAGTTTGACCATATGCGCGCGGACGCGCATCAGTTTCGGCGCG
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CGGCGAGCTGACGTGTCGCCCTGAACCGCATTCGCAAGAAATCCCGGACCAACAGCACATCCACCGCGCATCTGTCATCAGCGCGGCAAAACTGGATTTCGTAAGCGCTCAGCATAAC
GATTTTCTCGCGCGCGCTTCATTTTTCAGTGTGTTTCAGTAAATCATCAGATATTTGTTACCCCGCCCTTTTCAGACGCGCTTTTCAGTT

SEQ ID 3402

MFRSEGFPGDFGNIRPNRSLDAALPAHKVFDEFRRFARENTHEIIVHQNLTVAIRARPDADGRTGNSFSYLFQCFRRHAFHQYDSSGFIIMRLGIVKRLRLAAAPLNFISAEGRHGLRG
QTDVGTDRNSAHLQKFSRFRHFAHAFEDHMRAGSHQFGGGGKRLLLTLLICTKQRIADNHRIPCTACTYFVIAHLAQADRQRRLSPLNRHSQRIPDQGHIIAGIVHQRGKTGFSVQGNH
DPLAGRLHFLQCVHNSHQILPRPPTAFSV

SEQ ID 3403

TTGCAGATTGAACAAGGCTGCTGCGCATGCCCTGTGAAAGCGTTTCAGACGGCATTTGTTTTCGCGTGCGCGCGCTATAATCGCGCGCTTTTTCGCGGACAGGAGCCGGAAGGATA
AGGATTACCGTAATGCAATCATACATACCAATTCGAGAACTCGGACGCTGGCG

SEQ ID 3404

LQIEQGLLPMPSERFRHFVLPAAARIIGAFCRAGSPKDKDYRNANHTYHSRTAHVA

SEQ ID 3405

TTGGCCACCGTATCTCTCTACGACGATACCGCGTGTGATTTCGCGCGCTCAATGGTAACAGGTTGTGTAATCAGCGTTTTCGCTCTCTGTCATAACGCAATTTCCACATAGCCGAA
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TCGGGACAGCACTCGACGGTAATTCGCGCAAGCTGAAATGACTTTGCTGCGTGAATGCCAAGCAGCGGACGAGCTCTGTAAGTTTGAATGCTTCCCAT

SEQ ID 3406

LATVLLTDDTRCDFARLNGNRLVNHAFLFLVITFHIAGNREVFARMSDKAVIGQDAQVGVHVEDAVQIEGFALVPIRAVVNIGYGFYDREVVV*NPDAADALIVFNGQLTDMGK
AFALPCFVFSVIDAAQVQKLEMQIFMVQCGHD*NVLGQTLQDGNLAQS*NDFACLIAKHADGLV*VLNACH

SEQ ID 3407

TTGGTGATACGCTGCTGGCGCAGATCATGCGAGCAGCAGACCGGCTGCGGAGCAGTCCCAAGACCGGACGCGGAGGCAATCCGAAACGATGCCGTCCCGCGGCTGCAAACTTTGGAAG
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AACGTTTTCGAAAGCGCACTGCTCAGTTTATGAGCGGCAATCCGATGATCAAAATTCGAGCAGGTGAGTTTCGCAACCGAAGAGGAGGCGCTCAGGCGCAGCAGCTCTGCTCAAA
GGGCTGCTCTTTGAAGGGCTGATGAAGGTTATCCGAACGAGCAGGCGTTTCGACGTTTCATPATGCGCAGCAGCTTCCGAGCGCTGCGCTTCGCAAGTTTCCCGGTATGAACCGTG
CGGAGCTTACCCGCAATCCGCTCAAATTTGGGCAACGCTATTACTGTTCAAACTCGCGCGGTCGGGAAAAACCCGACGCGCAGCTTTTCGAGTTGCTCAGAAACGATTTGGAACAAAG
TTTTGAGGACGAAAAAGCCGCTGAAAAATCGATGCCCTTTTGAAGAAAAAGGTTGTCACACG

SEQ ID 3408

LVDTLVAQIMQADRHAESQRPDQAIIRNDVRLQFLVILKNRLKEGLDKDKVDQNRFKIAEASFYAEYVRFLESETVSESALRQFYERQIRMIKLQVVSFATEEEARQAQQLLKR
GLSFEGLMKRYPNDEQAPDGFIMAQQLPEPLASQFAGMNRGDVTRNPVKLGRYLYFLKAVGKINFDAQPFELVRNQLQGLRQEKARLKIDALLKENGKVP

SEQ ID 3409

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CGGCGAGGTCGCGACCATTTGACCGCTGCGGCTGCTGATTTGCGGAAATCCCGCGCGGATACGCTCGAAATGGCGCGGCGGGAGATAAGAACTGTTGTTCTTGGCGCGC
GCCGCTCGGGGACGCGCTGATTGACAAATGGAAGTGGCGCTGCT

SEQ ID 3410

VAFVPTMGNLHGHLLALVREARKRADNVVVSIFVNRLOFGQGEDFDKYPRTLOQDADKLAAGVAVVFAPDEKELYPNVEQRYNVEPPHLONELCKFRPCHFRGVATVVSXLFNIVLPDV
ACFGKDYQQLAVIKGLTDLNFDIEIVPVDGRAADGLALSSNRNRYLSVGERAEAPRLYRELQAVAESLKQAGLDYAGLERQADHLTAAGHLVDYVEIRRADTLEMARAGDKKLVVLA
ARLGTTRLIDNVEVGLP

SEQ ID 3411

ATGTATGATTTCATTACGGTAATCCTTATCCTTCGGGGTTCCTGCCCCGACAAACCGCCGATTATACGCCGCCGCGCAGGCAAAACAAAATGCGGTC

SEQ ID 3412

MYDLHYGNPYPGFLPDKTRRLYAPRTAKQNAV

SEQ ID 3413

TTGTCCGCGCATCGCATAAGGCAACCGCAATCTCAAAACACAGCCCTGCCCTTCGGGCGGGTTTTGCAAACTACAAACCGTTGGCTTG

SEQ ID 3414

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SEQ ID 3415

GTGAAACGGGCGGGTAACATAATCATCTTATCCGACATCCGTCCGAACCTTCAGACGGCATATTGAGTATCTAGACAAGCGTCACCTTATCACAAGCCAAACGGTTTG

SEQ ID 3416

VKRAGNIILYPTSVTRFRRHIEYLDKASLYHKPMGL

SEQ ID 3417

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CCACTT

SEQ ID 3418

MTMLPARFTLLSVLAAALLAGQAYAAGAADVELPKEVGKVLKRRYSEEEKNERARLAUVGERVNRVPTLLGGETALQKGQAGTALATYMLMLERTKSPEVAERALEMAVSLNAFQAE
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PL

SEQ ID 3419

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SEQ ID 3420

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ALPEPSRKPRK

SEQ ID 3421

GTGGAACCTGCGTCCGTTTGGCCGAATGCCCGCGCTCCCGGCAACCTTATGCGGCTCTGAAAGGATGGCGCTGCATTATTTCCGGGGTTTTCCGGAAGGCTCGGGCAAGGCGATTCCG

SEQ ID 3422

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SEQ ID 3423

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SEQ ID 3424

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SEQ ID 3425

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SEQ ID 3426

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SEQ ID 3427

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SEQ ID 3428

LHGTPHPSAGRMTPVKETLMKHTVSASVILLITACAQLPQNNENLWQPSHISFPAEBRLAVKAEKGSGYANFDWYQPPVETINLMTPLGSTLGQLCQDRDGLAVDGKGNVYQABGTZ
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SEQ ID 3429

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SEQ ID 3430

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SEQ ID 3431

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SEQ ID 3432

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SEQ ID 3433

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SEQ ID 3434

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SEQ ID 3435

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SEQ ID 3436

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SEQ ID 3437

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SEQ ID 3440:
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SEQ ID 3443
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SEQ ID 3444
 MNTPLPSPDYLTIRLITASVYDVAVETPLSPARSLSVRLKNNILLKREDLPVPVFSFKIRGAYNKMSKLFKDALACGVIAAASAGNHAQGVALSQRILGCRAVIMPETTPKIKVDVAVSRGGE
 VVLRGVSYNDAIDYAMELAEQEGLYTIAPFDDPDIAGQGVGMETVSRHPDPIRAVVFVPIGGGLAAGVAAPFIQVQPEIKVIGVQINDSCCMQSVRAGEIVHLKDVGLFSDGTAVKVV
 GNGTFRILCKELDEITITVDITAVCGAVKIDFPDTRSTTEPAGALALAGLKIYATAREGAENQTLIAVTSGANMNFHRLRHVSERSELGEGNEGIFAVTIPPERGSPFLKVFNII LGNRNITEFN
 YTRYGGDEKAIHFVGLQAAGPQDLAVGSRILDEAGLPNVDLTNNETAKITHIRYVGGRTDKVGHRELVSFPEPFCALARFLNMQGGWNITLFYTRNHEGADYGRILLVGIDVPPHDAAFD
 GFLSESLGYSHEETONAAAYKLFA

SEQ ID 3445

ATGAGTATTACCACTCAAACATTTAAACAAAAACGCTTCGGCAATTTTACACGCGCTGAAAAACATCAACCTCAACGTCCTCCGCGGCAAACTCGTTTCCCTGCTCGGTCCTCCGCGGCGG
GCAAAACCACACTTTTACGCATTATCGCGCGACTGGAAAAACGCGACGGCGGCCAAATTCCTCTTTGACGGCCAAGACGTAAACGCGCAAGCATGTGGCGGAGCGCAAAATCGGTTCTCGTGT
CCACACTACGCCCTCTCCGCGACATGAATGTGTTGACAACGTTCGCTTCGGTTTGACCGTATTTCGCCAAGCCGCAAGCGCGCTTCCAAAGGACAAATCCGCGCGCAAACTCGAAGAAATTG
CTCAAACTCGTACAACCTTCCCACCTCGCCAAATCTTATCGCCACCAACTCTCGCGCGGGCAACGCCGAGGCACTATGCGCTCTCGCGCGCGCTTCGGGTCTGCAACCGAAATCTCGTCTTTTGG
ACGAACCTCTCGGCGCGCTGGATGCCAAGTGGCGCAAGAAATACGCAACTCGGCTGCGCGACATCTCATACAACTTCGGGTAACACGACTTCGTGTACTCAGGACCAAGAAGAAGCCCT

CGAAGTTTCGACGAAATCGTCGTGATGAACCATGSCAAATCGAACAAACCGGAGTCCGGAAGCCATTACCGCAAAACCGGAAACGCTTCGTACCGAGTTCCTCGGCGAAGCCGAC
GCATTTGAAGGACGATCGAAAGAGCATCTGCGCATTAACACGGCTTCGCGTGAAATTTGGACCGCAATACAAATGGCAGGAGCAAAACCGCCACCGGCTATATCCGCGCGACGAATGGC
AGATCGCCCGCGAACACGAAACCGCGATGATCCGTGCGGAAATCGAAAAATTCACGCGCGCGCGCATTGACGCACGTTTGTGTAAACACGCGCAACAGAGCTGCATATCACACTGGC
TGGCAGCGATGCGCGCGCTACCAATCGCGGAGGCAAAAAATTAACCTTAATTCGGAACAGGTTTATGTTTTTCTCAAAACGAGTTGATGAATATTCGATT

SEQ ID 3446

MSITIQNLNKKRFGNFHALKNINLNPAGKLVSLGPSGGKTLRLRIAGLENADGGQILFDGQDVTAKHVRERKVGFPVQHYALFRHMNVFDMVAFGLTVLPKPERPSKQIRAKVEHL
LKLVLQSLHAKSYPHQLSGGQRIALALALAVEPKLLLDPEFGALDAKVRKELTWLRLDHNHGVTSILVTHDQEEALEVSDIEVMNHGKIEBTGSARAIYRKPENAFVTEPLGREAD
AFEGRIEKGWIHYNGFANKLDAQYKQEBTATGYIRPHEWQIAAEHETPMIRABIEKIHAVGALTHVLVKHGQDVHITLAGSDAARYPIABGKILNLPKQVYVFSQNELIEYST

SEQ ID 3447

ATGTTGCTGATTCGCGCCGCTGGGCTTTCTGCTGCTGATGCTGGTTCGTCGCGCTCTGTCGCGCTGTTTTACGAAGCCTTAAAGGCGGTGGGATTGTACTGAAATCCTTAAGCGATC
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GTTGCTGACCACTCTGCTGATTTGCGCTTCTCGTATCGCCGCTGGTTCGCGGTGTTGATGTTGCTCTTATGTTGCGCGCGCACACGCGGTGGGCGAGCGCGCTGGAAGCGCAAGGCATA
CAGATTATCTTCGCCATTCGCCGATTTGTTTACGCGCGCTGCTGTTACCTTTCCCTTTGCGGCACGCGAAATCATCCCTTAATGCAGACACAGGCGGACAGCAAGAACAGGCGGCAT
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CAGCGTGTATCGGACACATACGCGCGGAAACCAACATATCCGCTTTTGGTGGAAATCTTACAAAGCAATCAACTTCACGCGCGCATTCCTCTCGCGCGTATTGGCACTTTTA
GCACTGGCGACGCTGGCGGTGCAACATCATCAACCAATTA

SEQ ID 3448

MLLAAALGFLMLLVPLVAVFYALKGGWDLYLKSLDPEAWSAVKLTLITALIVPVNAVILGVAMNLLTRFDLFGQLLTLDDLPSVSPVAVGLMFVLLFGAHTALGSRLEAQGI
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ALATLAVQNLITKL

SEQ ID 3449

GTGCGTCTGCTCTCTGCTGGTTTTCGCGTTTTCGATGATGGCGCGGAAATCGGCTGGGCGCGCTTTCGGAACACGATTGCGGAGCGCAAGCTGCGCGCGGTGCGGCTGAGTTTCGCG
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CAGTGGCGGTGGCGGAGCGCTGCGGTGCGAAGGT

SEQ ID 3450

VPVASGGFAVCDGGGNRLGRLEHDCRAERAGGGAFAFADVVLCDAQCQVVFGLVAVNLVRYEPGKDLANALVDLPFALEPTAVTGIALAALYAPNGWIGRFFELGKIAFTFVGIMI
ALVVSLEPFIIVRAVPVLEELSGEYEEAATLGNRFTTFRVLLPEITPALLTGAGMNFARATGEYGVIFLAGSIPMISEILPLIITGKLEQFDVQASAVALLMILLSVFIPLFALNVL
QWALGRRSGARG

SEQ ID 3451

ATGACCGCCATTCAGCCGATTAAGACACGCAAGCGCGACCTGCAAGAATTCGCGGAATGGTTTCGACAGCTACTGCGCGCTCTGCGCGCAACGATTAACCTCATCGGTACCGCAT
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CGCGCGCACTCTGCTGCGGACATCGGACGCTAGCTCCCGGATTTGGAACCTTATGTTTTCGAGCGCTGCAACAGCACCGTTCGCGAGCTGGTCAAAGGTGTGGAGGAGTGCAGAACTT
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CAAAGCAACGCTTATAAAGTTTGCACACCGCTCATCTGCGCGCGGAGCAAGAGTGTGGAAGTGCAAATTCGCGACCTTCGATATGACCAATTCAGCAATTCGCTGTGCGCGCGCAC
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CCGCGCAAACTCAACGTTACGCGCGTGCACCAACAGTCCCGGACTTGAAGCCAGCATGAGTTTACGCTGCAAGTCAAAAGCTCAACGACCTTCGCGCGCTTCTGCGCGCTGCG
GATGTCAAAGGCGTATTGAGCGTTTACCGCGCT

SEQ ID 3452

MTAISPIQDTQSATLQELREWFDSYCAALPDNDKNLIGTAWSLAQEHYPADAATPYGEPLPDHFLGAAQMVDELDDLDPDAVAATLLADIGRYVPDNLVSRNCSTVAELVKGVDEVQKL
THFARVDSLATPEERAQQAETHMRKMLLAVVDIRVLIKLAMRTTLQFLSNAPDSPEKRAVAKETLIDIFAPLANRLGVWLKWLQLEDLGRHQBPEKYREIALLLDEKRTERLEYTENFL
DILRTBLKYNHIFEVAGRPKHISYTKMVKKLSFDGLFDIRAVRILVDTVPCEYTTLIGIVHSLWQPIGPEDDYIANPKNGYKSLHFTVIGPEDEKGEVQIQTTFDMHOFNEFGVAH
WRYKGGKGDSEYBQKIAMLRQLLDWRENMAESGKEDLAAFPKTELFNDTIVYLPFGKVLSLFTGATPIDFAYALHSSIGDRCGAKVBEQIVPLSTPLENGQREILITAKEGHPSVWNL
YBVGWKSGLAIGIRAYITQONADTVREGRVQLDKQLAKLTPKPNLQELAEHLVKKPEDLYTAVGQGEISNRAIQKACGTLINEPFPVPSATITVQSKIKKGGKTGVLIDGEDGLMTT
LAKCKPAPPDDLAGFVTRERGISVHRKTCPSFRHLAEHAPEKVLDAASWALQBGQVFAVDIETRAQDRSGLLRDVSALARHLNNTAVQTQSRDLEASMRFTLEVQVNDLPRVLVLAGL
DVKGVLSTEL

SEQ ID 3453

TTCCCATTCAGCGCACCTTTTTCATTCGTAAACAAAGCCTACCGTCAGGACGACGATAAACACACGACATAGACCAAAAGCGGTACGCGCCCAAAATCTTTGAACACGACTGCCACGCG
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CAATCCGTTANCA

SEQ ID 3454

FPFQRTFFPVFNKAYRQDDKHQHRPKAVRAQIFEHDCPRQHKRNLIQIEDEQVDEVIHVELHPCVFGFKTAFVRRVFPFIVAFRAQNRABEQDKQYAGREADEKDKGKISQGHYT
QIR*Q

SEQ ID 3455

ATGCCGGCTGTCGATTGATCCGCGAAGCGCTGCAGACGCTCGATCTCTGGTGTGGAAATCGCGGATGAGAGCCATCTGCACAAAGGACACGCGGCAATACCGCGCGGACATTATG
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GGCTACCCCTGACGAGTATTTCCATACGCGGAC

SEQ ID 3456

MPAVDLIRERLQTLPLVLEIGDESHLHKGHAGNTGGGHYAVLVVSGRFEGLSLNRQKTVKSLKDLFSGGMIHALGIRAATPDEYFHTAD

SEQ ID 3457

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SEQ ID 3458

MPPEKRRKKVCKDEFVIRLAVFQAGAMF

SEQ ID 3459

ATGCAGATTTTATCTTTTCAGCGGACATTCGCGAACGTATGCTGGAAGGTACGGAAGCGAGTCCGTCAACGAAAAACGACAATTTGTCGCTACGACACCGCTATTGGATTGCGTGGC
ATGAAGCGGTGGCGGCACTGCTTGGCCCGATACGCCCGCGGCACTTCCCTGTTTGGGTGGAAGGGCGGAAAGCCTTGAAGAGTTGTGCGCGATGGTGAACCGCGGAGTTTACGA
AGTGAAGAGTTTACGCGCATGACGACGCTGGCTCGAAGCGGCTAAAGATTGCGGACACCAACGCGACGCTTGGCGCTGCGGACAT

SEQ ID 3460

MQILSPQADLAREMLEGTEGESVNEAQAQFVRTDNGTWIAWHEGVAALLAPDTPPGIPCFWVEGAESLEELCAMVERGEFDEVEEFDGDDANLEAAKDCGHGDACAGH

SEQ ID 3461

ATGCCCTTAATGTCCGACGGCGCAAGCGTCGCCGTGGTGTCCGCAATCTTTAGCCGCTTCGAGCCACGCGTCTCATGCGCTCAAACTCTTCCACTTCGTCAAACTCGCCGCTTCCACC
ATCGCGCACAACTCTTCAAGGCTTTCCGCCCTTCCACCCAAAAACAGGGAATGCCCGCGCGGTATCGGCGCAAGCAGTGGCGCCACGCTTATGCGCACCAATCAATAGCCGTGTG
CCGTACGCAAAATGTGCGTTTTCGTTGACCGACTCGCTTCCGTACCTTCCAGCATAGCTTCGCAATGTCCGCTGAAAAA

SEQ ID 3462

MPMSAGASVAVSAIFSRFEPVVIKVLPHFVKLAAPHRAQLFKAFRPFPHKPTGNARRRIRGKQCRHAFHPRNPILAVVTDKLCVFDRLAFRTQHTFRNVLKR

SEQ ID 3463

TTGACGAAAAACCATCATATAAGGAACACTTATGACAGATTTATCTTTTCAGCGGACATTCGCGAACGTATGCTGGAAGGTACGGAAGCGAGTCCGTCAACGAAAAACGACAATTTGT
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TGCCTGATGGTGAAGCGCGGCGAGTTTGAAGAGTGAAGAGTTTGAAGCGGTGACGACGCTGGCTCGAAGCGCTAAAGATTGCGGACACCAACGCGACGCTTGGCGCTGCGGACAT
AAAGCATGGCAGGCTTGGCGCAAGGGTGAAGGCTTGGCGCTTTT

SEQ ID 3464

LTEHHHKEHLRCFYLFRTTLRNVCWKVKASRSTKTHNLSVRTTAIGLRGMKAWRHCLRPIRRRAFPVFWKGRKALKSCARWNAASLTKWKSLTAMTTRGSRKLIKADTTATLAPADI
KGMAGLPQGVQGFVAF

SEQ ID 3465

TTGAATAAAATTTATCTTGGTATTATAATAAGGACGATCAATTTATTTGGGACTGCAACAAACGCAAGCATTGATTGCGTTTGTGCAAACTTATTTATAGCAGTTTGGCGCGCG
ACTTAATGGGAATTGTTTATAGAGCA

SEQ ID 3466

LNKNYLGIIIRQHLPWDCNKRKALICVCKLIILAGCGADLHGIVYRA

SEQ ID 3467

ATGACAAATGATTTAAGCATTTAAGCCTGTTTATCATTAGACTGTTATTTTAGCCGCTCTCTATTAAACATGAAAAAGCCTTGATTGCCAAAGGGCGGAAACATACGAAAAACCA
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TATTTTAAACATCATACCCGAACTGATTGGCATCGCTTATTTATGTCAGCGTGGTATGTTTATTTGATTGGCTGCCCATTTATTTGCTGTCTTATTAAGCGTATCCGACAAGAAG
AACAGCGCATGGCAACACTTTT

SEQ ID 3468

MTMLISLISLFFIIRLLFLAVSIRHEKALIKAGAKQYKTNSTVLAAVHTLYYLACFVWVWLSDTAFNGISLIGLTVHASFVLSLIIKQLGEIWTVKIYILFNEHQINESWLFKTPRHPN
YFLNIPELIGIALLCQAWYVLLIGLPTIYLLVLFKRIRQREQANATLF

SEQ ID 3469

GTGTTCAACAACGCGGCTCAAACTTGAACCAACCTTCTACTGGCTGGGTTTACGCCCAAAGGCCAAGGCAAACTTCCGGCGAATGGCCGCCCATCGATGCCGAATGGGCGAGCT
TCGAGAAATTCGAAGAGCGTTCAATGCTGCGCGGCGGAACCTTCGGATCCGTTGGGCGTGGCTGGTAAAAACCCCTGCGCGGAGTTGGCTTGGTTTCCACTTCCACGCGGCAAC
TCCGCTGACCACTGAAACACGCGCTCTTGACTTGGGAGCTGGGAACACGCTTACTACATCGACTACCGCAACAGCGCCCCAACTACCTGGAAGGTTTTGGGAAATCGTCAACTGG
GACGAGTCCGCAACGCTTTGCCGCA

SEQ ID 3470

VFNNAQTWNHTFYNLGTFPKQKPSGELAAIDAEGSFEKQZAFNACAAGTFGSGWAWLVKTPAGGLALVSTSNAAATPLATTENTPLLTCDVWEHAYIIDYRNSRPNYLEGFWEIVNM
DEVAKRFAA

SEQ ID 3471

ATGGTTACACCAATCCGTTAACAAAATTTCTACAATAATTTGCTATTTTAGCGAATTTCAAAAACCATTAAGGTAAATATCGGCAAAACGCCCAAAAAACCAATAAATACAATCA
TGTTA

SEQ ID 3472

MVTPKSVNKLSTIISYFSEFQKPLGKYRQNAQKNPINTIHL

SEQ ID 3473

TTGTCCCGCATCTGAGCAAGAGACTTTGGAATTCCTACTACGCAACACCATCAAACTTACTACCAACCTGAACAATCAAAATCAAGGCACCGAATTTGAAAACCTGCTTTGGAAG
AGATTGTGAAAAAATCTTGGCGCGGCTGTTCAACACGCGCTCAAACTTGAACCAACACTTCTACTGGCTGGGTTTCAAGCCCAAGGCCAAGGCAAACTTCCGCGCACTGGCGG
CGCCATCGATGCCGAATGGGCGAGCTTCAGAAATTCGAAGAGCTTCAATGCTGCGCGCGGCACTTTGCGATCGGTTGGCGTGGCTGTTAAACACCCCTGCGCGGAGTTGGC
TTTGTGTTCCACTTCCACGCGGCACTCCGCTGACCA

SEQ ID 3474

LSPHLSKETLEPHYGKHHTYITNLNQIKGTPEENLPLEEIVKFI GRRVQQRGNSLPHLLLAGFHAQRPRQTFRRTGRRHRCRMGQLREI PRSVQCLIRGNFRIRLGVAGKNPCRRIG
PGPHFORGNSADE

SEQ ID 3475

SEQ ID 3475
ATCGGGGACAAATCGCTCCGGCTCATAAGGCAGTTGCGGCAGCTTATGTTCCATTTTGTGCTCCTAATGTTGTTTTGGATGTTGTGTTTTGGCAGTGTGCTGCAACGAATCGGGGCT
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C

SEQ ID 3476

SEQ ID 3476
MRGQCVRRLRQLRQLMPHFVLLMLFLDVFVWQCCCKRIGGSRILPVLSDGNQLNLLCVIILED CNFGMTDWMYHERLESYAA

SEQ ID 3477

SEQ ID 3477

ATGAACGATTACGCAGCTATGCGCGCTGAAGCGCGTGAGGTCGGCGCATTTGCTGCTGCCATTCGATGGAGCGGAACAATCCGTTTGGGCGGTTTGATGCTGGA AAAATCCGGCTT
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GGAAGATTTGCGAGCGGAACGAAGAATTTGGAAAGCCGCGAGGCGATTTTGAATATCTGATTACACTGGGCGAAAACACCCCGTCTGCCGCAAACATCCGCGCGTACGCCGGAATCGTACGCGAG
CGTTCCTATTATCGCCCACTFCGCGGAAGTGGGACGCGAARTCGCCGCGAGCGCATACAATCGCAAGGCAGGGAACGCGGGCGCGCTTTTGGATGAGGCGGAAAACAAAGTGTTTCAAAATCG
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SEQ ID 3478

SEQ ID 3478

MDNYAAMPPEGREGVALGSLPPHSMEAEBQSVLGGMLLENPAWDRIADVSGEDFYRHEHRLIFRSIAKLINEGRPADVITVQVEDLQRNKELEAAGGFYELITLAQNTPSAANIRRYAETIVRE
RSTINRQLAEVGTETIARSAAYNPQGRDAGRLLDLEANVKVQFIAESTAKSKQGPLLENPLLEKVVQIRIMLYSRDNPDVEVGTPTGFDLDOKKTSGLQPGDLIVAGRPSMKTAFSINIAEYV
AIEKHLPVAVFSEMMEGAQLVMRLGSGVGRDLQSVLTKGRLEDEHWGRNLNAAVVKLSDAVYIETDTPGLTALELRARARRLARQFNKLGGLIVIDYQLQMAASGRSDNRASLEGEISRSLSK
ALAEPLQVDTALSOISPTVEORTDKRPMNSDLRESGATEQDADLIMFYRDEYYNQDSPMKGLAECTIGKHRNGPVGKIFLWTWQGTFTKFDNAAYIPEAKIED

SEQ ID 3479

SEQ ID 3479

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CTATATCTGCTCTGTTCAAGTTTAAAAAAGACGGTGGCGTCCAAACAATAGATGTGACTTCAGCAAGAAGGGGTGGGGAATGTGGCTTTCGGCGACAAAAACGGCAATAAGGAATATGACGG
GATGTGGCGGATGTTTTCCTCCGACGCGTGGTATTGAATGATGATATCAATGATATAAGCGGATTGATTATGCCCTTCAACCATATCGCTTTCCGCTGCTCTCAGCGCCGACCGCTGTGATG
TTTGGACGTTCAATCAAAACGGGAGCTTCGGTTATACGACAGCCAGCATCTTACAGAGCATTCACGCTTTTCTTTCGACAGCGGTATATATCAAAATCTGCTGACAGATGCGAGAGCAGT

SEQ ID 3480

SEQ ID 3480
LNLIHLYTLPIVLLIMCTRKQGGFTLTTELLIVMAIAAIMATIALPNMSGWIASRRRIASHAEQVANLLRFSRGEAVRLNLPVYICPVQVKKGASNNRCDPSKKGWGLMAGDKNGKRYDQ
LNLHLYTLPIVLLIMCTRKQGGFTLTTELLIVMAIAAIMATIALPNMSGWIASRRRIASHAEQVANLLRFSRGEAVRLNLPVYICPVQVKKGASNNRCDPSKKGWGLMAGDKNGKRYDQ

SEQ ID 3481

SEQ ID 3481

ATGAAGAATAATGATTGCTTGGCCCTGAAAAATCCCACGTCCGGTATGGCGTTGATAGAAAGTCTTGGTCGCTATGCTCGTCTTACCATCGGTATTATTGGCATTGCTGTCCGTACAGTTGC
GGACAGTCCGTTCCGTCAGGAGGGCGGAAACGCAACCATCTGTCAGCCAAATCAGCGAAAAACCTGATGGAAGGAATGTTGATGAATCCGACCATTTGATTTCGACAGCAACAGAAAAACTA
TAGTCTTTTACATGGGAAAAACAGACACTATCAGCTCTGGATGCTGAGTTTATGCTTTGATGCCGAGAAAAAGTAAGCGCGAGTTGGCAGAGGAACAATTAAGAGATTATGTCATGAGCTGAAA
AATGCCCTTGCCGGATCGCGTAGCTATTCAATTACGCCGCTCGCAAGGATTCTCGGGTGACGGCGGCACATTGTCCGACAGCGGTGCTTTTCTCTCAAATTCGCACAATAAGGCAACCGGG
ATACCTTTGATTAAAGTATTGTGGGTAATGATTCGCGAGGGGATTTCGGATATTTCCCGTACGAATCTTGAAGTGAGCGGCGACAATATCTGATATACCTATCAGGCAAGGGTCGAGGGTCG
TGAA

SEQ ID 3482

SEQ ID 3482
MKNNDCRLRLKNPQSGMALIEVLVAMLVLTIGILALLSVQLRTVASVREAETQTIVSQITQNLMEGHLMNPITIDLDSSNKNKNSLYMGKQTLSSAVDGEFHLDAEKSKAQLAEQQLKRFPSHELK
NALPDAVAIHVAVCKDSSGDAPTLSDSGAFSSNCDNKANGDTLIKVLWVNDSSAGSDSIRTNLEVSGDINVTYTYQARVGGRE

SEQ ID 3483

SEQ ID 3483
ATGCTAAACGTACCAAAGGCGGTATGATGGTATGAAGGGTTTTACCATTGTTGAATTTCTGGTTGCGGGCCCTGCTCAGTATAATTGTCTGTATGACGGTCTGATCGAGTTACTTTACAT
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SEQ ID 3484

SEQ ID 3484
MLNVPRGGYDGMKGPTTVEFLVAGLLSIIVLIAVVSSYPTSRKLNVDANERLAIQQDLRNAATLIVRDARMAGSGFCFNMSEHTKIDIVDSSNQTSNLAKPGAKQENPLFLSKRSGMDQ
LIPVAESIDIKYPGFTQRLNALVFPQYGGIDDLDASETVVVSSCSKIAKPGKKISTLQEAQSALQITNDKQKNGNTITQKHVVNAYAVGRFGNNEESLRFQOLDGKGWGNPQLLVKKVRM

SEQ ID 3485

SEQ ID 3485

AATCCCTCTGCGGTATTGTATTCTACAATCATATTATCGTCAGTAATGACTTCGCGCCACGCCGAAGGTTCCGTCATCCGAATCAGCATACGAGAGACAACTTTGTGCTGCAGCATCC
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CGTAGCGGTATGCATAGGGAATCTGTGTACGCGCGGTAGCAAAAGCATGCGGGCTGTGCGTGGTATTAAACATTACAAATACCATCCGGGGTAAGGTGGCTTTGCACCTGTGTTTAAAAATTC
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SEQ ID 3486

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RTQVVSIGITPVPSRIHQNVVEFFIRMATQPPPTVIQYNFTFVLQKRCDLRLVRDKATVCRIDFRNDHRLHFRNGRQDARPRITCTQSDENAYAGLQG*QIGTFDAVDFTIETIGIVCA
VYIRPIINLIITISMVNRNNAVFVFNQPIRTASNLKDIRQ*EHEDAHE*GNCYRHCIQSETFLEQCTKQRDSSRNQTDQVNLGGQELIKYHKAADKDRCTAGNVGIEINIGLSSGPV
AIRTHMVYKWNQPPDDGRQGNEDTGVVDEAGTRQPPRSTQNKIGNTRPQZALPDKNINKAAAAANPFAKIRADGDTGQKTGSK*KLEHGLCCERKHPYQDPYTTAQ*SAKERKHI
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SEQ ID 3487

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AATTAAGCTTCCCTTGGTTGCTGATACGCTGGGAATTCATGAACCTTATGAAAGATTCAACAGATGCTCCGTTATATTTTACCAGAGAAGACATAGTCAACGTGCGATTTGATTAT
TACAACAAAAA

SEQ ID 3488

MCEPKDFRNRNIPCFEYDENSFIGKYYDDGVMDDEEYWKLENDLIEVRKYPIYPMIDIPDIVIGITIIDFLMVPNWELFEIKASFWLPDSVGIHERYFTMLEYIFTEKDIVNVRFDY
YNEK

SEQ ID 3489

TTGACTGTGAATATTTTATGTGCTGGCAACAGACGGGAGGATGTGATGAAGCGGTATGGCGGCACGTCCCGAACACTTTAAACGGCTGGAACCGTGAATCGGAAGCCGTCTGC
TGACGGCAGGCCCAACCTGCTGCCGGAATCCCGAACGTGTTTGGCGCAGCTTGATTGTGGCAGATTCGAGTCTTTGATGCGCGCGCAGCGCTGGGCTGAAGACGATCCCTATGTTC
TGCGCGCGTGTACAGCAAGTGTGATCAAGCGGTTTAAAGCGGTGTTCAAA

SEQ ID 3490

LTVEYFMLLATDGEDVHEARMAARPEHFKRLETLKSEGRLLTAGPNLLFDNPERVSGSLIVAQFESLDAQAWEEDDPYVHAGVYSEVLKPKFAVFK

SEQ ID 3491

ATGCGCAAAACAGAACACTTTGACAGGAATCCCGACTTCTGACGGACAGAGGGGTCCGCACTGTTTATCGTGCTGATGGTGTATGATAGTCTGGCCTTTTGGTTGTAATGCGGCCAGT
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CAGTAAGGTTACGTTTACGAAACCTGTGAAAGGCTCTGTGTACCGCACTGAATGTGCGGCAAAATAATATGATGTAAGAGGCTTTTGGCAATATCGTGTGCAAGCAAGCCCGCC
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GCAA

SEQ ID 3492

MRKQNTLTGIPISDQGRSALFIVLMVMIVVAFVLTAAQSYNTEQRIISANESDRKLALSLEAALREGEFQVLDLEYAADSKVTFSENCEKGLCTAVNVRTNNGSEAPGNIVVGKPA
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SEQ ID 3493

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AGGCTATAAGATGAATCCGAAATTTGCCAAAATATAGTGTTCGGTAAGGTTTGTGATGCGGAAACCAAGGGCATAAGGTTGCTGGCGTTCCGAACCGGGGAGCGGTTATATCT
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AA

SEQ ID 3494

HMSNMKEQKGFLLIEMMIVVTLILGISVIAIPSYQSYIEKGYSQLYTEMVGINNVLKQFILKNPQDDNDTLKSKLIFVSGYKMFIAKKYSVSVRFVDAEKPRAYRLVGVPNAGTGT
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SEQ ID 3495

GTGAAGCTTCTCTAATCGTAAAAATAGGGCTGTTTTCGCAATCCGCTCTGAAGATCAATTTTCAGACGGTATTTTATGGGCATTTTGAATGAATATGCCATCAACCATCCCGAGA
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SEQ ID 3496

VKLSLIVKRAVLEHMPSEDQSDGIFYGHPFEMNYAINHPEMPDEPTPIVNNIEKRAAKAVNAMAISSCGLSDTK

SEQ ID 3497

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SEQ ID 3498

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SEQ ID 3499

ATGATGGGACGACAAATAAATCTTTCAATTTCCGCCACTCCAAAAATAAGCGGACACAGGCCGACGCGTGGCGGGGAACATACACGCGCGCTCAACGGTCAGGTAAACGGCGGAT
CGGACAAACAGGTTGACAAATCAAGGTAT

SEQ ID 3500

MMGTTINLSFPPTISGQQAGQAGGNI PRAVNGQVNGCDKQVDSRY

SEQ ID 3501

ATGGCATTTCTCGAAATCCAAAAACGAAAGCAGCGGTTTGGCTGCAATCAATATGCTTTTATATGGGCGCATGCTTTATCTTCTACATTACTTGGATAGGTTTTCGCGCATTCGCG
CGGCGTAGCGCCCATGTTCCGCAACGTGCGAGCTTGGGTTTCCGCAATGGCTTTCTGCGGCTATTTCTGTTTACTGAGGGGAATGTGGAAAACTTTTCGCGCATCAATACCT

SEQ ID 3502

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SEQ ID 3503

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SEQ ID 3504

VANSEPPAKPIPVISSISSRPFPCCIPISINAQKSPISMGELSPMRNNSRGEAVCVMLMFIYEETGRYHTQABCF

SEQ ID 3505

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SEQ ID 3506

VFTSILSVTPY*SSNQKVKAGCQRNGLGEGKRDVEKFGGKRSECRTOSEKI*GTDRLANIMYFVVKKTQQGQGRAHKGKQ*KEIGSSDDQISLN*KNPQAGNQFLAYQTEQT
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SEQ ID 3507

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AATAGGTCGAATTTGAAGATTTTAAACAGCTTTCCATCACCCTAAATCATACGCTGTGTATTAATATTTATTCATCAATGAATCTTATCCGACATATGCTATGAGTTTGTATGAATA
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SEQ ID 3508

MVDVAVKTFEFLPFTSVGIPRFGADITQYKNILETFMYEPPDEFGTETYESPDSNLLISVEKNKIIIFCYQELYFMGVNLIIGLNFEDFKQLFHHKSYGVDKYILSNESYPTTYVEFDEI
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SEQ ID 3509

TTGCTTTCTCATTGGATATGAAATTTGTGACGCGACTTTTGTCCGTCATCTGTGTTTTGCTACTTATACCGTTACCAAAAAATGATTCGCCCTGCGCGCGTTGCCCTGGTTCGAGCG
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SEQ ID 3510

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SEQ ID 3511

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GTACGGGTTCTCAC

SEQ ID 3512

VYNLSLPAVCRSRMTNIEVENKVLDERMADFIAPAYATEGSAGLDLRACLDEEVVLQPGETFLVPTGLAIYLANPAYAAVLLPRSGLGHKHGIVLGNLVGLIDSDYQGLKVSILNRRGSE
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SEQ ID 3513

ATGCCGCTGAACCGTCTCTCAGACGGCATTTCTATATCTTATGAGAACCCGTACTGCCGAAGCCGCCCTACCCCGGCTGCTTCCGACAAATCTCTGACACGTTTGAAGCCCGCTGT
ACGACCGGCACGATAACCATTTGTGCGATACGCTCGAACCGCTTGACCGCAACCGTTGCTACCCCTGTTCCA

SEQ ID 3514

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SEQ ID 3515

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SEQ ID 3516

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SKRSNVPGLRSGFVAGDAELLKNFLLYRTYHGSAMSI PVQRASIAWNBQHVINDRRMYQKPERVPILOQVVDVKLPDASFYIWLKVPNGDDLAFARNLMQKAAIQVLPGRFLARDTE
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SEQ ID 3517

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SEQ ID 3518

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DLIQYRLHMGTSFANLRGKNLYEPWGGIITNLNDTLAQAGSNTLVNLAQSEYFKSVNTKKLRARLITPIFKDEKNGKYKLIISFYAKRARGLMVRYAAEHNTDPEMLKNFNVEGTAFND
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SEQ ID 3519

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SEQ ID 3520

LAKCINFIIPITLQEDGSVAERFNATVLKTVEG

SEQ ID 3521

GTGGGTTCGAATCCCGCGCTTCCGCCCAAAGCAAACCGCCCTGATTAGGGCGGTTCTTTTGTGTCAGGTTGTGTTAATTACTATA

SEQ ID 3522

VGSNPAVSAKQNRPSGRFFVQVVLITI

SEQ ID 3523

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SEQ ID 3524

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SEQ ID 3525

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SEQ ID 3526

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SEQ ID 3527

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SEQ ID 3528

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SEQ ID 3529

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SEQ ID 3530

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SEQ ID 3531

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SEQ ID 3532

FPQFF*FKFQQLFYPPGEV*LIGKQ*ISFFSVK*NVL*NALRFVAFGLFGVHSSPLLKIIIVDTFYSI*NH

SEQ ID 3533

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SEQ ID 3534

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SEQ ID 3535

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SEQ ID 3536

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SEQ ID 3537

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SEQ ID 3538

LSGGGLALNVYPTGRRSWKLSFMQDGRQPTLSLGRYPDFSLAEAREWREVRKRAHGENVNNKVRADFAFEKVARDMFVWRSKGRSEKYAQVMNFRWVPAIGNLDIRQVRTADV
VGCLRVMEARGIVDPLRKTNSLKNVFAFVAGSGMMEINPVAQIGSGVFERVKTNTALSPSELPRLIDFLBQRNEFAVYAGRVHIHPVTRFCIYVLLI/TNTRIREAALME#SELDGEVW
RIPAERKKERRRGRDVP LSRAMRWVLDQARGLVNNGRPFVFSVNFQGHINKSPHVAMRSGDITTAHLRLSLARTYLREVLKVYNDVAEKLALHSLGTRTQTAYNRSELWBERKDAPERNG
NDVLRADNGK

SEQ ID 3539

ATGAACATCAACAAACGGGCGCAAGGATAGACCGCCGACCATCCGCGAATGATTGCTACGCAACCTGCCGCAACCCCACTTCAAACTCGACACTGCTGCGTATGAAAAAGACG
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CGCAACCGGTGCGCGCTCGTATCCAGCCCGACCGCATCGCCACGTCGGGACTTTTCCTTATGATATGCCCTTGAAAAATTCACACTTTCAAACACAAACCGCCCGTTCACATTCAGCC
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SEQ ID 3540

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IADSRKNPPFKI/PHNLGILFRPLRPLRPHKPI/THLLKSKIRPHLLIDIDIFFVCP/SAHLPLPPFRLSQRIRIPQRNCLLPSVLHKKQLPTPPARRIDPQSQPSAVRQLIQLIARLIF
NLICRQRDDFCHYKFPFVQNLPTLP

SEQ ID 3541

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ATATAAAAAATCGGGAAGAAGAA

SEQ ID 3542

MESSDVQGRMETLAFATAPKKGGIRKSGFGRVILIKSGHVIHNDGDSFATGYGVIADIVSPDLKTDIFPPESLRYKKIKKK

SEQ ID 3543

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ATTC

SEQ ID 3544

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SEQ ID 3545

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GAAGCCGCTACCTGTCACGGCA

SEQ ID 3546

LYVGRILHCFADRFFDGRLLNTSYSSSILFPLIPICPGRFTTANHAALASFIPIGIFSPQSAEVSASAAVSIHVCPICFTKVPVPTA

SEQ ID 3547

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SEQ ID 3548

LDGRAVIAVSSAQAVRDPVLVFRIGAGAQVREYTAILEDVPGSPKTSALSDGKTHRTAPKAESQENQNAKALRRTDKDSANSVAVKPAHNGKTHVVRKGETLKQIAAAIRPKH/LEQV
ADVLLKANPNVSAHGRRLRAGSVLHILNLR/IKAAAPKKIKABQPKPQTA/KAETASMPSEPSKQATVEKPIEK/VEK/VEK/PEAKVA/PEAKAEKPAVRPEKPAVSETPASATERQGP
VPAANTAASETAESAAPP/RSRRP/CHRHADRRNR

SEQ ID 3549

AAATGGAACAAGAACTTTTATCTCACTGTTGTTAAACGCGCTTCGCACTCTTTAAATACGGCTCAAAATGCTCTTTGGGAATGCGCTCAAACTTCGCTAAATGACGTTTTCGCGGTTTC
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AAACAATGCTGTGACGGCTCTGTTCTGCTTTCGAGTTAGCGCTGCGCAAAACAGTTCAATGAGTTTATTTGTTTATACCGGCTTAGACGGCTTTTCTCAT

SEQ ID 3550

KNNKMFYLVVKTFFALL*IRLKM/LPGNAVLA*MTFCVPKVPNSINMVL/SFGKMC/VIDTEM/KFACI/QYIIATITIRINN/VRLCCSCSY/ACKQ/NEFIL/FIPA*TAFSE

SEQ ID 3551

ATGGATAAGAGAAAGTCTTAGACAAAATCAAGAAATGTTTGGCTTTGGTTCGCTCGGTAATGAACATGAAGCCGACAGGCGTTAAGCGAGGCGAGGCTTAAATGGAAGTACAAAG
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SEQ ID 3552

MDKEKVLDKIKKCLALGRSVNEHEAAQALRQAQALMEKYKVNEDIALSKVSEQADRKMAFKLAGWQVNMADIIFGCKSYQRKTMFYGIGNRAETSAAYFDVWYRQISADRRKFL
KTCRAGKPSHRTYLD/DRPCGGW/LASAWET/VKKF/EM/DEEKA/IMDGY/KK/ET/PDMA/EARTRDAKSSILQ/GSKMEY/EA/IRG/ESGKQ/VKLHY/VNGTGF/VKQ/IGGT

SEQ ID 3553

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SEQ ID 3554

LPPKSADTAANTRAYLTARQEAGSLNGLSRNFTTPWRYSPKPAKPCCKTTLPRPVISAGGNKKSPEFVSVALAENPDRIESKARDENARVEN

SEQ ID 3555

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CAGGAAGCAGGCAGCTTTGAACGGTATATTAAGCCGTCTGAATTTACGCCGTGGAGATACAGCCGGAAGCTTGTTCGAAACTACCTGCGCGCGCGGTAAATCTCGGCAG
CGGGAACAAAAAGCCCGAGTTCGTAAGCGTATCAGCCCTAGCCGAATGGCCCGACCGAATCGAAAGCAAAGCGAAAGACGAATGGGCAAGGTGCGAAATTAATAATACCGGACAAAT

SEQ ID 3556

MLSGARVSEDEALTCGIMRLVAAKVRVRYCGEHPGVFDGAAGSRQLEKRYIKPSEFHAIVEIQPEACKALLQNYPAAGNLGRRKQKPKPVVRKRISPSRHARPNRQKSERRMKGAKLKYRTN

SEQ ID 3557

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SEQ ID 3558

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SEQ ID 3559

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SEQ ID 3560

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SEQ ID 3561

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TTAGA

SEQ ID 3562

MPALALYRCADVDQAALDYFDSETEREDTLEAVIGQFEVKAQSVIAYIKNQBITKMLBGRHRRMTGKLKAVKQNSLKDYLARNMQAAGITEIKADDGTFKASFRKSEAVVILDEAQI
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SEQ ID 3563

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SEQ ID 3564

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SEQ ID 3565

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SEQ ID 3566

VLSSLMDCDGFVAVCRFDQGAVERAGVGFLKNLVFNILPQMKEMPSN

SEQ ID 3567

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SEQ ID 3568

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SEQ ID 3569

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SEQ ID 3570

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SEQ ID 3571

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SEQ ID 3572

LLSSFTLKINDIFGLLLKVSSIGLALFYALRGGGYLILMLMPSACFSVIRRVSAVSGALPGI

SEQ ID 3573

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SEQ ID 3574

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SEQ ID 3575

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SEQ ID 3576

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SEQ ID 3577

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SEQ ID 3578

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SEQ ID 3579

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SEQ ID 3580

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SEQ ID 3581

SEQ ID 3581
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SEQ ID 3582

SEQ ID 3582

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SEQ ID 3583

SEQ ID 3583

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SEQ ID 3584

SEQ ID 3584
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SEQ ID 3585

SEQ ID 3565
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SEQ ID 3586

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SEQ ID 3587

SEQ ID 3587

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SEQ ID 3588

SEQ ID 3588
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VSLVDGRCSEPRRPGSCGCGPRPLREGLEPRFFFCYCFRPDPDUTIRNVKHAARTOSAVCGNT^{VV}CVLOOHIGNLF^{EROV}FR^TDGGGNLF^{ER}FA^{FAD}MG^{FAV}MRRFDG

SEQ ID 3589

SEQ ID 3589
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CAACGGCTACAGCAACGGCAGCGCAACGGC

SEQ ID 3590

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SEQ ID 3591

SEQ ID 3591

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SEQ ID 3592

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SOICGELDSVWLEPAIEILPVTGGAESIRTALEVAQS

SEQ ID 3593

SEQ ID 3593
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SEQ ID 3594

SEQ ID 3594
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SEQ ID 3595

SEQ ID 3595
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SEQ ID 3596

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SEQ ID 3597

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SEQ ID 3598

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SEQ ID 3599

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SEQ ID 3600

MELTVHFNAEQDLRLFEKDEEAVGYLENVIAMIQADSAIFDGLYKNRYFREYGEFIGIDLEVKPIILSLNGKDIKVLVRVPDSEBAAGYRIIYAPCHEKQPNGTPIRRIDILAVNKKITD
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SEQ ID 3601

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SEQ ID 3602

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SEQ ID 3603

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TGCCTCATCACCTTAGGGAACCGTTCCCTTTGAGCGCGGGCGGGCAACCGCTACCGGTTTGTGTTAATCCGCTATACAGAGCGGTTGGTGGAAATCCCGAA

SEQ ID 3604

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SEQ ID 3605

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SEQ ID 3606

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SEQ ID 3607

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SEQ ID 3608

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SEQ ID 3609

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SEQ ID 3610

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SEQ ID 3611

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SEQ ID 3612

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SEQ ID 3613

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SEQ ID 3614

MPSDLSPILAKELIRSGSIRLSGSTARGQAGELAVFIRTLRQKPESEPNITDEYILGLSK

SEQ ID 3615

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SEQ ID 3616

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SEQ ID 3617

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SEQ ID 3618

VTQLAARITDLEGRGFVFAKPKYKVGNCNPFVAHYSIAKSGIEP

SEQ ID 3619

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SEQ ID 3620

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SEQ ID 3621

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SEQ ID 3622

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SEQ ID 3623

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TACTATATCGGAAATGGAATTTTGAT

SEQ ID 3624

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SEQ ID 3625

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SEQ ID 3626

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SEQ ID 3627

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SEQ ID 3628

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SEQ ID 3629

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SEQ ID 3630

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SEQ ID 3631

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GAGGCATT

SEQ ID 3632

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SEQ ID 3633

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SEQ ID 3634

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SEQ ID 3635

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SEQ ID 3636

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SEQ ID 3637

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SEQ ID 3638

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SEQ ID 3639

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SEQ ID 3640

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SEQ ID 3641

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SEQ ID 3642

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SEQ ID 3643

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SEQ ID 3644

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SEQ ID 3645

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SEQ ID 3646

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SEQ ID 3647

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SEQ ID 3648

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SEQ ID 3649

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SEQ ID 3650

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SEQ ID 3651

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SEQ ID 3652

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SEQ ID 3653

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SEQ ID 3654

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SEQ ID 3655

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SEQ ID 3656

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SEQ ID 3657

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SEQ ID 3658

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SEQ ID 3659

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SEQ ID 3660

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SEQ ID 3661

GTGTACGAGCTTGAGACCTTCAACCGGTACAACCTGTGAAATCGTCAATCGACACGCGCCGAACCGGAATCTGTGCCAACTGCGGAAAACAAACCGGAAACCGTCGATACCGATTCT
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AACAGTTGCGGAAGTCCAACACCGGAAGAGTTGCACGATTTCTGAAAAGTGTACGAAACCGGTGCCGTCGCGGAAATCGGCTGAAACCGCCGATTTCACCGCCCGCAGACGATTG
TCCGCATGTCTCAACCTGCGGAAGCACCGCGCTTGAGGAAAATGCAGCGGAAATCACTTTGGAAACCGCTGATCCAAACACCTCTGAGGCAGACGCTTTCGCCGACTTCTGAAAGACA
GCGAGGAGGAAACCGGTAGATTGGAGCATCTACCTCTCGGAAGAAAATATCCAAATAATGCAGATACCTGTTCCTCTCGGAATCTGTAGGTTCTGACGCGCTTCCGAAGCGAAATACGA
CCTTCCGAAATGTATCTCGAAATCGCGACCGCATGCCGTGCCGAGACAGTGCAGAAATGTCTGGAAGAAGCGGAAGCGGACGTACTCAAACGTGCCCAAGCATTGGCGCAGGAATTG
GGTATT

SEQ ID 3662

VYEPETFNPNFVEIVDTTPEPESVAQTAENKPEVDTDFYNNLFSNNHIGTEETASAKPAAPSGLAGLTKASSPETILEKTVAEVQTPRELHDFLKVYETGAVAETAPETPDFNAADDL
SALLQPAEAPAVEENAARETLETPTDSNTSEADALPDPLKDSEETVDWSIYLSEENI PNNADTFPSESVSADPSEAKYDLAEMYLEIGDRDAAAEVQKLLERABGDVLKRAQALAE
GI

SEQ ID 3663

CGCAACGCTGTCTGCTTGGCGGGCGCGGTGGCGGGCGGGCGGTTCGTGCTATGATACGGAAGTTCCGATATACAAAGGGCGGGCTTCAGCCCCCAAAATCCACCAACTCCGCCGAAT
CCGCCGATTCCGCCCGCGCTATCCCGCATAGCGGGAATCCAGACCTGTGCGTGCAGAACTTATCCGATAAAACGGTTTCTTTAGATTTCGCTTCGCGATCCCACTTTCGTGGGA
TGACGAATGTAGTTTCGCGGAATGACGGCGCGGCTGCGGCAAAATTGCCCTTCCCGTTTCAGACAA

SEQ ID 3664

RNGCLPWAAGGGRAVCRYDTEVPIYKGLQPAKSTNSAESADSRRRHSRISGNPDLVSRKLIG*NGFFRCVPDSHFRNDGM*VRGNDGGCGKIALPVFRQ

SEQ ID 3665

TTGTTATGTACGGCTTAAAAATCATATCCTTCGGCGTGCAGAAATCCCGCAAGGGTAAACGATTGAATTATACACCTATTGCCGGAATAAACACAGGCGCTTGAAGATTGAGAG
GCATTTGTATTCCCTACTGCATCAAACCGCGACAGGTTCGGGATTTCGGGCAGTATCGGGCGGATTTTTCTGCGTGTTCGCGTTCGCGGTGCGCTTAAGGCTTCGAGGGCGTTTGC
GCGGCTT

SEQ ID 3666

LLCTGLKIHILRACENPRKGNLDNYTPIAGKNNRPSGICIPYCIKPPTGCGFRAVSGGFLRVPRRRVRLRLRGLRL

SEQ ID 3667

ATGAGCGGCACGAAACGCAAAATAGGCGCTCCGACAGATTACACGAAAGACATGGCCGATAAGATATGCGAAAAATCGCAATGGCAGAACCTACGTTCAATATGCGCCGAAGATGGTG
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TAGTGCAACAGCAGAGAGCGCGCGGTTCAAAGCGGAAATTCAGATAGATGCCGAAAGTGGCGGCTTCCAAGATTGCCCGGAAGAAATACGGCGACAAATCGGAGCTTGACGTTAA
TCGGCGATGGGAGCATGAGGGCGCTGTACGCTGTAGGAAATATCCCAAGATAGCGGAAGATGTGTTCGCTAGGGT

SEQ ID 3668

MSGTKRKLGRPTDVKMDADKICEKIANGRSLRSICAEDGVPPMKTIYRWLEANEFRHQYARAREKQADYFABEII EIADSAQAESAAVSKAKLQIDARKWAASKIAPKKYGDSELDVK
SGDGSMAAARLDAAEYRKIAEDVLRV

SEQ ID 3669

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SEQ ID 3670

MALGQFDVDETSVIRSLSSASLYMFTTRMFPYQRRGVWQRANHHAPICNALERVFNGETKRLIINIIPRYSKTEIAVNVFLAWAMGRVDPCEFIHASYSAAALAVNSVQIRNLVQHEEYRA
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SEQ ID 3671

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SEQ ID 3672

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RQVHALEYTAGSVPDALVGPETWSADDIRFPQYNDLLSGETAQRKRMRFPVPGELSRNFRFETKQPLKDVYDEWLARVVCFAFSVEPTFPVQVNRSAETSREQLSDGHSGLKMW
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SEQ ID 3673

TTGGTTTCTCTCAAAAAAAGCGCGCGCGGAGGGGCGGCAAAACACACCGCGCTGACCGCAAGGAATCAAGATTTCAGGCATATCCCTGCCAAAAACAGGCACAAACCGCGCACCGCGAGT
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SEQ ID 3674

LVCSSKKPPREGAAKHRLTRRNQDSGLSPARTGTTAHRQFG

SEQ ID 3675

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SEQ ID 3676

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KLFEISLVDRPANPDVPTFKADKPKDEAGAADKDGKSDKPTFEEDENPKDGKPKTEKDGKDGKDEAGKSASVNLSESEIALKAVLAKADKPKGGPAKSMYQVSPADVLHS
LKWLVEDASYDNIDEAVTAQIKESAAGLAESLKALAASEADKPADGLAAKAGSGDLAKAESADELAKAQDALKKSNDALAKAQAEISLKKQAVPPKSGTKAISKAEDNGEDPLKGFQPI
VKNDGTLDVATLILAKQTRGL

SEQ ID 3677

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SEQ ID 3678

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SEQ ID 3679

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SEQ ID 3680

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SEQ ID 3681

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SEQ ID 3682

LCLELVHVLSSLILKKPVSQVTDGLFVLV

SEQ ID 3683

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SEQ ID 3684

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 RLSPTDTPVGNARDLAAFLKLIIGNSGAPLKLKLVNDVNTANIRAGVVGVSVMNKITDGLDNI VVHPNLPAQTYLYFYSSRLPAYVQGVGNLLQVRTRQEYTLQLEWPLRTMRYEYGVYADEVL
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SEQ ID 3685

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CGGCGAGCCGGCAGGACAAATCCGAACCTGCCGAAGTCGCCGAACCTGCCGAAGCCGAAGCGAAGCTGCCGAACCTGCCGAAGCAGAAGCCGAACCTGCCGAAGCCGAAAAGGCTGAA

SEQ ID 3686

MPSENQAFSEGDFFMTVKLKAPGGFTDVSFGSOSYAADENGIVEVPSEAAEFLYQFGFNVASEPAEGPEKAKRGRKPKTCQAPAGQSEPAEAAEPAAEAEAAEPAAEAEPAEAEKAE

SEQ ID 3687

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CGCGTGATGATTTATCGCGGTGACGCGCTGAACGAAATCGGCGCAAGGGCGTACGGAGCAAGACGCTTGCAGCGGAAACCCGTCGCTTCTACGCTTCGGTAAATTCGCGCGTTCGCGG
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SEQ ID 3688

MAAPVSLSEEFKQRIQVEHRRDDFFLSVIDVGSAAAEAYIGRSLAADYVGRYDNGKDRIVLDNYFVLSVSSVKINGADAGGWEFDNWLLMRPEGFARGLKNVEVSYRAGYERMPADIRE
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SEQ ID 3689

SEQ ID 3689

GTGTTGGGGGTAAGGACGGGGGACCTGCGAGCGTCGTACACCAGCGCGTGAATGTTTCCGGCAATTCGTTCGCGGCAAGTCGATACGAACGTCCTGTACGGCATCGCGCATGAAGTATG
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SEQ ID 3690

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SEQ ID 3691

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CGGATT

SEQ ID 3692

SECRET
LQVVELRRLQIAQCRTEERPLRLQHITGNGADVDI.SRRFPQRLAERLPDLAQRSINVDITARETILMRDAVTDVRIIDFARNDIAGNTHALVYGASQVRFPYPQHPPTITGSAQLRFAGANPTCP
PI

SEQ ID 3693

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SEQ ID 3694

PPHKRESRPVGAFYRIKREL*ILRSGFPLSWE*RNVGSR*RRRLRONCPSRFOPTICLVLATVFCRRSDSRIRHFQORFFGNDKRVKCFPCRIRLSGLHFKFTSLPLSQ

SEQ ID 3695

SEQ ID 3695
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GAATCCGCTGATTGACGCGGTGTGCAATGCCGTGAACGCCGCTCCACCCGTTACGGGCAAGACGGATTAAACGGCGGACGGCGCGGATATCGAGTATTGCCCGCTCGAGGGTACGCTGGA
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SEQ ID 3696

NRREAVYSALNAKLDALDGFVTKSRKLVHWNDVKRYDQPALFMAQGDNQALFLTGRETKWILRADVYLVVQTAGQPPAPVMNPLIDAVCNVAVNAVHPVTGKTLDTADGADIEYCRVBEVTVE
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SEQ ID 3697

SEQ ID: 3597
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SEQ ID 3698

NQLTFGSGEVFAQMITDAYGNRVQNAFVRINGLQEMSVLDAELKRFYQNRYPPLAVAGQKVKVSGKMGALINGLTNLTLPFGTEYATGTMKALMAFTTGRVLDGDNYSYLQAAAPGGG
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SEQ ID 3699

GTGGATTTCAGGAGTAATGTTTATATGCCGCTCGAAAAGGCGGCTTTTTTATTCAACCAAGTCAAGGAAATAAAATGACCGTACGGAT

SEQ ID 3700

VDSGVMPICRLKRLFLFNQSQGNKNDRTD

SEQ ID 3701

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SEQ ID 3702

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SEQ ID 3703

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GCTCAAGCGAAGGAATCATC

SEQ ID 3704

VIAHVCASTGTWYVDNLDLPRIKHLNEYWREHPPVHILAAASYMGVKPSSSVQSEADEARAVGMLGGGELSEDEFDALLKAKGII

SEQ ID 3705

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SEQ ID 3706

LRRVENQNALVGNVIAFVRQRRADLDGGPFLDRRHRLDKSAHRTDKLITRNALHRVSDRLVGVGVGVVKETPKAAGVVEESRQFQLVYGRFCFYLERQRKPLFRVGVVGGSEL
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SEQ ID 3707

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SEQ ID 3708

MGNVAFPEFPLKRWGRKKTAVWSTGTQKASGREFTAYITTPQWRP SLSFELVTRKASVNELEKLAGFPNARKGSFESFLYEDPADNAVTDQPVGNTVQGVARYQLVRSMGPIEPVSAV
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SEQ ID 3709

FTGAATATGGGCAATGGCTTTGTAGCCGCTCTGCCGTTTGAACCAAGTGCTGCCGTGGAAGGAACAGGTGTAGGATTTTTGAAGAACTTAGTTCCTCAATATCTGTTTTAAATAAGGGGAA
GGTGCGCTGAAAAAT

SEQ ID 3710

LNMGNFVAVCRFPDQGAABESTGVGFLKNLVPNLFKIRGRSPEN

SEQ ID 3711

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SEQ ID 3712

MKLLRRKDYPEGRTFLAFVGYDEFTDSTVLELTHNWDTRYDLGDAYGHIAVEVDDAYEACERVKRQGNVVRAGLMKHGTFTVIAFVEDPDGCKIEFVQKSGDDSVAYANT

SEQ ID 3713

GTGGCAITGGGTACTTCTGCTAATGCATCGAATTTGGTATTTCCTTAGGAAAAACAGTGTGCGCAGGTGACGAAAGGAATTCAGTGGGACATCTTCTCAGGCAACAAATTTAAGT
CGGTGGCAATGGTACTGAAAGTAAGGCACAAATAAA

SEQ ID 3714

VALGTSANASNFISLKGSSAASGTGIAVGTSSQATNLSAVAIGTESKAQNK

SEQ ID 3715

AGAAGCTTTTTTCGGATTTGTTCTTTAAACCCATTGGGAAAACTAATTTTATTGACACCTTATTTCACCTTTTTTATAAATATAATTCAC

SEQ ID 3716

RTLFGFVL*PIGN*FYLHLICTFFINIIQ

SEQ ID 3717

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TGGTG

SEQ ID 3718

MKAATSGRLIGLLHGGDEFOQADLYTITLSGGRVLRHTGADMFVVWDGQAYCAHELVIKRGATRTAVGLEVDNSHTLQISAAPDYRLBGLQWAEALAGVLGDARVKIDRVFFDAGLRFPGAV
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SEQ ID 3719

ATCCGCTCCGAACGCGATTTCAGGGCGCGGATCGTCGAAGAGGCGGGTCGTGGCTTGGCACGCGGTACCATCATCATGCAATGGTCAAGGGCGCGGGTGTGTGATTGCGCGATGCTCCTGG
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SEQ ID 3720

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SEQ ID 3721

ATGGAAAGCGCAACCTAATCTCCGTCATCTTGAAGCACTGTGCGACACGGCTGCCAAGCCGCCAATATGCGGTTGCGGCGCGGCTGATGATGCACATGCGCGATACCGTCCGCGAAA
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SEQ ID 3722

MESETLILRHLDALCDTPAQAAAMRLRAGLMMHIADTVRENGWTFQQAEEHCGLTRPRINDLLNGKIDKPSLDALVNIINAGLGQCISLSFAPA

SEQ ID 3723

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SEQ ID 3724

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SEQ ID 3725

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SEQ ID 3726

SEQ ID 3726

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VFSQGLRLKIPYGDGSHSGNGAVVYADNKAAAYDLTDDDFIVSQAQDPVKAGRKTNADAFNQIQVEYELDRDNDYNVAIAEKQDQANIEQYGLRPKDAVRMHGICDAKVAQKVAQQLLQALY
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SEQ ID 372

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SEQ ID 3728

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SEQ ID 3729

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SEQ ID 3730

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SEQ ID 3731

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SEQ ID 3732

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SEQ ID 3733

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SEQ ID 3734

NTEDKKTVALNFAVEDGNTGASAAVHVVEHTGADYRNGYVTATLNGYVSENAPKSGKRYLLARTLDFQETDITAPDPGWVYRKALEGAAGIPKDAQPVYAE

SEQ ID 3735

GTGACGGGCTGTGTGAGGTTTTTGACGGGAACGGCGGTTTTTGCCCGCGGGTTTCAGCGTGGTTGTTCGGCACGGCGACGGGGTGCTGGAGGCGGTCATCGGTTTGGGCTGTGCGGGT
ACGCGCGGATGTTTCGCGCTTGCGCCGACAGAGATTATGCGCTGGCGGATTATTAACAATAATCCAGGATATTCCGGAGGCGTGGACGGTGGGGTGCTGGCGCGCGGGGCTGCTCTACGAC
GCGATCTGCTGTTTTCGCGCGGGCGTGAGGGCTTTGTGGCTTCGGCTACCTGCTTTTGTGTTTCGGGCTTTGTGTGGTTTGTGGTTTCGGTGGCGTTTGGGGGGGTACCCGCTTTGAAC
ACGGGTATGTCGTTCCCGCGCTGTGTGGCGTTTTTCTGCGCGCTGGCGGGGAATAATCGCTGAGGTTTTGTGTTTCGGCGCAAAAGTCGCGGGTTTGGCGGATGAGGGTTCG

SEQ ID 3736

SEQ ID 3736
 VTGMLRFLTERPLPAGFQANLFGTATRVLEAVIGLGLSGYAAVFLAPDEITYANRIYYKQDIPEAWTVGVGLAAAGLTQALLFARGVVRACVASAYILLFSGFVNFVLSVAFWGAYPEPLN
 TGMVVVPLLPAPFCALAGNNALRFLPSAOKSRGLADEGS

SEQ ID 3737

SEQ ID 3737

ATGGGGTTTTCGAGTTCGGACTGCTGTTTGCCGCGGCGCGGCGCTGCTGGGCGCGGTGTGGGCAAGCCTTCAGGAACCGCGGCCGCCGGTGCAGGCTGTGCTGGAGGCTTTTATTTCG
CAATCGCGCGCGCGCGCGCGCGGAGCGGTTCGTGCCGTGGATCAGGCGTGGACGTGCGCGCGCGCGGGGTGTTCGCGGGGATGATGACGGGGCACGCGCTCGATACGGTGC

SEQ ID 3738

MGFLOFGLLFAAAGGVLGAVWASLOERGRPVQAVLEAFISAIAAAAAERFVPLDQAWTCAAGVFAGMTGHALDTVRALAPKVLRGYLGGLAEKLTGVKDGSSDGKD

SEQ ID 3739

EQ ID 3739
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SEQ ID 3740

SEQ ID 3740
MNCVSRTLPGTQRHLHAPRYRSKSIFSIIRPSVFHTRKLFRAAQVTAQHLGRERAHRIERVPRHHPREHPRRRARPRLIQRHEPLRRGRRRDCRNKSLQHS LHRAAFLKACPHRAQHAAG
RGKQQSSELOKPHSPRLIRQTPRLLRKQKQKQRLIQRQRAEKRQQRNDHTVRQVRVPPKHRNKQKPHARKQKQVGRSHSPHAPRQKQCRLLQPRRRQHPHRPLENILEFVINPRVNV
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SEQ ID 3741

SEQ ID 3741

GTGCGCCGCGCCCTTTGACGGCGTTGATTTGGAAGCGCGCGGATATTTTGAATGCTTTTGAATAGGGCGGGGTATGGAACCGGATGCTTCCCCCTGCGGACAGGCTTCGCACTCTGAAGTCA
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TTGCCTTGTGTGTGCGCTTCCCGTGCAGGACATGTGTGGAATACTACCGCCGCTTCTTGTCCGCCGCCGCCCTGCCCTTGTGAANTCGGCAGCGGTAAACCAAGCCGGTTGCGCGGTTGTAAAG
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ACATCGGGCATTTTCTTCCAGCCTTCCGCGCGCGCGGGCGGCTTCGCTTTCGCAAAAGGTCGGACAGCGCGGTAGCGTTTGAAGCGGGCGGATGAGCAGCTTCGCCGTTGCGGATTTCTG
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SEQ ID 3742

[illegible]

SEQ ID 3743

SEQ ID 3743
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CCGGCTTGGTTTACGCCCTGCCCGATTTCACAAGCGAGGCGCGCGCGGCAAGAAGCGCGGTATGATTTCCACACTGCTCGGCACGGGAACGGCAACACAAGCGCAATGTCCACTGCCACCG
GATGAAGGCATTGGATTGGAAAAATCCCGCGCGCGGCTTCCGCGAAACCGTCCCGGATTACGTGATTGAAGACGTATTGGCACGCATCGCGCGAGTACTGTTCGAC

SEQ ID 3744

SEQ ID 3744
IMVTPERGDIPIHLAFDPAAGTEMKGGHYAIALSPRAYNRATGLVYACPISQGRAAAARSGGHISTLLGTGTATQGNVHCERMKALDWKIRRAAFRETVPDVIYEDVLARIGAVLFD

SEQ ID 3745

SEQ ID 3745
ATGTTGCGACTGCAAAAATGGGGCAACAGCGCGGCACTCGGTCTGCCCGCCGCTCTCTGACCGCCCTCAACGCCAAAATCGGCGACGCGCTGGAACAGAAATCCGCAACGGCGAGCTGC
TCATCCGCCCGCTCAAAACGCTACCGCCTGTCCGACCTTTTGGCAGAAACGGAAGCCGCCGCCCGCGCGGAAGGCTGGGAAGAAATCCCCGATGTCCGACAGGAGGGCGCTT

SEQ ID 3746

SEQ ID 3746
 MRIRKQNGNSAAVRLPARLLTALNAKIGDALETEIRNGELLIRPVKRYRLSDLLAETEAAPPRAEGWEENPDVGQEGV

SEQ ID 3747

SEQ ID 3747
TTGGATAATAAAGTGGGTCGGATAGTCGGCAAACGTAGTCCGTTTGAACACGCTTTTACTTTTCAGACGGACTTTCTACCAATGGGAACAAGCGCTTTTCTCTCAATCCGCTTTA

SEQ ID 3748

SEQ ID 3748
L-DNKVGRIVGKRSPFETLLLFRRTFYQWEQGVLSQSGL

SEQ ID 3749

SEQ ID 3749

ATGGACACGAAATTGTGGATTATCTGCTGCCGATTATCCTTTTGGCCGCTCTTCTTCACGATGGGCTGGTTGCCGCCCGCGTGGATATGAAAAACGTAATTGAAGCAGGCAAAAAGCATCC
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CAAACTTTTACCGTCAGCGCGCGCAAAACGACAAAGCCATCAACATACACCGGACAATGCTCGATTCTCCGATACGCTCGCGGAAAGCGCGCGCGCTCTGTTTGAATTGGCGCAAAAC
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TTCAAATCCCAAGTCTTTTCTGGCAGCTGCCCGCTGCAACAAATGGCAGAGCTTTACGCCGAATAAAATCGAAGTT

SEQ ID 3750

SEQ ID 3750

MDNRLWILLPILLPVFTMGWFAARVDMKTVLKQAKSIPSGFYKSLDALVDRNSGRAARELAEBVDGRPQSYDLNLTGLKYRQRGENDKAINIHRTHLSDPTVGEKRARVLFELAQN
YQSAGLVDRABQIFLGLQDGEHAREARQHLLNTYQDQDWEKAVETAQLSHDEQTYQFETAQFYCLAQAALPKFSNDFDARFNVNGKALEANKKCTRANMILGDIETRQGNFFAAVEAYAA
IEQQNHAYLSMVGEKLYEAYAAQKPEEGENLRLTGYMOTFPELDLINVVYKSLSLDLGKEGEAAQTAVELVRRKPDNGVYRILGLKLSLDLPWKADADMRSVIGRQLQSRVMYRCNRCH
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SEQ ID 3751

SEQ ID 3751
ATGAAGAAGATTGAAATGGATTGAAGAAGCCCGTAAATACCTTGGCGCTCAGCAAAAAGTGAATGGCAAGTCAAAACCTGTGCTTTTAGCGATGCTGCAAGAAATGGGAAATTTTAAATCAGG
AGCAGAAAGCGTGTTGGAAGAAGAACAGATACGCCGTGGTGGCGGCTGTTTGTTCGGATACTGCCCTGGGCAAAAGCGGACGCGCGGTATCATCAGGGACTGGTATCGCGCCAAAGCCTGGTCAAT
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GGCGGCAATCAGGCAATATGGTATCCATCATCCCGTTTGAACCTCGGCACATTGACGGCTACTTCTGGCCGTCCAAGCTGATTGGCGGCAAAAGCCGTGCCTTCTGCTCCCGCGCGGAAGGGC
GTTACCGGTTGTCGGACGTTGCGCGCCACGGCGAAACAGGGCGCGGGCGAGGCG

SEQ ID 3752

SEQ ID 3752
MKELKWIIEARKYLGAHEKVNKSNPVLHLAQEMGNFNOEQKAWKETDTPWCGLFVG YCLGKSGRAVIRDWYRAKAWSMSGLTKLEAPAYGCIADVPRGGGHVFPVVGKDAECRILGL
GGNOGNMVSIIIPDPADIDGYFWPSKLI GKA VPSPAEGRYRLSDVAATAKQGAGEA

SEQ ID 3753

SEQ ID 3753
ATGATTGGGGCTTGCTGAAAAATTGAAGCCGCTCTTATTTTGTCCGCAATCGCGTTCTTCGCCGTTCTTGGCAGCTGGACAGGGCGGCGCAATACGTCGCGGATACGGTGCGCGG
TGTCCGGAGTTTTCGAACGCCCTCAAAGCCGCCCGGTGAACACGCCGGAACACGCCCGCAATCGTCGCCGCGTATCAGGCGCAAAAGCGCGCGCGAGGAAAAAGAAAGGTCGCGTA
TGTGCAACCGCTTAAANTCATTGAAAACTGTGTACCGCAATGCTGTGTTTGTAGTGTACGGCGTGCCGGAACCTCAACGCCCGCGTGTGACGACGCGGT

SEQ ID 3755

SEQ ID 3756

SEQ ID 3757

SEQ ID 3758

SEQ ID 3759

SEQ ID 3760

SEQ ID 3761

SEQ ID 3762

SEQ ID 3763

SEQ ID 3764

SEQ ID 3704:
MSDLEAKVRITVFNHTKQGFDSAAADAKAAEKRSSGDNAAKGFKAAIDSMHETHRNLHADVKAGFEAGNQAQQAASEKVRAEVKGKIGSGLSGLTKLLAGLATADPAKSVLDTADAMQSI
NSQVRQVTSSETYELAVQQQLDPTANRTRASLESTANLYVSTRALKDYGYTQOBLKFTPEAANNAMTIGGVGAQQQAAALMQLSQALGSGVQLQGGDFPKSISRAAPILLDTIAEYMGKSHD
ETIKLKGSEGLKTADVIFKAI SGASEKFGEOAAKMPVTMGQALTVFSNNWQSMVSKLLNDGTHSGIAAVIKLILADNLALVVPVAVGFAVAVAAAVAPTLALNALLANFPGLIATAIGTVV
GLIAKPGDEIDVFGGGSNLSDDVIRAVWQIIITETVGRBAVTVKSNFQGLTGRNLBGAGGWPLPGRVMSVSSAIGAYNVVYINIFATGWMILKEAANDMPQFPANLGAIGNVFI SAIER
MINKAVGIMNSMIDPANKAASMAGISGIGKLNKVRMRMDGGELGERIHDSLTKDRAGAMANAVRERAADIHEADALKRGGGGHAKTARKPGANQGGGGKGRSGGGGCAAGDPQAWB
GETIKARKLAHREMQRETLAHQEWDLAREAYWRAKLATVDANGKTGVKIREKILNLEDQLSKQSTEAQNMQAABEQLDKHLEKKEADQALADGRIQLERLDLIEFENRRYRIAYD
ALQERIALAEQDPAYSQAATGKLAQMGELGRGHERTQAKNEGKRENQRKADPNVVMELQDGGNRVNVQEAQWQKQOAPTAMILARQNFRQAMNGFFKSNQGTFTIQEMVTKPLTGLMRRNV
QBSAIYKIMFGTKTLETA AAAKTAATKATETATTVVSSNAVQAASGAASAQAHI PYVWGLLAVAAAMASAVNGMLGGGGGSQTTTTTTRIPSAAGGWDPAGINPLTQLHENEMVLPAB
HAOTPIREMDQOGGGSVTYINSTGGDFIHKNDLAKLLKQMKRDFKFV

SEQ ID 3765

ATGCGCTATTTTAATAGAAACGGAAGGATGCTTGACAACCTGATTTTGATTTCGGTTTGGCAAGCCCTCGCGGCACACAGCAGCAGCAAAACCTTGATAGGGCGGATATCATATTGCGCGCT
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CCTATCGGTTGGGGAAAATATTTCGGTTTGGCCCTGAAACATAGGAATAACCGCTTTCGAATTGCAAAACACCGAAATCGTACCGATTGTTCCAGACACAGCCAAAAACAAATGCCCTCG
AAACCCGGATTGTCAAGGCTTCAGACGGCATTTTTGTTCAGGCGGTTGCGCTTCCTCCCGGAACACTTCCCGCCCAATTTCC

SEQ ID 3766

MRYFNRNGRMFPDNLILISVLAKPSPHARTKTLGGYHIAAPQTDLDGRIDRMADLPSTLHVKLKGKPLPRKGGIRIGFDIALSVGENTSVCRLNIGITAPQFANNRNRRTDCSDTAKNKCRL
 KPGLSGFRHRHLFRRLPLPPPTLPATIS

SEQ ID 3767

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CGTCCAGGCTTCTATAAAATCCGAAGAGGCTTTTTCGCTGCTCAATCAGGTTTTCATATCCACGCGGGCGGCAAAACAGCCCATCTGTGAAGAAGACGGGCAAAAGGATAATCGGCAG
CAGGATATTCCTCAATTTCTGTTGCCATATCGGCTTTCTTAAAGCTGTTTGGCAGATTTCGACGACTTTTGTATCGGCGGTGCACTCAATTTCTGTCCGCTCAAGCGCGCACTTTCTTCAC
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SEQ ID 3768

VPEKLDGFEVAAVATVHHALELPSDNRTFHVIGIGFPSRIQIAEFQTEQAVHVKVGLAADKLDGGLRGFFLALRQOGFLVHVIDQVKFGKRLHISCOTVQAFRFRSLRGIGFVKLLADHA
QVCMVLLLDGGIGFDGGREIALSVFNVAQNHVGAAGAFFVGFECCLADIETRGIEIGLBQRLGKGFATKLCNLKILCLFVVTKLGGFNRFFPIVLLVDIEQVLSGFTTRHPTVLQPKNLFG
TIDQTRALVVLVRQFKQDARALFADRIGRIEHCPPVVDGFFVFAALTVKPAEGKVQITLRLPAVDDFRQLPCRAPNAVDDQSVQAFIKSRDAPCLLQYGFHIIHAGGKPAHREEDGQKDNRO
QDNPOFVVHIGFLKAVWQIROHFPVSAQGISVRSASHFSSLPHAGGCFRRARTAAARTGTFTTRACRRQTRRTIROSAAD

SEQ ID 3769

GTGTCATGACACATAAAATTCAATACTTTGGGGGTTATCTCTGAATGGGGTCAATCTCTGAAGAAAAATTCATAAAAAATTATGATGGCCAGGAAAAATCCGGTGGATTCTTGATACTGTTATCTTCAAAATGACAAATCTCTCATCAATTGACAGTTACGATGACTGGGTGCAAAACTTAGAATAATTAAAAGAATACTCGCAAGAACTCATTTGGATAATAAAGTGGGTGCGA

SEQ ID 3770

VSMIDIKFNTILGVILNGVNPERKFIKIIDGQENTGGFLILLSSNDKFSFSDSYDDWVENLEILKEYLQESHWIIKHVG

SEQ ID 3771

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GATTTTCGAATACTCCATCTGTTTACCGGACTGGGACAACTTAAGCAGCTTCATTTTGAATAACGCCGTATAGGAGCGCGCGCCGCTTTCAGAAATTTGAAGCCGTAGCCCCGGAAT
GGAAGAAAAGCGCTTCAAGAACCAAA

SEQ ID 3772

VISA PQTAGTAMTDNLNLIQIATPILAVIGVFVAAAGIMRNFFENAKKRATTIIMTMAERNNAALQEAITTVNGLAKTDGCILATYTSDDTPDKKKDREAILTVLNQREFVCAGVLGGALHEKHVK
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SEQ ID 3773

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SEQ ID 3774

SEQ ID 3174
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EVSPTSVGRELTTLSAVCEHAMKEWGLLRENVPVRKISKPKKSRRARRRPTQEQBIADICALLYRPNKPKMAVQVAVLFAIETAMRAGKICGLKWADVMMRRRIAHLPITKNGDSRV
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SEQ ID 3775

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SEQ ID 3776

LGOFGGTKYKLSAFORAAFYLP MCFNTONGT

SEQ ID 3777

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GATTCGTTGCGGAACAAATGGCGTGCTTTATGTCCGTTTGTGTGTTGAAACACATAGGCAGA

SEQ ID 3778

LADGRKGFFDAITKINIFFFPVKPTLGAANPLAGGSTRFRFGAEOMAVLYVPPCVLKHIGR

SEQ ID 3779

SEQ ID 3779
ATGCCCGCGCGTGTCGGGTTTGGCGGGGCCGTCGCCAGGATTAAACGGCAGAAACCGCCCTGCGCCTTCCCTCAATTCTCTATATATCGCGTCCATCAAAAGACGCATTGCTTTTCTTAA
CAATTCTCTTTGGCAGACGGGCGGAAGGCTTTT

SEQ ID 3780

SEQ ID 3780
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SEQ ID 3781

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SEQ ID 3782

LRGRAGGFLPVNPADGPAKPDTRGHMADCLQYCLKI

SEQ ID 3783

TTGCAGGTTTCAGATTTTAGACAATATTGTAAACAATCCGCCATATGCCCGCGCTGTCGGGTTTGGCGGGCCGTCGCGAGGATTAAACGGGCAGAAACCCGCTGCCCTTCCCTCAATT
TCTTATATATCGCGTTCCATCAAAAGACGCATTGCTTTTCT

SEQ ID 3784

LQVQIFRQYCKQSAICPRVSLAGPSAGLTGRNPPALPLNPLYIAFHQKTHCFS

SEQ ID 3785

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SEQ ID 3786

LSKNLNLQTRNKVEYAPLFYRPIPIYQKTMSTSLSYRDAGVIGIDAGDLVEIKIPFAKTRMEVPLDGLGFGALVEIKKYQNPVLVSGTDGVTGKLKLAFLDWDKHDVTGIDLVAMSVN
DILVQGAELPLFLDYFACGKLDVPRATDVIRGIAQCCEESGALIGGETAEMPGMYFVGEYDLAGFAVGVEKENVTGLSIGAGDVVLGLASNGHSNGYSLIRKIHERNDPLDABFDN
GKTLREAVLAPTRLYVKPILAALEKPTIKGMAHTGGGITTENVRVPLPKNTVAQIDAESWELPKLFQWLQAGNVETQEMRYTFNCIGMVVIVAEDADAVRSFLSQGGETVYRLGCIRE
RQGNHQQTQVA

SEQ ID 3787

ATGCGGAAATGCCGTCTGAACAAATTCAGACGGCATTGATGCTTGGAAATCAGGCAACTTGGGTTTATGCTCGTTCCCTTGACGCTCTCGGATCAACCCAAACGGTACACTGTCTCG
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SEQ ID 3788

MRKRLKQIQAFDANKSGNLGLMLVPLTSLDATTVEHCLALPAQE

SEQ ID 3789

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SEQ ID 3790

MVFSTQPTLFFVSSHTNQNLHNNHFFVQYQIT

SEQ ID 3791

TTGTCCATATCGGCTTTCTTAAGGCTGTTTGGCAGATTCGGCAGCATTTGTATCGCGGCTGCAGTCAATTTCTGTCGCTCAAGCGGCACTTTTCTTCACTTCGCGACGCGAGGCGGCTG
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ACAGCTTCGCACTCTGAACCAAGATTGCGT

SEQ ID 3792

LSISAPLRLFGFSGSILYRRCQFLSAQARTFLHFRTOAAVFAAQGQPPBQKHSHEHDADKRAEQYDNQRQIDTLPRIKIGKNGIHHNDGKQBEQDNDFFDGDGDKFHVCSVNKNAAR
TASHSEPLRL

SEQ ID 3793

ATGCCGTCTGAATTTGTTTCAGACGGCATTTCGCGCATCTTCCAAACGCGTATCGGCAACACAGTTCTGCAAACTGATATTTTCCCGGTATGGCGGCTAAACTTCTTCATCATATTTGCA
TAATGCTA

SEQ ID 3794

NPSEFVSDGISASSKRVSATQFCKLIFCFWRLLKLLHHSIML

SEQ ID 3795

TTGTTTATCTACATCGTATTCATCTTATTTCCGAAATGTGAGCGTTTATGAAGCAATCCGTCCATAATAAAACAATTTAAGTGTTTGTATTCATCTATGCTGTAAACGGCTTTT
CCGCCCCCACCACCCCGCGA

SEQ ID 3796

LFIPTSYSSYPKCRFMKQSVHNKTILSVLISSMSVTAFSAPHPPPR

SEQ ID 3797

TTGCTCGCCTTGCCTACTATTGTACTGTCTCGGCTCGCCGCTTGTCTGATTTTGTAAATCGCTATATTATTAAGCGAACTTCTTGGTTTTGTGTTGTTGCTTACGCTCGCT
CCGA

SEQ ID 3798

LPRLAVLFVLSAARRLVLI FVNPLYLSELLGFLVRYGRSG

SEQ ID 3799

ATGAAGATAACACTGCAAAATTAAGAAAGAGTACAGAAAGAACCGCTCCGTTCTTTTGTACCAGGATTACCGCCGCTTCTGCCGCGATATTTGGGTATCCATCCGATTGCGCGG
CACTGTTTTACCGTAAATCCGACGGTACCAACCATCGTTTGGCTTGGCTGCGGATGAGGTTTTCAGTATGCCCCGCGGCGCGGCGCAAGCTGTTTTCGCGGTACGCGGTAAAGCGAG
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CACACCGTCCCGGAGCTAAAAATCTGCGGGATCGGTGTGAATT

SEQ ID 3800

MKITHCKLKEVQKEPLRSFVPEVTARSAADILGIHPSAALFYRKIRTVTNHRLALADEVFECAPGAGSCFVRRKRRRGRGAAGKAVVFGIPKRNRAATTVAEDDAEPETLPPAVK
KIMPDGIVYADSPSGSRGSDAGGPTRCRINRSKEFADRNRHINGIGNFWQAKRALRKYNIDRKPFPLLRCEFRFNGTTPSRQLKILRDRCGI

SEQ ID 3801

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SEQ ID 3802

LSLSEFIERTSPFNPMVILTLFFVCLVVLVLTVPDQVQMWLDRAKEVIFTEPSWFYVLTFSIFLGPLLILSVSLGNIRLGRDEDPVEFGFLSLMLAMLPAAHGVLMPFGVAPRIMHY
PSDITVGAPEHRQOQALLHTVPHWVHANSVYGTIALALAYPGFRYKLPALRLSCFYLLEKI SGRFGDAIDIMALLATFPGLIITTLFGASQLGAGLQEMGWIENSFGVVLIIAAVH
SLAVVSAISGVGKGVKVLSELNLGLAPLILFFVLAADPTVYLLSAPFDNIGNYLGNLVRSLKTYAYEREHKPFESWTVLYWAWCSWAPFVGLFIARISKGRFTIREFVFGVLLIPGLFG
VLWPTFVPGNTAIWLDNGVAGGMLERMTSSPETLLFKFPNYLPLPELT/SLVSLVLSLFFVT/SADSGIYVIANIT/STRDGLSAPRQVAMWVGLMSAVAVLLMRSGGLGNLQSMTLIVSLPF
ALLMLIMCPFLWKLGLSADKKYPETRVNPTSVFTGKWKERLVRIMSQTQEQDILKFLKHTASPMHLELRELSEYGLSVRVDMFPHQDEPAIEFVIRKETHRDFMYGLKSVGQDVSDQL
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SEQ ID 3803

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SEQ ID 3804

MRAPAVRNHKGSPFNRTYANFYEMLAACRKNNGTAVFDGKEKTAIRALKQAEAVAAVYLNIGVKPGDTVALAVSNSTEFITAYFAVSAIGAVAVPMNTFLKSEYAYIILNCKARFLP
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PIYMACSIIIVKSVFFSNVLKQALLKRATVFLVPAITYAMSKAKIPWYRWFNRILRFISGGAPLAEQITLDFKAKFPRAKLLEGYGLSEASPVVAWNTPERQKARSVGIPLGLEAKA
VDEELVEVPRGEVGLIVRGGSVMRGYLNMPAATDETVNGWLTGDFVTIDEDGFIPVDKDLIISKQNVYPREI BEEIHLDAVEAAAVIGVKDRIYADEIVAVQLKEGMDLGED
EIRRLHRTVLNFKIPKQIHFKDLPRNATGKVLKRLKQFEGNK

SEQ ID 3805

ATGGTTGCGGACGGCGAACGCCCTCATTTGAAACAAATATGCGCTGTAAGAACGGAAGCGGCGAGTTTATCATCTTTGCTTCAGACGGCATATCAAACGCCGCTTTGCGCGCATGCGG
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SEQ ID 3806

HVADGERPHLRTICRLKTEGSLSSLPDGI SNAAPFAPHAGGSPSPFLCLT

SEQ ID 3807

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SEQ ID 3808

LRILAGMGKYQILDDKFDVDHAAARVFDVAVGRRMGHEHFFAHFDDFACQGLVAFSGHFGADAVECRLNFGCAADEAGAGEGLVFPFCVPTLVFSKGGDAVREETGVAIRAQAVGVFV
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SEQ ID 3809

TTGAAACTACGTTATTTGGTATTCACAAAAAATGATTGAATTATGAAGGTTTTGGTTCGTATGGGAACAAACAAAAGTGTAGGTTGGT

SEQ ID 3810

LKRLYLVLKMKIVIMKVLVRMGFNKKRLG

SEQ ID 3811

ATGCCGTCCGACACGCTGCCCATCTTATCCGAAACGTCGCAATCGTTTAACTAACGCAATCTTGGTTACAGATGCGAAGCTGTCGCTGGCGGTTTTTATTTACGAGGCAACATGA
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SEQ ID 3812

SEQ ID 3812
MPSEHAAAFYPKPKCSFKLTQSWFRVRSCPCGVFTYGANMKLIYTFVIKIITLLFLLLAVINMDAVTFSYLPQSVNLP LIJVLFGAFVVGIVFGHFAIFGRLLSLRGNSRLRAEVKXSA
RLSGQKLTAPPIQNAESAQDP

SEQ ID 3813

SEQ ID 3813

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SEQ ID 3814

SEQ ID 3814

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HSGNWQSFSTRNNTGDPPLGGILAQITSGGGMTLTPASDGTGKQRVSLFAKPLLAQTLTNMGHTVSANGGGWQVLDTGAAFLPAIQTEPMDIGFINIENPAGGITVSANGINGAQLTQW
SKWRADRMNDLAQTGADLVLSYGTNEAFPNNIIDLADTEQKWLDTVRQIRDSLPAAGILIIIGAPESLKNVLGVCGRTPVLLTEVQDMQRVARQQTTFMSWQNMAGGICSMKNWLNQGWA
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SEQ ID 3815

SEQ ID 3815
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GGGG

SEQ ID 3816

VEIPSAPPVRLPCDCGADEFEAVGKHFRRAPVALGGEVYAVFGGPSLVEPVFHAATAAHCVLPRFRARHFBIGDAPLHMS QJGZGZLHMLH
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SEQ ID 3817

SEQ ID 3817
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CGCGCTACACCGGATTCGTACACGCTCAACGGCAAAACCGCTCGCTACCGCAGTAAGGACGGCATACACTTTACCGCGGAGGACAAAAACTGCTGCGGAAAAAATATGTGAAAAAATCGT
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SEQ ID 3818

SEQ ID 3818
MPIFRGLDMKFNLSLPASTILMSALIAVWFSQNPINAYWQQTTHRNSPLEFLAAYGWWRSGAALQENAYALSDGIKTFLSGETPTTAQDGSADMPPEAAASEAAPPAGGTWQQTAAAV
RSGDKVFPAGDSLMOGVAPFPQKSLKQOYQIESANLSKQSTGLSYSPFPDWPKTITETLKKHPEISLAVFLGPNDPWDFPVVKRYLKFASDEWAQEYLRVDRILEAAHTRVQVWVLGI
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SEQ ID 3819

SEQ ID 3819

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SEQ ID 3820

SEQ ID 3820
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SEQ ID 3821

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SEQ ID 3822

MPSEGREGLOTASLGQVRIWNPFRQTRKPAAAVSIPATPMQEMPEYCVT

SEQ ID 3823

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CTGCTGGGACAT

SEQ ID 3824

VGIVLTHAVFWSTIASLAVRIAPVQKGNQALGILLSTGTVMAMVAGIPLGRMVQVGLQWQASFLILIGLCSAAVMMAVLAKSLPRLPVSNTGSLSSLPILLKKRKLMLLYAVTVPVTHAFTAY
SYIEPPVIQIGGFSARQVTVVPGLYGLAGFAASYLFGKWFPAKHPRAPLAGAVSLIALSSGILLPLAHFPAATYALVFVWGTATVVSLSGMVAVLDFASDAADLANSTISELYNVGIGGGA
LGH

SEQ ID 3825

TTGGCAATCGGCGCAFTTATTTTCAACACGGCGGAATACATCCCATCGCGCTTTTGAGCGACATCGGACGAAGCTTCGGCATGGCGCGGACCGAAACGGGTGTGATGATTACGGTTTATG
CTGGGATTGTGCGCGTGACTTCGTGCGCGCTGCGCGCTGACTGCTGACGCGCAATATGGAACGGCGCGGCTGCTGCTGGTCCGTGTTTGGCGCTGTTATTACTGTGACGCCATCCCTGTGCG
TTTGCCCTCGTGGCGGTTTGAATACTACTCGCAAGCCCGTGGGGATTGTGCG

SEQ ID 3826

LAIGAFIFNTAEYIPIALLSDIGRSFGMAATETGVMITVYANIVALTSALPLMLLTRNYGTARPAAGFVCAVLLSATSCRLPRGVLSYSQAAGLC

SEQ ID 3827

GTGTTCGGACGGGCATCGGAGTATGCGATTGCCGCACAAATTTTACCAAAATACACCGCTCCTTTCCATTTGAAAAATAACGGATTGGACACGCGATCGACAGAAAAAACCOCGCCCACTTGT
CAAAACCCCTGTTCGAGGCGTATCTTTTACAACCTTCAAATTCAAACCGTTCAT

SEQ ID 3828

VFGRHTEYALADNFTKYTAPFHLKNNGLDTASTEKPAHLSKPCLQAYLYNLQIQTVH

SEQ ID 3829

GGCGGTTGCCGCTTCCTCCCCGAACACTTCCGCCACAATTCTCGACATTGCCGTAATGGGACAGCAATTCTGCTCGCTTACTTCGGTTTTCGCCGCTGCGCGCAATTTCGGTGTGTGCTCTG
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CGGCTGTCAAGGCGGTGGTCGACAT

SEQ ID 3830

GCGRCFLPEHPFPQFPDIAVMGQQFVAYFGRCVAQFGVVLPAVEAVGGAALSGEGFVNQTAVGGDVQ*GDVAVVVQELRLIAGMGKYQLDKDFVDHAAARVFDVAVGRRMGGEHFFAH
 FDDFACQGGVLVAFGSGHQFGADAVECRLNFGCAADEAGAGEGLVFPCCPVFTLVFSGKGDVAREETGVAIRAQVQGVFEAARAGGGKPVQGAAGEAAVEHVACFGMGIVVKID*VEVGVA
 EPPFAELAVADDGELRGVAVFFGHIRPRARKGGGNDGVCBEGGLVREBGFYRPFQSGSVLDGEAFDLGLVEMAQVHLIRFGTIAAGPDVAV*KGCGECLPIKRGIQKLRADEFPQQNRILVQIR
 RHPRALAHNLRLQCGGLRMFVEBEGIGGAEDVFEKIQQPHQIRCVVLILCRLRYKQRHNGVKARLGVCGKAAVFMVSADLFEPCDGFGEIPVFFQTA*PFFVFGFLPCPLPFAIALRL
 FFRPAQDFVEQILDFVPMNTEAV*KSGITVETHAFGEQLPLFGRDRQGLGLFVVPVLQAVFDIAQAEAVGGKQGFVFRRHNAHLGNFLQRLRAFQLQRAHLAAAYHLENLGDKFLNADAA
 RAEFDVVRHAFFADFAADLAVQVAHRLIRAVIQIFAEHEGAHQRFVVRIRRDYAAPRIAPFPAPLRLNQILLQHGFAQYQARARITVVRPQHIDAEHLVPGSNVACQCNQFLPDFGEKLL
 IPPFAVAGVGARFGINDGQIDVGRFVLIAARLAGEHQAQFVIRFVTRDRAVHVPIIGVGEQTCRGIDGKIGKQRNAGNFVQIADAVYIAHNLRHHTAQLAQLPRQFPFLAFPRADFV
 PCKGLFETLITRORI.VOHNQENGLFEAVFVVLAGEHQAQFVIRFVTRDRAVHVPIIGVGEQTCRGIDGKIGKQRNAGNFVQIADAVYIAHNLRHHTAQLAQLPRQFPFLAFPRADFV

SEQ ID 3831

ATGATAATTGACCAAAAAATCTACTTCAGATGTACTGAAACAATATCAAGAACTAGGTTTGATTGACAAAACCTATGATAATAGAGTTTTTTATAGGAGGTCTCAAAAAAATCTGCAAT
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TTTAGCTAGCGAACTACGTTATTTCGGTATTCACAAAAAATGATTGTAATTATGAAGGTTTTGGTTCGTATGGGAAC

SEQ ID 3849

ATGGGAATAAAAAATGAACAAATAAATTTGTAATAATATATATATCTCTGTTCCGATGTTTCAAAAAATCGGTGTGCTGAAAAATGTCAACAGACAGCGCTGTATCCGA
TTAACGGGTAAAGGCACCGTCCCAAGGTGATATAACGGTGGTATATCTGGGCGGTGAAACCTCTCCATGATAAAAAATTTTCTGCCCTTGACATAGCTTCAATTTGCAAAATATG
CGACCCGAATCATCCCTTTTGACACTTCCGCGGTACCGTTTAAATGGGGAACCGGTATGAAGACGTATGGTTGATGAATTCATTAATGATAAT

SEQ ID 3850

MGIKNEQLIICKYNTETIYPVSDVSKIGVAENVKQFGLYPINGLRHPRKGD/TNGWYTWAGENPSYDNFPLPLHTFHLQIWRPEIIPFL/PLPGYRFLIGENGYEDWVDFDELLINDN

SEQ ID 3851

GTGGAATGTCTCTCTGCTCTGCTGCTGATGGGGGAGAGGCACTGTAGATGCTATCCGACATCTCTTGACCTAGAGAAAAATGTCTCCAAGTGACAGGACCTTTTGGACAAAAAGAG
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CGGCGAGTTTCTGCTGAAGATTGCTTCCCTTACCATTTGAAAAATATCAAGCTGCTTTTCTATTGAGAGAAAAAGTGAACCTTAGAAGATAGTTTGAAGATGCCAGTCTTTATTGGA
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SEQ ID 3852

VECLLPVGDGEGTVDAIRHSLDLEEKCLQVTGPFQKEVHYRQKEQLALFEVADLVGLKPILEKRNPLQIQTRGIGELIRHLISQETKEYIVGGTAGNDGGIGIAAGLGYQFYDE
DGNALPACGQSLNLPASVSTENRYEIPEDVHIRILADVSPICGHQGYATTYFGKQGLDSTMEAVDQAIQDFYKVPPTLKLKAGAGGGIAGGLCAFAQASTVSGIDTCLDLIDPDKK
VSDVDLVIVGEGRLDRQSLAGKAPIGVAKRTPVGVVVAICGSFAEDLPSLFFENIQAAFSILEKSEPLKEDSLKASLYLEHTASNI GYLLNMPKI

SEQ ID 3853

ATGTTTGGCAGGTTCTCTCTTATGCGGTACGATTAAACCGGCGATGCGGCTCTGAAAGGGTTTCCGCTTCAGGCGGCATCGGTTTGAACAGGGATGGGATGAAAAACCGAAAAATCC
TTTTGTCTGCTCGGCAACATCTGCGGTTCCCGATGGCGGAATACATTTCGCGCGCGCTGCGCGCGAAGCGGCAATTCCTCGAAACCGGACCGCGGAGCATCGGCGTGGCAGCA
CGGCGAGGATATGACCGCTGAAACCGCAAGATATTGAAAAATACGGCATTGACGCTTCAGGCTTTACCGCGCAAAATCCGCCAAGCGATGCGAGCGCGTTTGACTACATCATGCT
ATGGAACGCAAGAAATTTGCTCGAATTGGAATAAATTTTCGGCAGGCGCGCGAAAAAATATTCAAGCTGACCGACCTGATACCGAAAGCGGTTACGACCATGCTCCCGATCCGCTGACA
TGGGTGATTTTGAAGAAACATACAGGCTTCGGGATGACGCGTGTGCGGCATTATTGGAAGAAATTTCCAAA

SEQ ID 3854

MFVQVLPYAVTINRPMPSERVSAAGGIALEQWDMKKPKILFVCLGNICRSPMAEYILRRRAEAGIPLTDSAGTSGWHDGEMHRETAKLKRYGIDASGTSRRIQSDATAFDYIIA
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SEQ ID 3855

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AGCAACCTCAGCCAGGAGTGGGCGGCACTGCGTGCGAGCGGTTCGCGAAAGCGGTTTTCGCTGAAAGAAAGAACAGCTGTTTAACTGGAATCTGTAAGAAATGTCAGAAAG

SEQ ID 3856

LRMQAVGHYWRFPNKAIEYKHKYKTASCRIGSDGINRFMTNFKQKIIIEQARRDLQVTLALREQLDVLQSGVVIKAYNVLSQMQQSEGVLPPTAYRALDFWADQGVHLKVAVN
GYLLCSHAQHECHNDHCHDEEABAHHSAPILVCTECGADEQTLSEWAAALRAGVAESGFALKEHVVLITGICKKQK

SEQ ID 3857

ATGTCAGAAAGTGAACAAACCAAGTCCACCTGATTTCAGGTTTCTGGGAACAGGCAAAACACCGCGCTCAAAGCCTGATGGCGCAAAAGACCGCAACGAAATGGGTCAATCATCG
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TGAAATACAGCTTACCGCTCAAAGCCCTGCGCGCAACACCATGCGGCTTCAGTTCGCAAGGTTTTCATATCCCGCGCGGAGCGATTTCACGCGGCAAAATTTGACCACTCTTCAAT
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CGGATTCGCGTTTCGAGCTGATTGCCAATCGTTGACGCGGATTATTCGAACAAACCTTAAAGACCGATTGGAA

SEQ ID 3858

MSEVKTKVHLISGLTGTALKSLMAQKDPNEKWVIIIVNEFGEIGIDGAVLSDNGIPVARIAGGCLCTAGPQMGVTVQKMLERDAKPDRLMIASGLAHAASVIDELKAKPLDSLLEI
GAVFTVVDPRQFINPDYAQALYKQIGICDVLAAASKTDLCTPEQLAEFHDKAKLFPKARVVEVQNAQLDIQWLDIPVVEKSRYLKALPDNTMGFSQGPFPAGRDFNGEKLNTNFFN
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SEQ ID 3859

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SEQ ID 3860

MKPKFTVLTALLLAVSLPSMAATRVLMETDMGNIRLVDESKASKTVANFVRYARKGYDNTIIPHRVIGGFVIQDGLTEDLVQKATDKAVANESNGLNKTVGTIAMARTAAPDSAAAQ
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SEQ ID 3861

GTGTTACTGCCGACAAACACGCGAGGATTGTGACGGCGTACGGGTACGTTTGTATAAAGCGCGCGTGGCGGTTTTCAGCGCGGCGATTTTGGAACCGGTGTCATTCCGCTTTCT
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AATCCCAACGTTTTCCAGATTTCGAACTGCGTTCAGCGGCAGCAGCTTCCAAGCTGCAAGAGTCGGACGCGCGCTGCGCTGCGCGTAAACGAGCTGATGGCGGGTGGCGGATG
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TTGTGATTGAAGCAAGGAGCTGACGGGCGGAAGATTTCGCAAAAGCGAAGAGCGGAAATCAACATGCGGAAAGCTGTTTGGCGAGATTTCGCAAGAAATCAAGGTGTTTCAA
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SEQ ID 3876

VVESAKNNKGGKSNAPITIEQVKAENKKEIHVLLINAGNVNSSMNDTGKALKDLFDNPVDALAAVRPFMIVDEPHKPTRDSARTWGNIKRLKPYILRYGATFNDEYNNLYRLTAV
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GVVFTKIPRNSIKIPVAGGTYSPDFAYIVTKSGEILNPFVIEAKGTGDAEDLRKSEERIKHAEKLPAEISKEIKVVFQTFDGERIALIQLQMPAGHSENGH

SEQ ID 3877

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SEQ ID 3878

MTBPGDKIMVCLSGGKDSYALLDILRLQASAPIDFELVAVNLDQKQPGFPPEEVLPTYLESIGVYKIVEEDTYSYTVKRVLDGKTTCSLCSRLRRGILYRTAKELGCTYKIALGHRDDIL
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SEQ ID 3879

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SEQ ID 3880

NLATLP*NSISRTFLPCGIFKRTITLYDFMQLLT*FLRIHFQRLMLIAGFNQSLAYCFCCFSHTTPKTHNHVLQSFQINKVVSVKQROFQINCRKTKRLNAG*RFRRH

SEQ ID 3881

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SEQ ID 3882

MKRTLLPFFGVARVSGEDQTFLLHGLSNDINNLTQACATYNTPKGRVIANMTVNRGDDLLILMAQDLLEATVKRLQMFVLRKAVFREILEDYAVGAELAAAEPLAAQEPSLAFTS
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SEQ ID 3883

GTGTTATCGGATAGTGTGTTTACTCATTTTCTGTCATGCAAAACATGGAATTCGGTCAAGCGCAATGTTACCATATATCCCTTTATCGAAGGAACCGATATGGATATCCGGTATTTCC
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CGCGTGGTGGCGGAATGCGGCTCGGACAAGGACACGCTTTTGGATGCGGTATCTTACCTGCGGTATGCGGAGTATGCGGAAATGAACGCGGTGTCGAGCGCTTGGGTTGCCCGCGC
AGAAGCGCGCGCGCGCTGCGTGAAGCGCGCTCGCGGCTCGCGAGTGGCGGTCGAAATCAAAATAACCGCGTGAAGAGAGACGCGGCACTGCA

SEQ ID 3884

VLSDKCVYSFFVQNMMEIQACQYHISPLSKETMDIRYFGTTPRYSEAVCAGGLIFLSGHVPENGETAABQTDVLAQTDKWLAECSGDKAHVLDVAVILYRLMDGYAEMNGVWDAHVAAG
RTPARACVEARLARPEWRVEIKITAVKRDAATA

SEQ ID 3885

ATGAGTAACACACTTATCCGATAACACCTGCGGTACGCGTTTTGCGTGAAGAACCGCATCGAATTTGAACCTTTTACCTATGCTATGAGGAACACCGCGGCAAGCGGCTTTGCGGAC
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SEQ ID 3886

MSKHTYPTPAVRVLRNGIEFEPTTYAYEEHGGTAQFARLFGKDEHLVKTIVLQDENGKPIVLMHGDQIISTRNLARHLGAKHI EPAAPQAQNKHTGYLVGGTTPFGIRTKLDIYVQ
SYMDLETIYINGKRGFIIGIRPDELINILNPKTIQAAV

SEQ ID 3887

EQ ID 3887
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 AGCGCGAAGAAAGTCTCAAGAANAATCAACGGGCTTACGATACGCTTTCCGACCTTCTCAAAACGGACGCAATACGACGCGTCTTCAGACGGCATGAGGAACCGGGCGGCAGGAAGAGGC
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 AACGACCGTCTGGTATTCTACCGCAATCATCGCGGCTTTATCCGCTTCAACGACGGCAGGCGGTTTGGCGCCGAGAAATGGATA

SEQ ID 3888

SEQ ID 3888
MDKDLAYVLGVSPQAGADEIKRAYEKLAMKYHPDRNPQNLQAEKFKELQRAYDTLSDLSKRTQYDASFRHEERGQEEAFRRQARREQFYGBQMRBQAFRRERFERQASRSRHAYEPS
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SEQ ID 3889

SEQ ID 3889
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CGTGAGAGCGTGGTCGGCGGCATACTCTTGGGCGGTTTGAATTTTATGAACTGATGCTACATCACTGCGCACCACAAATGATGAAGGACAGTCCCACGCTGGTTTTGCCGGTATGAAT
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CAGAAGTTAAGGCTATTGTTCCGCCATA

SEQ ID 3890

SEQ ID 3890
 MAYILLISIVFSVSVSILLMARKKRIDIAQAVAVNVVAVILTVSLVKPDVGNIGAFLETPWPLFAALGVLLPSVFMGKSVESAGIVKSDAAQRSLFLPIVAALTLFGEKLSSEKKLIGL
 CLAFAPALFCLLWKSDSGKSGSANRQALLLGGVWAGYGIIDILPKQIAKSGTAFAGNLLVAPALAGVIMFACLFAKSVNRKSVSVVGGILGLGNFMNIVYITAHQMMKDSPTLVFAGMN
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SEQ ID 3891

[illegible]

SEQ ID 3892

SEQ ID 3892

MMSGFSPPKPTTILSLAGAFGALAFADTPNNTEQQKELNTWTVVHGKGSADQKGADDDVYKNSVNAVGVKEILERYRVQSGADVGLKGLNGVYNNMFRTAGGAIPTPNIRGITGKGRIPVTIDG
TEQTDLDVWMNNYVGVGDRNYLDLPALFSLIAVLEKSPALTRGVKSVGGVMSIRKTIPESDIIEPGRNWGLEVKTEFSGNTVAQKNDLRQLPLGRDYRTLSPIGATADGVSGMPDVLTYGTGKPS
TALLLDDEGIADYKPSGKSGSHNFKDDRGLQMLSAFKTIDTIDGLAAVSHRQKGNITYAGKRGYQSYLNNPIYGADACDYQYPDKSWREKIDILCKSSASLVPMAVLFVRPGEIIMNSHTDTKLL
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PYTELADEEDIANQKRMQLQYDPRADGQVAEYQDLNRRFKEKNGYDFDPHDILWQDTRFVAKSDGNFVFWAKGNKHTDVLVILRRRQIIPMNAKGFDPGKVQITPEMYRERVNNPQGS
GSYRRYIPGSHITYTPGVSREEMERMANENQIPSKEDNNQALEFNSDLNRTANIRKHQFGDARDWRMPQEQRAHSSWPHLAVSYDLADNHRLFARYARMSRFPVSLYELZFAATGSGGGLYGS
VAEYSLKPKESHTYVGVNFPFAPKALRQGDRLITYYSNKIKNQIDTSNEDGGMITYDKAVSKGVELQSRLLSGRFFASFGGYTYRLKMHVMDCKGIAFKFDYLYLQVPECLGGPGLSRF
FOSLOKPYSLTLWVGTFRFPNEKLELGMRAIHSKAEERNYDKLIADGAGQVYARNGKPYGWHAAFTLLDAYARYIGKHIDLNFVSTNLNARYLYDPMSSTPVPGPGRITTPGIGKRF

SEQ ID 3893

SEQ ID 3893
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CCTGGAAATACGCTTCAAACGGCAACCGCCGCCGAAACCGGACTACTCGGCACGGACGGCGCAGGATTTGAAAACGGCGGATTATCCCTCGGTGCTCAAGGCATTATGCTGTAAACCGCC
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TGCCATCGCGGCGAGCTGTATCGGAAATTTCTGTGCGGTGTGAACGCTTCGCGGTGATGCTGTCGAGGAAGTCCGCGCTCAAGGCTTCTTTCGCGCGAAGCGGATGGAATGCACC
AAACCGTCAAGCCATCCCAATGTTTGGC

SEQ ID 3894

MPSVRLPTSTVWRKTNTAGWSKADALNKKMPSETRLAFTAFSRSDRFRRTCSKSVQRQSVKTSVRISHPACRKSGLISLEIRFKQTAAARNRYSAHTAGFENGSLGAQGINAVTA
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CQCGQAVCGNPFVCGVERPADAVEEVAAGQFFRREADGMHTVQAI PMPA

SEQ ID 3895

ACCTCGCCGCGCGCTTGTTCAAATAGTGTCCAGTGAGAATAAACCGGCAATATTTCTTCATAAGTGTGGGCGAGAAGGAATATAACCGTCTTTGGCGGCATATACCTGACAAAT
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GGAAATACCCCTCGTTCCGAGCCAAATCTTCAGAACAGCGCTTAAATTCAGAAATATGGATTATTGGTTAAAGATAGCTTGAACACCGGTCATCATGATCTGAAGCGGCTATT
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SEQ ID 3896

TLPAVVQIVFVRI*PGNIFISVGRNITVGRHIDPK*FYFRIIEIRINFNPQRAVKFPLSMEYVI*EDVQPIFRGITPRFRSQIF*NRL*FKNIGFIG*R*LEHAFIHI*KRHF
SGISCHISPTQVILIPQNLPRKADFLSG*IKVH

SEQ ID 3897

ATGGACTATAACCAACTGTTTATCTCACTTGCAGAAATTTTGGAAACATCATGATTTAAAGGATTTACTTGGACTTTAGGAAGAATTTGTAAGAATCTCCCGATTTCAGATTTC
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SEQ ID 3898

MDYNQTVLSHLQKFKHHDIKGPTWTLGRIVEELPDFQVQVPIPNHEDEPMVYVSSIGIQFLGQEFFIISPFTPEPHIETLAMLASASMHYPDQFLGKTVINIGRPFWEQSSFRHPLISLP
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SEQ ID 3899

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CAATAATCAGTAACCATCTGATTGTGCGCTTAATTTTCATCGCGCGCGCGCTGTCGAAATACAAAGATTGGAAGCGTTCCAATATCTTATACGCAATTTGGATATGGCGGTCTGTCCA
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SEQ ID 3900

MLNVLQTTAAESARLITPGYVLTIVCLGLPALAYIAVKYRVWYKELLRLVLAASFLCALGLIAMQYQDYASFFRNKSVTHLIVPSNFIAGVSKYKDWKRSNIPYQLDMAVVQ
NRPAAGLRRFVTVVGETTTRAAWGLNGYSRQTPFLAARGDEIVNFPQVRSCGTSTHSLPCHPSTPDRDIDYDEIKAEHQDNLDDIVQAGVEVTVLENDGCKGVCGKVPMTDVTSLNL
PEYCRNGECLDNLITLTKFDEALNKNDKDAVLILHTIGSHGPTTYERYTEAEKPTPTCDTNEIDKCARATLVNTYDNTVLYVDQFIDKVIKLENRDDLESAAVYVSDHGESLGENGHYH
AAPYAIAPSGQTHIPVMVWFSKAFRQHGIDFQCLKQAAENEYSHDHYFSVFLGLMDISNSQTYRKEMDILAACRRP

SEQ ID 3901

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GTCGCGGCGAGTAAATCTCGCGGATCGGTGGGAAT

SEQ ID 3902

MPDGIVYADSPGSRGKSDAGGPTRCRINRSKEFADRRNHINGINFWNQAKRALRKVNGIDRKPPFPLKCGWEFLNSGTPSRQLKILDRDCGI

SEQ ID 3903

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SEQ ID 3904

GLMAVTYAGVDRLAAHFQQAITHSITGAPQ

SEQ ID 3905

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SEQ ID 3906

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SEQ ID 3907

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SEQ ID 3908

MTDIFTPSKRSFVMSKISHKTEKPEVLVRKFLPSQGFYRKNDKRYACKPDIVLPKYTKTVFVHCGFWHGSNCNGHIPKSNMDFWLEKITKNRERDINKNETELEKIGFKVIVVWCELEKN
KAICRELRNLVBEIKDAV

SEQ ID 3909

TTGTTTGTCTTCAGCGGCAAGATGTATCGGCTGTTCGCCAGAGGTGCATATTAGTACGAATGCAATAATAATCTAATTAATACTCATTATCAATATTGGTTGTAGATTGCATTGTGTC
AATATTTTATTTTAAATATCATTGCATTATCATCTAATAAATACAAATATCATAGTAACGGCAACAGGCTG

SEQ ID 3910

LFCLQRQDVSAVDRVHISTNANNLIKTHYQILVVDICQYFIPNIALSSNKYKYHSNGNRL

SEQ ID 3911

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SEQ ID 3912

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SEQ ID 3913

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SEQ ID 3914

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VRQFAARYAKLPRHXPALIHLDALQKRDEGDFRAAGNSPQTALEAEPDNPRLLEAGRPYAEWNQKESAAAFKVLKTDIPAEATRPIVENYLSLGRKRRWHQGISLGYNSNVNQGN
GINQCVWELAGMCLMERLPAPTDSTPSSYSATAERTVPLKGNHGVQVRGLVGNRYTEKDKDSAAAMPDYGYRNGSLYAGIYADARSFSLPLPYEYDFRNRNTHYRWAGADADWSRTLS
PWRINSHAGAKKTYGGQSKTYFADFQYELGAGAEFSITLKSGLLVNFDARKAYPEKSSSKETARLGAIRLPSGGTYLNAVLLYRRSLYDAASFVSDNKRDRDKQYIMAAAGFPQ
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SEQ ID 3915

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SEQ ID 3916

MAHFPNINYPYKGNMTVRIEHDLLGDREIPAEVYWGHTLRAIENFKISTQKISDVPQFVRSIVMVKKATAQANGELGAVKPELAAAEKACDEVLLNRRCLDQFPSPDYVQGGAGTSVN
MNTHEVIANLALAEALGYEKGRIYDIVNPMOHVNASQSTNDAYPTGFRILAVYISIGELLDKLTVLKNFAAKAEAPKIDVLKMGRTQLQDAVPMTAGQEFQSPQVLLLEKILNLDRTQLLELV
NLGATAIGTGVMPPKYAELVVKLSEVSGLPCKLLENLIEATSDCAGYVHVHGLKRTAVLKSICNDLRLSSGPRAGLKEINLPELAGSSINPAKVNPIVBEVNVQVCPKVIQNDPT
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SEQ ID 3917

ATGAAAAATCATCTTCGCGCGCTCGCAGCGGACGCGTCCGCACTGCCCTCCGCCACTCAAAAGTGGAGCAATATCAGGCCAACGTCGCTTTCGCCATCGACCACTTCAACACCGCA
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CGGCACTGAAATCGCGCGCATCTTCGATGCGGCTCAATATCCGACATCCGCTTCGTTCCGTTCAACCAATTCACCTTCAACGCGCAAAACCTTGTTCGCTGACGCGCAACCTGACCATG
CGCGGCAAAACCGCCCGCTCAAACTCAAGCGGAAATTCACCTGCTACCAAGCCGATGCGGGAACCGAAGTTTGGCGGCGGACTTCAGCACCACCATCGACCGCAACCAATGGG
GCGTGGACTACCTGTTAACCGCGGTATGACCAAAACGTCGCCATCGACATCCAATCGAAGCTGCAAAACAA

SEQ ID 3918

MKKIIFAAALAAAVGTASATYKVDYHANVRPAIDHFNSTNVGGFYGLTGSVEFDQAKRDKIDITIPVANLQSGSPPTGHLKSADIPDAQYPDIRFVSTKFPNFKKLVSVDGNLTM
RGKTAIPVKLKAEPNFCYQSPMAETEVCGGDFSTTIDRTKMGVDYLVNAGMTKNRVIDIQIEAAKQ

SEQ ID 3919

TTGAAAAATCGCCATCGGAAGATGCCGCGAGCAGGACGAACACTATACCGGCCCGGATGAAATTTGCCATATCGTATGCGGCTGAAAAACGGAACGTTGTTTTTCGGTTCGTTACTTTC
CGGACTTCCGCGAAGCCCGCTGCGGCCAAATATCTTTCGGGGGTTGTCTCCGCCATATCGGCTTACGGTTGCGAGGGCGGTTTGTATGAAGAGGCGATTGTGCTGATTCGCAATCA

AGGCTTATTGTTTTCAGCTTCGATTGGATGTCGATGCGGACGTTTTTGGTCATACCGCGTTAACGAGGTAGTCCACGCCCATTTGGTGGGTGATGTTGGTGTGCTGAAATCGCGCC
GCAAACTTCGGTTTCGCCCATCGGGCTTTGGTAGCAGTTGAATTTTCGGCTTTGAGTTTGACGGGGCGGTTTTGCCCGCATGTGTCAGGTTCGGCTCAACGGAACAAGTTTTTTCGG
TTGAAGTTGAATTTGGTGGAAACGAGCGGATGTCGGGATATTGAGCGGCATCGAAGATGTCGGCGGATTTTCAGGTGGCGGTGAAGGGTTGCGAACCGCTTTGCAAGTTGGCGACGGGAA
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GTGATATTCTGCTCCATTTTGTAGGTGGCGAGGCGATGCGGACGGCTGCGGAGCGCGGGAAGATGATTTTTTTCATGATGATAATCTTTTGTGGGCGGTAAAGGGCTTTATCC
TAACA

SEQ ID 3920

LKKCAIGKMPQDDEHYTGPDEIVHIVCRLKTGNVVPGRYTFDFPASPACRQNI FRRVVLRLHIGLRLAGRFDEGICADSHQGLLPCSFOLDVDVADVPHTGVNEVVHAPFGAVDGGAEVAA
ANFGFRRLALVAVEFFGFEDGGFAAHGQVAVNGNKFFAVEVEFGNEADVRLLSGIEDVGGPQVAGEGLRTALQVGDGNDVDFAVAFCLIELDGTGCTVKTADVAGVEVVDGETDVG
VIFVHFVGGGSADGCR CERGEDDFHDDNPLCGPVKAFILIT

SEQ ID 3921

ATGGGGTTTCATGTTGCGGACTTGGTGGCGTTTCGTACCAAAATATCGAATTTACCACAAAGTTGGAACAAGGTTACCTTCTCTGCTGTCTGCTGCTGAGCCCTTGTCTCATCTGT
TTGAGAACCTCCATAATCGGTTTGACGATTATAACGTTCTGCGTTTTAGTTTGGTTGGACAATCATATGAACCCAAACCCCTTCGGTTTCGGCTTATCGCCTT

SEQ ID 3922

MGVHVADLVRFSYQISEFYHKLKRVYLLLPVLLPEPLHLFENLHNAFDDYNVLSVLWLDNHYEPKLPFPFYRL

SEQ ID 3923

CGAAAAGCTTTCAAATGACGGCTGATTCCTCTTCAACAGTCGGATACCAATCTATGAAAATGCCGTCTGAACGGCAAAACGTCGGTTACAGCGCAT

SEQ ID 3924

RKVFQMTADCLFNSRIPIYENAV* TAKRAFRRH

SEQ ID 3925

ATGGGTTTTCTGCAAGGCAAAAAATTCGATTACCGGCATGATTTCCGAGCGTTCCATCGCTTACGGCATCGCCAAAGCTGCCGGAACAGGGCGCGGAACGCGGTTTACCTACGTTG
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TACAGCCTTGCCCGCATTTGGCAAAAGCGCCGCTCCGATGATGCGCGCGGAGGAACCTCGCCATCGTCCCTTAGCTACTTGGGCGCGGTACGCGCGGATTCGGAATACACAGTGATGGGT
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GGCAAACTCACTTATCTTACGCGCGGTACAGCATTAATGCCCTTGAGCACCAGGGA

SEQ ID 3926

MGFLQKKLITLGMISERSIAYGLAKACREQGAELATYVVDKLEERVVRKMAELDELVFRCDVADDEINQVFDLGRHWDGLDGLVHSGIFAPKEALSGDFLDSISREAPNTAHEISA
YSLPALAKAARPMRGRNSAIVALSYLGAVRAIPNYVMGMAKASLEAGIRFTAACLGKEGTRCNGISAGPIKTLAASGIADFGKLLGHVAHNPLRRNVITIEVGNTAFLSLDSLGIT
GEITYVDGGYSINALSTEG

SEQ ID 3927

GTGTTATCTTCATATTTTCAGGGTAACATATCTGCTAATCTGGTACAGACCCAAAAACAAAGCAGGATAACACCGCGCTTTTCATCGGCCCTGTTCCGCCGCCCGCTTCGTCAACCGCC
TGCAAAACCACCGTTTACCGCGAGGAATGCCATAAATCCCGCTATGT

SEQ ID 3928

VLSYFEGNLSANLWQTKQKSTDNFALFHPPCSARFPVNRLLQTHRLPAGNAINPLIC

SEQ ID 3929

ATGAAGATAACACATGCAAAATTAAGAAAGAGTACAAAAAGAACCGCTCCGCTTTTGTACCGGAAGTTACCGCCGCTTCTGCCGCGGATATTTTGGGTATCCATCCGATTCCGGCGG
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ACGCGGTGCGCGCGCGGAGGAAAGCGGTTTGTCTTCGGCATTCGAAACCAACCGGCGGCTTATACCTTCCCGCAGACGATGCCGAGCTGAAACGTTGCTCCCTGCCGCTCAAAAA
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CACACCGTCCCGGACGCTAAAAATCTCCGGATCGGTGTGAATT

SEQ ID 3930

NKITHCKLKKVQKEPLRSFVPEVTARSADILGIHPDSALFYRKIRTVANHRLALADEVFEGPAGPGSGFCGRRKGRGRGAAGKAVVFGIPKRNGRAYTVAADDAEPETLLPAVKK
KIMPDGIVYADSPGSRGKSDAGGPTRCRINRSKEPADRRNHINGIGNFWQAKRALRKYNGIDRKFPFPLLRCEPFLNFGTSPSRQLKILDRDGI

SEQ ID 3931

TTGTGCGCGGAGATGAAACCGCTCAAAATCAACAGCGGATTAAGGCAAGTTTTTGTTCATGAAACCGCTCTCTTTTTAAGTATTGGGGAATTAAGATAAAACAAACAACTTAT
CGGATATTTCGGGCGGCAATTATAT

SEQ ID 3932

LSAADENALKINSIGIKASFLPKTSLFSLSIGELKIKQNLSDISGGNYI

SEQ ID 3933

TTGAGCGCGTTTTCATCTGCCGCGACAATCTCCGAGCATGGGAACTCGGACAGGTTCACTGTCGCGCGGATGCCAAGCGCGTCAAAGCGCGCATTTCTACTCCATCGCCAGCGATG
GCGACTTGCAGCGACCGGTAATTTGGGCGTATTGGGTAAAGCCAACCGGTTTACCGCGCGGATTACCGTGTCACTACGACGAACAAGCCTTCAACAAATACGAGCGCGTACTTTAGT
GGATGCCGTAGCCAAAAAGACGCTTCCGTT

SEQ ID 3934

LSAFSSAADNTPOHGELQVHVRAADAKRVKAHSYSIASDGLDRDVRNLGLVKANAFAPITTVVNYDEQAFNVEARTLVDAVAKKDAV

SEQ ID 3935

TTGGCAGGAATGTATGGCACGCAAGGCACGGCGAGCGTGAAGTGGCTTCGCACAATGATTAAGGCGCGTCCACCGCGTAAACGGCATACC

SEQ ID 3936

LAMGYGTQGTASVQVGAQLIKGASTAVNGIP

SEQ ID 3937

TTGTTCGCCGAACCGGCAACCGATTTTCGGTTGCCCTTCGTGGCGGCTTTTTTGGTTTCGATGTTGACGGAACCGGATACCGCGCTTCAGGATATGCCGTTTACGCGGTGGACGCG
CCTTTAATCAGTTGCGGAAGCGGACTTGCACGCTCGCGGCTTGGTGCCATACATCTCTGCCAAGCGGTTTACGCTGAATTTGGCGCGCATCAAGCTGATTAACACGGAATACAGAC
CGGTACGCGTGTCTTTCCGCCCAACTCTCAACGGAAGCGCTTTTTTGGCTACGGCATCCAC

SEQ ID 3938

LIPNRAKPIILRPSSAAFLVSMLEPDTAPSGYAVYGGRAFNLCEADLHARRALRAHSCQAVYAEARILKITTEIQTGRVFAAKLSNGSVFPYGIH

SEQ ID 3939

SEQ ID 3939
TTGGCCCGGTTTCGGCAACAACCGCGCCCAAGGTACGTTTCGACTTAGGGCAACGCTTCGGCGAAAAACAAGCATTCGGCGTTCGCTGCCAACGGCAAACTGGCCACGGCGACACCCCGCGCC
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CGACGATATTCAAAACGCGCGGACGCTTGTTCGACGCGCCGACGGCAAAATCAACCTGCTGCCTTCTTGGAACTGGCAAAATACCGTCGGCGAAACCAATATGCTGACGTTTGAATGG
GATCGGTTTGACAATACC

SEQ ID 3940

SEQ ID 3940
LARGFNRAQGTFDLGQRFGENKAFGVRANGKLRHGDTPRHGYREDNKEFALNADYRGEKLRVTFDSIYAKRKINGGRARMQDIQAGGRLFDAPDGKINLLPSWAWQNTYGETNMLTFEN
DATA

SEQ ID 3941

SEQ ID 3941

GTGGTATTGGTTGGCAGCCATGCAAGTTTGGGTTGGCTGCTCGCACCGCTTGTAACGCCAAACGGTTGGGAAATCAGCGTACCGTAATAACGCGCTTTGGTTGTAGCCGATACCGCCGTA
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CGCGCGCGTTTGGATATCTCGATACGCGCGCGCGCGCTGTGATTTTGC GTTTCGCGTAGATGGAGTCGAACGTCACGCGCAGTTTTCGCCCGGATAATCGGCATT

SEQ ID 3942

SEQ ID 3942
VVVVGSHAGFLAARTACTANGWGNQRTVITRFVVDATAGNLGIVKRIPIFKRQHIGFADGILPVPRRQQVDFAVGRVEQASAGVLDILHTRAAAVDFAPRVGDVERHAQFFAAITGI

SEQ ID 3943

SEQ ID 3943

ATGGCTGCCAACCAATACCAACACCGGCACGGCAGCGCCTGACCGACCAATATTTCCGTACTTTGAGTAGTAACCTGACCGCAGCGCGGAATTTGAAACCGGCCCGGTACAGCATAACTGGA
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CGACTATCCCAATCTTTGGCGGAACCTGCGGCAACTTGGATGCCAATATCAAAGTCAACAGCTTGGCTTTGTCGGGATACTTTGGGCTTCGTTGATAACAAATACCCCTGACTTTGGGCGGA
CGTTTCAAAGCGGTTGAATACACTGATTAAGAAGAAATACAGAGCGGGCGATGCCAAACGTTTCAGCCCGATGCTGATGCGCGCGTGGGTGCCCAACCTGATTGGTCTGTGTCGGCAACT
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TGCCTGTTAACGCGGTACAAGTCGCCAACCCGCGCGTGATTTCGAACACAGCGCTTGAACCGGATACACCGTTTGCACAAAGGTTTGAGCTTTGAACGCGCAATGTTTCGTATTTCCGCAAGTC
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SEQ ID 3944

SEQ ID 3944
MAAQYHYPTGARLFDQYFRTLSMNLTARGETFETGPVTHNWSTAFDRVIRQKRTINGSGNGNSKIEVKANENTIANQASPKADYPNMSWANSANLDANIKVNSLALSDDTLGFDVKYFLTLGG
RFQAVSYTDDKKKSGSDAKRFPSPMLMAAWVPQDPLVCGNYMEDLERADIKTDSSGETTMAKPRVSRQFETIGVRKNWGDVPTTLNAPQIKRPGYWRGNTKKGTDFAAAYKAAGGAAGDEQGN
ERNRGIEFNAYANLNLNKLRTLPFGVMYLIQSSYQNPARNRMLVNGVQVANPRVIVKTKVERDTPPAKGLSLNGVNSYPGKSYQDTQKQYAFPSYTLVDVGARYKTKLGNTLTVSSSVENL
FNKNYWOVORGQDRSFVAVGLPRTYWNLKAELDF

SEQ ID 3945

SEQ ID 3945

GTGAACCGCTGCGAGACTGACAAACCTCCCTTGCCGCTTGCGCCGTAGCGCGGTCGCACTCATACAGCCCGCCCTCGCGCGGCACTGGCGCAAGACCGCTTCATTACCGATAACACCC
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SEQ ID 3946

SEQ ID 3946
VKPLRLRLINLLAACAVAAVALIQPALAADLAQDPFITDNTQROHYEPGGKYHLFGDPRGVSVDRTGKINVIQYTHQMGNLLIQQAIIQGNLGYTVRFSGHGHHEHAPFDNHAADSASEEK
GNVDGDFTVYRLNWEGHEHPADAYDGPKGNGYKPKTGARDEITYHVNGTARSILKINPTDTRISIRQRLFDNYNNLGSNPSDRADENRKMFEHNAKLDRWGNSMEFVNGVAAAGALNPFISA
GHALGQDILDIYGRTRAYDKAAMRNTPAPKAGFKPAIIGGLGSAAGFEGKQTRAVDRWIQENPNAAEIVALVNVLPFAKVKNLTKAAKPGKAIVSGDPSKSYTCSFHGTSITLVKTADGKYAI
AHIQAGDRLVLSKDEASGETGYKPVTRYAGNPNFYQETVYIEVSDGIGNSQTLISNRHIPPYSDGKWIKAEGLKAGSRLLSESQKPTVVRNIVVKPKPLKAYNLTVADWHYTVFKGDKAETEGV
WHNDPCPTKLKPTERYNRQTHYGGSGTGDGARAQAARQAGEGKPCPTCGRIQIFGTKTAPSQHEPPLVKHYIEHGGHSMNADRAKHARESISQTCQLTCQKEGAMMSRYSRQAKKHGL

SEQ ID 3947

SEQ ID 3947

TTGTTTGAAGTGTGAAAAACCTTTGATTTTCAGTTGCGGCAGTATTGCTCGCGCTTGCTTTGGGTACACCTTATTATTTTGGGTGTCAAAGCAGAAGAAAGTCTGACGCGAGCAGCAAAAA
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TGAGGCGGAAGCGAGCAAGCAAGTTCGCGATATTGAAATGAACATTGCGCTGATGTTGGACAGTACGGTCCAAAGTATGGCAAGGAAAAATATCTTACTTTAGACGGGTAATCAGATTGAT
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SEQ ID 3948

LFVEMKKPLISVAALLGVALGTPYYLGKAEESLTQQQLKQKTGFLTVESHQYDRGWTSTETTVIRLKPPELLHNAQKYLNDNLKIVLEQPVTVLWHITGHPFAGGFGTQAHIEFEKY
APETEKVLERFPKGQVPSLANVYFNGSGKHEVSPAFDYERLSGIRLHWEGLTGEBTVYQKFKSYRNSYDAPLFFKIKLADKGDAAFERAHFDSSETSDGINPLALGSSNLFLKFSLEWK
EGVDYNNKLNELVNLVTDLQIGAFINPNSIAPSKIEVGLAFSTKTGESGAFIDSEGRFRDFTLVYQDEKYGPLDIHIAAEHLDSALTVLKRKPAQISAKMTEBQIRNDLIAAVKGD
SGLFTHDFVLNIKIPKFTLPQKIDVGGKINFKGMKKEDLNQLGLMLKKTETANIRMSIPQKMLDLAVSQAGNIFSVNAEDAEARASIASIDINETLRIMVDSVQSMAREKYLTLGNDQID
TVISLKNALKLNGKTLQNEPDPDFDEGDMVSGQPH

SEQ ID 3949

ATGGAATTCGGACGGGATAGGGGAACATTGAAATCCAGTTGAAATCTGTTATTGGAAGCATGGAGGAAAAATAAAGGCTGTATTTTAATA

SEQ ID 3950

MEFRDRGTIEIQLKSVIGKHGGKIKGCILI

SEQ ID 3951

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CCGAAACCGCGCGCATCATCGCGCGCGCATTTGCTGCTCGAAGCGTGGCGCATGATCGCGCAAGTCTGCTTTCGCTATCGAATGGGCTGCGACGCGCGCAGACATCGCGCAAAACCATCA
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SEQ ID 3952

MALVELKVPDIGHENVDIIAENVVGDITIAVDDTLITLETDKATMDVPAEAVGIVKEVKVKGDKISEGGILVVVEAEGAAAAAPKAEAAAAAPAEKAAAPAPQAAQFGGAADAEDVDV
VLGGGPGGYSAFAAADEGLKVAIVERYKTLGGVCLNVGCIPSKALLHNAAVIDEVRLHAANGIKYKPELIDIMLRAYKDGVSRLTGLLAGMAKSRKVDVIGDGGFLDPHLEVSLTA
GDAYEQAAPTGEKKIVAFKNCIIAAGSRVTKLFFIPEDPRIIDSSGALALKEVPGKLLIIGGGIIGLENGTVYSTLGSRLDVVEHMDGLMGADRLVKVWQKNEYRFDINMVTKTAV
EPKEDGVVYTFEGANAPKEPQRYDAVLVAAGRPNKGLISAKGAVAVTDGRFIEVDKQMTNVPHTYIAGDIVGQPMALHKAHVHGHVAAENCAGHKAYFDARVIPGVAYTSPEVAHVGE
TELSAKASGRKIKANFPMAASGRALANGCDNGFTKLIFDARTGRIIGGGIVGPNGGDMIEVCLAIEMGCCAADIIGKTIHPHPTLGESIGMAAEVALGVCTDLPPQKKK

SEQ ID 3953

GTGAAGATGCAAGTTTACGCCCATCAAATGAAACAGATCTATATGACGATGTTATATATCTACGACAACAGCAAGAAATTTGCCAAGAAATTTGCAACAGCTCCCGGCATCGAAATG
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TATCTCTGAAGAGTGAATTATGCTAAGAGTGTATAGAAATTAAC

SEQ ID 3954

VKNVAVAHQIETDLYDCYISTTTDKELAKKFATSSGIENGYIYVLRDLFGQYSIFEYVEHPENPDEKEVTIRAECCGICEEVIIAKELIEIN

SEQ ID 3955

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SEQ ID 3956

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SEQ ID 3957

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GCCGTGTAATCAAAGTTGGCGACACCGTGGCGAAGCAGCAGCTGATTACTTTGGAACCGGATAAGCGGCAATGGACGTACCTTGTACCGCTGCGCGTGTCTTAAAGCGGTATCT
TAAAGTCCGCGACAAAGTGTCCGAAGGCTTGCCTATTCGAAGTGAAGAACCGCGGCTTCCGCGCAGCAGCTCTGCGGCTGCGGCTCAAGTGGCGCACCGCGCGCGGTGCTTACATC
TGCGCACCGCGCGCGGTGCTTACATCTGCTTGCCTGCGCTGCCAAATCGATGAAGCGGCTTTCGCCAAGCAGCAGCGCGGTCTTCCGCGCAGCAACCTGCGCGCGCAATTTGGCGTG
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GGTGGTGAATCTCTACGTTACCGTACACGAAGAAGCGGATATGACCGAATGGAAGAAATTCGCAACAGCTGAACAAGAAATGGGAACGCGAAGCGGTGAACCTGTCCTCCGTTGCGGTT
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CGCGTCTTTACATTTCCAGCTTGGCGCGCATCGCGGCAAGGTTTACCGCGATTTGTGAACGCTCCCGAAGTGTCTTGGCGGTGTGCAAAATCCCAATCAAACCGGTTTGAAG
GGCAAGAGTTTGGCGCGCGCTGATGTCGCGGTGAGCGTCTCTCGACACCGCGGTATCGAGCGTGGCGCGGTATGCGCTTACCGCTATCTTGGCGAAGCTGTTGAAGACTTCC
GCCGATTAACCTA

SEQ ID 3958

MSIVEIKVPDIGHENVDIIAENVKAGDTIAVDDTLITLETDKATMDVPAAGVVKVVKVKGDKISEGGILVTVETGAAAAEAPAAAAEAPAPAAAGGATVQVAVPDIGHETDVIDI
AVEIKVGDVFAEDDTLITLETDKATMDVPCTAAGVVKVFLKVGDKVSEGSIIIEVETAGSAAAAAPAPAAQAAAPAAVPTSAAPAAVPTSPASAAKIDEAFAKHAHGPSARKLARELV
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IIRASVSALKAPPEFNASLDGDLNLVKNYFNIGFAADTPNGLVVPVIRKVDVQKGLKQISQELTELSKAREBKLPQEMQGACFTISSLGGIGGTGPTIVNAPEVAILGVCKSQIKPVMN
GKEFAPRLMCPISLSFDHVRIDGAAGMRPTVFLANLLKDFRRTIL

SEQ ID 3959

ATGTCCACCAATACACGATGTTGACCTATCGAAACCAAGAGTGGCTGACGCGTTAAGTCCGCTCTCGAATATGAAGCGCGGCAACCGCGCAATACCTCTTGGAAAACTGCTCA
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CGCATTCGTCGCTGGAACCGCGCGCATCTGATTGCGCGCGCGCAAGAAAGATTGGAATGGGTGGGCACATCGCATCTTCCAACTCGCGCGCAACATGACGAAGTGGTTTCAAC
CACTTCTGGAAGCAAAAGGTGAAGTGAAGAGCGGATTTGGTCTTCTTCAAGGTACGTTGCCCGCGCATCTATGACGCGCATTCGTCGAAGCGGTGACGGAAGACCGACTGA

[illegible]**SEQ ID 3960**

EQ ID 3960
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 HPFKARGCEBEGDLPVFPQGHVAPGIIYARAFVYBGRLETFEQLNNPQFQEVGDHGLSPSYPHILLPDFWQFPTVSMGLGPIMAIYQARFLKYLESRGLAKTKGRKRVCFQCGDGEWDPEPESQALIA
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 POKVYNYADRAANHADGKPTVILAKTIKGYGNGASGEGQVNAHQAKMKDKASKQFDRDRPITVPTEDEQIESGLDLPYLTFADPTEEYKYLHARRDALGGYLPQRKPTQEVLEVPELSAFDAQ
 LKSSGEREFSTTMAFVRIILSLFKDKKIKGRVVPVVPDESRTFGMBGMFRQYGIWNPKGQQYITPQDKQLMFKYESVDGQILQELBNEFGAMADWIAAATSYANSDFAMI PPYIYYSMPGF
 QRI GD LAWAAGDMHARGFLGGTAGRTTLNNEGLOHEDGHSHIQADLI PNCVSYDITPQYEVAVIYQDGLARMYANNEDWYPIITLNNYTHYTHPDMPEGAEO DILKGWYLLKAGGKDKKY
 QLMGSGTILQEVIAAGIELKADFGVEADIWSCP FNLLHHRDAIETERFNRLHPLEAEKVPVFTSQLQGHDPVIAATDYIRSYADRIIRATIPNDYHVLGTGDFGRSDSRANLRFFFEVDKY
 NVVAALAAALAEQGVKSKETVQQAIEKYGIKADSAPSWKR

SEQ ID 3961

SEQ ID 3961

TCGCGCCAAATGCGCTTCAACATCTTTGACCAACGCCGGGCGCTTTGTATATCAATCCGCTGACACTGGACGCCGGTCGTGCCAAGCGGATTTTCTCTGCGCGGTCCCGGCTTCCATA
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CGAGTCAAAACAGGATGCGGCGGGCAAGTGGATACATGACAGGGCTTTCTGCTTCAGATGGAAATGCCGCCATTTTAAACGAAATCCGCGCAACATACGCGCACAC

SEQ ID 3962

SEQ ID 3962
SRQCLQTFPFDQRRAPVYQSAVHLDDGGRQAQDFLCRVPAPFHNAAYADNRQCAVYVFPQFQHPVAFFAHGKTAQTALLACERMAAEA*FVDGGVGSDDAVPFDGFDGADGVDFLCFTQIGGD
FDG*RDIPAVGGGKLRLPVQGFQEQCAQFAAALQRAEVFGVGRGNVDGNAVCVRVGF*FEAD*IIIGVLDDGRNRVFDADVQAYALIFAFNIAIYHRVDAVVVTKHSVDDALVFGNAEERL
RVAGLRVARNRADDPEAEATERAQSDVDPVTFVETCGKPDVGVQIHTHQFYRFGTVVGYGNQAQFINRVERVEREVVGF6IGCKQDAAGKWIHDRAFCFRWKCRHFNNRNPAKHTAH

SEQ ID 3963

[illegible]

SEQ ID 3964

SEQ ID 3964
MPSEERRCGIKVPPPPCIDSGAEKDICLPPARFRNAGIRQACGAADGRAFFVHNSTFVPVAMPSEBQYRQASRNISNQGNIMSLQNIETAFENRADITPTTVAPEVKEAVLETIRQLDSGX
LRVAERLGVGGEKVNENAKKAVLLSPRIQDNEVLNDGVNKYFDKVPKTFADWSEDEFKNAGFRATPVGAVARRGSGFVARNVAMPSPYVNI GAYVDEGAMVDWATVGSQAQIGKNVHLSGGV
GIGGVLEPQAAPTILEDNCFIGARSEIVEGAIVEGGSVIMSGVFIGQSTKIFDRTTGETIYQGRVPAGSVVWSSGLPSKDGSHSLYCAVIVKRVDQAQTRAKTSVNELLRGI

SEQ ID 3965

SEQ ID 3965
TTGTTTCGGTTTGATTAGAAATTTTCGTTTTTCGCTTATTATTTTCACAAACGAAATAAAGGGGTGGCTACACCCTCCCTTCGGATTAAACACTCAACA

SEQ ID 3966

LFRFDLEIFVFAYYFSQTKIKGLATPSLPIKHST

SEQ ID 3967

SEQ ID 3967
ATGTTTTCAAAAATTATAAAGCTTGGAAAGCAAGGAAAACCTGAAAAAAATGTTCCGGTCTGCTCCGACGAAATCCTATCAGCAATCGGGTCTGCTGGCAAATAACCATGCTTTTAA
AAGCAGGTTTATACTGAAGTTGGCGTTTGGTAAGGACAGGTCCTTTT

SEQ ID 3968

SEQ ID 3900
MPSKNYKSLGSKGLEKKCSVCSARNPISNRVCWQITMLLKAGFILKLAPGKDRSF

SEQ ID 3969

SEQ ID 3969
GTGGGATATCGAATCGTTATGCTCTGTCGGCAATTTCTTATTCAGAAATCTATACACAAGCTTTGTGGACAACCGTGTGATAAGCCACGGCTTGTGT

SEQ ID 3970

SEQ ID 3970
VGYRIVMSLSAIFLLQKIYTQALWTTVLI SHGLC

SEQ ID 3971

[illegible]

SEQ ID 3972

LEVGAKPAFFALQSPADLLNLPLVWKNTPFMASQFFISTLKEAPEAAFAASHKLMIRAGLIKANASGLYTWMPGLRVLVRKVENVVREEMARAGSVELLMPVQPAAELWQESGRNEFTGKE
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AESGDEVIAYSDTSYAAINIELADPTLPLKGERAAQAQVLTIKVHTPNVKTIESLVEFLNIPVBQTLKSIIVGEBENBELVILLRLGDHPEFNDIKAEKLAGVSKPLTHASGPAIIVEFGFANGG
SLGFGVGTGKVVYDAFTEKGADWVIGANEDDYHTYGFNFRGDAEAEPFDLNRNVEDESPDQGRLLKARGIEVGHVFPQRLGKTYQVKNVNSFLDNNGKSGTOMHEGCGYIGITRVVAAATE
CNDEKGIITWFKAMAFPEFVTVPMNYKXSTVRRAADRIYAEELAAAGADLDDDRERAGVGLNDESELGIPHRITVIGDRALKEGNVYEAERRGNEAQAVAIGRIVARVTASLNA

SEQ ID 3973

TTGGGGGAAAGTGAAGTGGCTTCAGTATTTTAGAAGGAGAAGCAGTCGAGGTCGGCAATATTTTCTGTATCGGCAGGAACATATGCGGCACATATGCGAAGAGTTAAAAACGAAATACCTT
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CTGAAGGCAAAAGGGTTACAGGCAATTCCTGCGTGCCTGTCTGGATTTTGCCTGGCGCAGACAGAACTCGGCAATCAAGATAAGGTGTTGTTTTCATTAAAACAAACCGCGTATTGAACAGCGCG
GGGAGACCTGGTTTGATGATTATACCGGATTTCGGGAAATTTTACACAACTGGCGGGCGGATTCAGGTTTGGGGAAGGGGATTTGGTGTTTACCGGAACGCTTCCGGCGTGGGCGCAATTCGG
TGCGGGGGACAAATTTGGCAATTGGAGACTGGACGCTTTGGTGTCGCCCTTTTACAGTATAGGGTGT

SEQ ID 3974

LGSEVASVFLGEAEVEVGNIFCTIGRNYAAHVEELKNEIPSEPVVFMKPSGSIILSSGGTILLPEFSRDVQFCECLVLLIGRDSDGTGEGEDILGCVAGYGVGLDLTARDIQCRKAQGLPW
LKAKGRFRHSCVSDFAAADRI GNQDKVLP/SLKONGVLKORGETGLMIYPIRETLHLKLAADYGLKGKDLVFTGTPTSGVGAIGAGNDLALBLDGLVCASFTTGC

SEQ ID 3975

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CAAGTTTGGACGCAAGGCTGAACGGCAGGTTCAATCTCCCGCTATTGGGTTGACGAACGGCTGTCTGCTCGTCTGTGCGCAAGACCTGCTTTTCGGAAGCAGAGTCTTGGGCAAAAAACGC
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SEQ ID 3976

MHKIPGKTALAFDFGEARIGVAQGDARLGLSHPLATVITGGSNDEKFAAIAKLQVEWQPRYTVVGLFVHADGTEHEMTHLSRKFGRRILNGRFNLVYVWDERLSSVCAESLLSEAQVLGKKR
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SEQ ID 3977

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CTTGAACCAAGCTTGGCGATTGCCCGGAATTTTCATCGTGTGCTCGCGCGGTCACCGGTGCGCAGCGGATGGGACAGCCCCAATTCGCGATTCGCCCTGCGCCACGCGGATGCGCGCTTCGCGC
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SEQ ID 3978

VQDGLRRHLVHRFAFFAQDLCFRKQAFGPDGRQFPVNPIDGEIPEAVQPSKLARQVHRHMFRAVGMHGQSDDKITRLFPFLNQLGDCREFFTVAAAGNGGQRMHQPOQFRIALRHADARFA
EVBCCRSFPMNEMHGRI.PKTGAGRCVVRMRRRRGVRRCRTGCVRRRERSATHCROVVRVAALCSSNSLNC

SEQ ID 3979

ATGACAGCTGCTCCCAACCACTTTCTCGTCGCCATGCCGATATGGAAGACGCGTTTPTTTCACAATCGGTCGTCTATATCTGCAAAACAGATGAAGAAGCGGCACCTCGGTATCGCCATCAACA
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CCACACTCCGATCGGCAACTGCGAAAGCAGCATCGGCGGTTTCAGACCGCATCGCGCTCACTCTCTCCCGGATGTGCTTTGAAAAACATTTACGCGGAAGGCGCGGTTGACAAAGCCTTGATC
AGCATAGGCTATTTCGAGCTGGAGCAATAGGCGAGCTCGAAGCGCAACTTCCGACCAATGCTGCGTGGCTGACGGTTCCCGCGGACGAACACATCTGTTTCGACATCCCTACGAAACACCGTTACG
CGCGCGCTGCTCCCAACTGCGGCAATGACACCGCTCGCCCTGTTTTCGGGAAGCGGCGATCGCA

SEQ ID 3980

MMLSNHFVAMPDMEDAFPSQSVVYICKHDEGALGAIANKPSPITMDHIFSATGKNIPMRHQHDSVMMGFPVQVERGVVHTPIGNQSSIGSVSDGIALTSSRDVLENTSRREGAVDKALI
SIGVSSWSKGOLERELADNAWLTVPADHILFDIPYEHRYAAAFKLGIDPLALFSGAGHA

SEQ ID 3981

ATGAAAGACCTCGCTCCTCTCATCGCCCTCGTACTCAACGCCCTGCGGCACACTGACCGGCATACCGGCCACGCGCGCGGCAACAGCTTTGCGGTGGAACAGGAACCTGTCGCGCGCATCGT
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CGCACTGATACGCGCGCGCTACCAACAACCCCGACAGCGCCACCCGATACAGCTACCCCGCCTATGACACTACCGCCACCAACCAATCCGACGCGCTCTCGCGCGTAACCACTTTCACA
TGGCTTTTGAACGCGCCCGCGCGCGCTGACGAAACAAACGGACGCAAGGCGAAGCGCTCGCGCGGACTGTCTCGTCAACGGCAACGCGGCGACTACCGCAACGAAACCTGCTCGCCAAAC
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CGTCCGCGAGCGCTCCAGCAACTGCACCTTACAGACGCCAAAGCCCTTAAAGCCCAACCAAGCTCGAATATTCTTCGCCCTCGACCGCGCACCGCGGAAACTGCTGATTGCGCCCTAAACACGGC
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ACCAACCGCCGCAAAACCGCTCGCGACTTCAACAAACAAACCGGTAAACACCCGATGTGCGCAACGAAGTCATCCGCGCGCGCAAGGAGGA

SEQ ID 3982

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SLNAPAAAL/KPNNGKRGERSAGLSVNGTGDYRNELTANPRDVSFLTNLIQTFFVYLRGIEVPPYADTDVFTVDVFGTVRSRTELHLYNAETLKAQTKLEYFAVDRDSRKLIIAPKTA
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SEQ ID 3983

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SEQ ID 3984

VRPSKQSKPCLRPENGSDTKETLMNRLLLLSAVLTACGSGETDKIGRASTVFNMLGNDRDIEVEGFDPDVQGVACYISYAKKGLKEMVNLLEADASDVSCVQTASSISFDETAVR
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SEQ ID 3985

GTGTCGGAACACAATATCCGTGACGATGAAATATGCGGCACAATATAAGGCTGTTTGAGCCGATTGCAAGTATCCGCGCAAGAAGGTGCAAGATTGGGCAACCGCATTTTCAGAC
GCATAAC

SEQ ID 3986

VSEHNIRCSIENMHPNIRLFEPIASIRAKVKQDWANGIFERHN

SEQ ID 3987

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SEQ ID 3988

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KAHGKPVSGSKENAKTQFENKQKKGAKGQPRKGGAKBKDTVSANKKARS DNKGAVKRDKKHTEENKAKTDSDELKAAVAATNDVENKALLKQSEGMLLHVSNLSKQLQBEERIRQ
ERIRQERIRQARGLASVNRKQREAWDKPQKLNTEFELNRLKTEVAATKAQISRFVSGNKNRPNALVLFKNAEPGQKRNFLRYTRYVNASNREVKDLERQKALAVQEQKINRELARK
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DGFSRMQRLLKKEVDFGVPGLFGQNRSGGDVWKGVPYSTAPATVESIAPGTVSYADELDGKGVVVDHGENYISYAGLSSEISAGKGYTAAVAGSKIGTSGSLPDGEEGLYLQIRYRGQVL
NPSGNIR

SEQ ID 3989

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SEQ ID 3990

LPFAVVFSGFWKSRKVKBCRNLLPKRSHFILWVQSAANP

SEQ ID 3991

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SEQ ID 3992

VSDQVRLAFAKSTPLIFYPDI GNNPLCLNGTVVRVIOGGRQLDRAAVGQRNQSINRTTREALRDDRAFVVLQ CAGDNLRRGSRGTGIDQYRHRNRFQ LGRNTRQVAANTVHI ILGNF
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RITLAGNFAQTGIDADVLAVIDHDFAVAVQLVRLIAYRSRRNAPNRCRRSLIEHAFNIAAFLVPEKPGRHVTNRFPQTSLHAASTVGTADTNRRLDLVVPVGGQVGHFRTSRFSL
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GVYITRITQKAVLFRPGVFPQEGNRIRPAVFIIVRYETGNLFRSGDFRPTQVLGIFLEFVPSLALFAVDGSKVAARLTDTLLADTFLADTFLKLFEGDIADMKQHSFALFEQGFVFP
DIIGSGNGGPFQVIGFGLFPLKVFVFLPHCFVNLVGTGPFICRNSVFRILAALARIALSPPFFALFVFLRCVFFPGSGHGLAMCLFVFLRLIIPASFAARRLPGRLLLCFFAVF
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SEQ ID 3993

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SEQ ID 3994

LGASGVAVSLAVQFAAEKGRDNEVLFPVQSIRTAIEVYQIKANYTHDKPDADLFEGAMKGMVAGLDPHSEYNDKKGVAEIKESTSGEFGGLGMEIGQEDGFVKVSPIEDTFAERA
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GVSAALFPEAVVSTKRGDKGMLKAVPEYVYMGGDPLAGI PAELKTI PMTVLVNSGSASASEI VAGALQDHKRAVIVGTQSPFGKSVQTLPLSNGSAVKLTALYTYTPNDRSIQ
AQGIUPDVVEKDKERTFESREADLVGHIGNPLGGEDVNSEPLAVLEKADPAKAEKGGKKKEDLSRRRI PNPAKDDQLRKALDLVKSPEQWQKSLGLAAKRPVSNKDKDKK

SEQ ID 3995

ATGTCAAACATCGAACAAAGTTAAGAAATTTATCTGAACAACTGGGCGTAAACGAAGCGGACGTGAAAAACGAATCTTCTTCCAAGACGACTTGGGCGCGGATTTCTTTGGATACCG
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SEQ ID 3996

MSNIQQVKKI IAEQLGVNEADVKNSSFODDLGDASLDTVELVMALEAFGCEIPDEDAEKITTVQLAIDYINAHG

SEQ ID 3997

TTGTTCTTGTATTGGGATTCTAGGCGCGGTTTTAGGGGCAATCAGCAGTTTCCGCTGTGCGGTCGAGCGGCAATATTCGAGCTTGGTTTGGGCTTTAAGGTTTTCCGCGTTGTAG
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CGGCTTTACAGCGCAATTTTGTGTTGCTGTAC

SEQ ID 3998

LFLVLGFGGFRGNQFPAVAVDGEIFELGLGPKFGVVEVQFTAADGAEYVDGYEYGVGVFGYDFDAAQVEDGLDEVQEGNVAGVGEQGFVAVVARVDQSGGAFAPASVVRQ
GGGGVQKRCSSGYAGERVGPGGGSGVIGGAVSGGAVGVVVAAYQCVDGVASAAYVARTLVARNGDVKGGFASFGQGVHFFDGGAGRCDEFLPDGKAFAAVGGYAGQCAAGGEYE
GDEEBQGFHGRVCFVNGFECKWILRVCKRCKWCRNLNGRAGFTALFLHL

SEQ ID 3999

ATGGACGAAATCTGCCGCTGAACGGCTCGAGCGCTTCGACGACATTCGCGGCGGAGGTGCGATCCGCTATGCGGATGTGACAAAAATCCGCAATCCGTTTTCCGTTATCCCTGGA
TA

SEQ ID 4000

MDGNLPSERLERLHAHCRPEVGSAYADVDKIRNPFSGYPLI

SEQ ID 4001

TTGACGATGCGCTCTGAAAGGATTTCAGACGCGATATTATGTTTGAAGGACAGGTTATGAGCGATTTTTTACCAGAAATTTGAACCGTGGCGCAATTTATAGTGGATTAAACAAAAATCAGGA
CAAGGCGACGAAGCCGACAGATACAA

SEQ ID 4002

LTPSERISDGLCLKGQVMSDFLPEFEPGIIYSLTKIRTRRSRRQYK

SEQ ID 4003

ATGGAAGTTATCCGATACCCAAATTCCTCTCAAACTCCACCAACCTTCCGCGCGGAGCGGACGAGCCACCGCATTTGCGGCGCTGATCGAAGGGCTTTGACAGCGCTTGCCTACC
AAACCTGCTGCGGTAACCGTTTCGGGCAAACTTACAGATGCGCAAGCTCATGCGCAAGCGGACGAGCCGCTATCATTTGCGGCAACAAACCTTTCGCGCGGAGCTTTATGC
CGAAATGCGCGAGTTTTTCCCGCAAAACGAGTGAATATTTCGTGCTGATTACGACTATTACGAGCCGAGCCTATGTGCGGACCGCGGATTTGTTTCATCGAAAGACAGCGCGATC

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SEQ ID 4004

MEVIRYPNSTFKLHQFPFAGDQPTAIALGLIEGLSDGLAYQLTGLVTSKGYTYMANVIAQSGRPAIIMAHNKTLLAQLYAEHREFFPENAVEYFVSYYDYQPEAYVPSRDLFIKDSAI
NEHIEQMLRSATKNLMTDRDDVIVATVSAIYGIDPTEYQOMVLSVKEGDTIEQRDIATLVSMQYERGLDFKRGSRFVRGVDIVDPYAESSEALRISLFDDEIDRLIMFDPLSGSLHQ
RVGRYTVFPSSHVTPRDFVLRACESIKEELRERIEFFAREQRPVEQRIEQRTRFDLEMLYEMGFCKIENYSRHFSGKKESEPPTLMDYLPDNAMEFIDESHVITVTQIGMYKGDASR
KQNLVDVGFRLPSARDNRPLKFHEFEKVMPTVFSATPAKYEEHAGQVVEQVVRPTGLVDPQTIRPVATQVDDLMSEINDRIQKGERVLVTT/LKRMABQLFDYVSELGKVRVLSHD
IDTVERVEIIRDLRLGLFDVLVGINLLREGLDIEVSLVAI LDADKEGFLRSHRSLQITIGRAARNVNGVAILLYADKITDSMAA VDETERRREKQIKFNEEHGIVPQIKKQVKDIDGV
YHEEDSGKRRQGNKVKVGEIHNEEDAIKEIAKLEKAMQQAARDLQFEAAVLDRISNIKENLLFGAE

SEQ ID 4005

GTGCGCACACGCTATGTATTACAGGCTGCGATTACTATTTCAAAATCACTCCGCCCAACAAACAANTCTCTTAAATATGCTAATCTCTCAACACAGCAGCTTCTTCAAACTG

SEQ ID 4006

VAHTLCIQAAITISKSLRPKQQLLFNIANPFIQHSSFFKL

SEQ ID 4007

ATGCCCTCGTTTCCCGCGCACTTTACCCCGCTGACCGCTGTCTGCTGTGCGCTGTACCGCTTCTCCGCCCGCACACGGCAATCACACCCATTTGGGGCTATACCGGACACGACTCTC
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CAGCCTCTGAATGCACGCTGTATTGAA

SEQ ID 4008

MPRPRTTLRLTAVLLACATFASAAAHGNHHTWGYTGHDSPESWGNLSEFRLCSTGKNQSPVNITETVSGKLPALKVNYKPSMVDVENHGTIQVNYPEGNTLTVNGRTYTLKQFPHV
PSENQIKGRTFPMBAHFVHLDENKQPLVLAVLYEAGKTNGRLSSIWNVEMTAGVKINQPFDASTLLPKRLKYRFAGSLTTPPCTEGVSWVLKRTYDHIQDAQAEKPTRAVGSENRRV
QPLNARVVIE

SEQ ID 4009

TTGAATCGGATTCAAATATCTTGTGCGGCTATTATATATTTTCCGGAATAAGGTAGCCATGCCTCATGTTATCCAAATAAGCAGGACTTATAGAAAA

SEQ ID 4010

LNRIQISLLRLIFRIKVMFPHGYPNKAGLIEK

SEQ ID 4011

ATGACATATTTAAAGTAATAGCAATTAGTATAGTTTATACATTTTATTATTGCAATTAATCTTAAATGTTAGAAAAAGGATTGATTCTTAGTAGAAAAATAGATAAATATTACC
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AAGAATGATAAAGACTATACTATTTTAGTCATGGGTTTCTCATCGAAATACTATTTTTCATCTCACAATAAATAAAGAAATTCAAATTCAAATAAATATGAT

SEQ ID 4012

MTYLVIAISIVLYILLQINLKMLEKRIDFLVENIDKYQQYGSYPNDFPISKTFDFTESYCDFWDKNLAGYGNCFVKNDKDYTLVLMGPFSSKILPSSHNIKEFNSNKYD

SEQ ID 4013

TTGGGACTTGTATTCAACCGGATCGGATAACAGACCGCGGATAAAAAATGCCGTCTGAAGCATGTTTCTTACAGACGGCATTTTCAAGATAAAGCAGCGGGCGATTTTCAATAC
AAGTTTGAACAATGGTTTGAACGGCAAAACCGGTATACCGCACGCATCTTGTAGGTTTAACTGCACATCGGTTTAAAGTTTATTCGCGCCGCGAGA

SEQ ID 4014

LGLGIQTDRIITDRRIKKRLKHVCLQTAFFQDKAAGDVSIQVLKQWFERQKRVYTARILVGFNLHIGFKVYSARR

SEQ ID 4015

AACATCGAACAAAGTTPAAGAAAATATTGCTGAACAACTGGGCGTAAACGAAGCCGACGTGAAAAACGAATCTTCCTTCCAAGACGACTTGGGCGCGGATTTCTTGGATACCGTGGAGT
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CCGACACAACAGCCTCTGCTGCACCGCGCAA

SEQ ID 4016

NIBQVVKIIAEQLGVNEADVKNESFPQDDLADSLDTVELVMALEAFGEIPDEDAEKITTVQLAIDYINAHNG*FVVAREHNSLOCTAQ

SEQ ID 4017

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SEQ ID 4018

MKITHCKLKKVQKPLRSPVPEVTARSAADILGIHPSAALFYRKIRITVTHRLALADEVFERPAGPGGSCFGRRKRRRGAAGKAVVFGIPKRNRAITVAEDDAEPETLPPAVK
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SEQ ID 4019

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GGCA

SEQ ID 4020

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SEQ ID 4021

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SEQ ID 4022

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SEQ ID 4023

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SEQ ID 4024

MYTFQGTADYNKARKWFEQATSQKNSMAFYNLACIHYSGHGVKPD

SEQ ID 4025

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SEQ ID 4026

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SEQ ID 4027

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SEQ ID 4028

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SEQ ID 4029

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SEQ ID 4030

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SEQ ID 4031

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SEQ ID 4032

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SEQ ID 4033

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SEQ ID 4034

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SEQ ID 4035

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SEQ ID 4036

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SEQ ID 4037

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SEQ ID 4038

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SEQ ID 4039

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SEQ ID 4040

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SEQ ID 4041

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CAA

SEQ ID 4042

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Q

SEQ ID 4043

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SEQ ID 4044

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SEQ ID 4045

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SEQ ID 4046

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SEQ ID 4047

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SEQ ID 4048

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SEQ ID 4049

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SEQ ID 4050

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SEQ ID 4051

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SEQ ID 4052

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SEQ ID 4053

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SEQ ID 4054

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SEQ ID 4055

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TGCTGAACAATTCGCAACAGATGATAGAGTGAACATATAAAGAAATACGCTCTCCCGAAACGCGCTATTGTCGCGCGCGCTATATGAATATCATGAAGAAACGCACTCGCGCTGCA
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SEQ ID 4056

MVACLKFRQRSSNRKHGFRRLVLTVCISRCIITDLPNNKYTGAMTESITRDSMQYDVVIVGAGPSGLSAAIKLKQLABQNGREISVCVVERKSEAGHSLAGAVIDPIALNELIP
DWKEKAPLRTVTQDKVPLTEKAPNLPITPNFNDHNGYIVSLGEVVRWLABQENMGVEIYPGFAAEVLVHEDGSVKGATGMDGVKDGPTDSFQPMELNARQTLFAEGCRGSL
SKQIIEFQLDQNSQPTTYGLGKEVVEPSEQHGPGLVHSAGWPLDSKTYGGAIFYHFDNKNVAVGVVGLDYQNPYLSPFEEFQRFKTHPEIRKTFEGGRRIAYGARSILBGLQSLP
KLSFGGVLIGDAAGFLNMPRIKGIHTSMKSAMLAABAVPPLLENFEEVESDGGKAGNYQKLFEBQSWLYQELYAARNVRPSFKWGVYLSGLTYGIDQIMPRGKAPWTLKEHGRDNEQLK
KAAVCKPIDYKPKDGLVTFDLRLSVFLANLAHEENQPDHLVNNPQTMIDVNYKEYASPEYRCPAGVYIEENGSPRLQINAANCVHCKTCDIKDPTQNTWICPEGASGPNYGM

SEQ ID 4057

ATGAAAACCGCGACATCCCGCTGCGGGCGGCAACCGGACAGAAATCGGATGCGATTATACCTTATTTAGCGGCTGTCCCGCATTTATGCGCACACAATAAATCTGCAAGATATTGTT
CGCGGTCAAATGCCGCGCGGAGGTA

SEQ ID 4058

MKTADIPPAGGRDRICDYTLFRLSGIYAHTINLAGYCCGSNAGRRV

SEQ ID 4059

TTGTATGCCGCTATTATGCGGAAATACCGTTTGGGAGGAGTCGCATCGCATGAGTGGCAAGCGAGGCGATGCGCGGATGCTTCGGGCGTGAAGCGAGGAAATCGGAGTTTGA
AAAAGGCAATGGAATTCGCGAGTGGTGTGATTGGGTGTTGAAAGCAA

SEQ ID 4060

LYAGHYGGNTVWEAVASHVGVTAGDAPMPGKAGSAVWKKAMESAGRCRLGGERQ

SEQ ID 4061

GTGCGCCGACTTATTGCTTTTACCACCCAAATCGACACCTACCTCGGNTCCATTGCTTTTTCAAACTGCCGATTTCCTTGCTTCACGCGCGAAGGCATCGGCGCATCGCTGCGG
TGCGGACTCCATCGGATCGGACTGCTCCCAAACGGTATTTCGCGCA

SEQ ID 4062

VRPTCLSPNRLPADSIAFFQTADFPAFTPEGIGASPAVPTPCDASQTVFPP

SEQ ID 4063

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SEQ ID 4064

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VAFKTLHTGRQTASRPLPLGLTAVSTLFGAMSSWVGIGGSLVPLIHCGFPAHKAIGTSSGLAWPIALSGAISLVNGLNLAGLPEGLSLGLYLPVAVLSAATIAFAPLGVKTAHK
LSSAKLKESFGIMLLLAGKMLNLL

SEQ ID 4065

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ACGCGCTCGCGTGTTCACAGCTCATCGGCAAGGTGGACAAACGCTGTTTATCGCGGTAACCGAGTCCGCGCGCTGATTGTCGGGCTGATTGGGTCAACACAGCGCTCGAA
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SEQ ID 4066

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SEQ ID 4067

TTGCCCGCAATGCCCTCTGAAACACAGCGCTTGGCGCTAAGCGCGCAATATGAGGATTTCGCGCTGCGCAACCGGTTTGTCTACAAACCGGCGAG

SEQ ID 4068

LPAMPSENGLPLRRQYEDLRNRFPATTRQ

SEQ ID 4069

TGTGTTTCAGACGGCATTGCGGGCAACCTTTGCGGGCGGGCAAAAACCTTGTCCTPATATTTATCCCGCTTCAAANAATCAGCATACGGTCGGAATGCAAAAAATATCTTTCAATTTGTGTGA
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SEQ ID 4070

LFSDGIAGNLCGGRKTLSYNLSRFKISRSEMOKISFNLLKPTNSLKIGKYRPGNGAPHIPMPSLRYLPASAEMPGNNIHPAKSETTHPVAGRVKPPRKASAIRKTNRLRGLHPKGRIVR

SEQ ID 4071

ATGATGAAAAGAGATCTGGCAGTATCGGCATATGCCGTGATGACTCGGGCGGCACAGGCTCCGATACTTACGGCTATCTCGCCGTTTGGCAGAATCCGAGGATGCAAAACGATGTTTTGC
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GGTCGTGTCGTGAACAATACCTGTGTCTCGCTGGCATACCGAAAGCCTTGGCGCGATGCGCGTTGAAAACCGCGTCGTGATTACTTCTCCGCGTTTACGAGCGTTCATCAGGTGCGCA
CTCAACCAAGTGCATAAAAAATACGGCGCACAGGACAAATCGGGCTTGGAAACAGTGTATTGCAACGTCATCTTCTTATPACGGCGGGCGTGTGCTCTCTTAATCCAACACCTGAAA

SEQ ID 4072

MMKKILAVSALCLNTAAQAADTYGYLAVHVNQDANDVLQVTKEDSAKSEAFAELEAFCKGQDTLAGIAEDEPTGCRSVVSLNNTVCSLAYPKALGAMRVENAVVITSPRFTSVBQVA
LNQCIKKYGAQGCGCLETVYCTSSSYGGAVRSLIQHLE

SEQ ID 4073

ATGCTTACATTTTCAAGTAAATCCAAACAGAAATGCCGCTGAACGTTGAAGCCAAGGTCAGACGGCATTTTTTGTTCATAGGTTCAAACGGGGCAGGTCGAACAACTGCCCATTCCTT
ATTCC

SEQ ID 4074

MLTFSSKSKQKRLNVEAKVQTAFVIGSNGAGSNNCPYPYS

SEQ ID 4075

TTGAACCGATTGAAAGAAGATGGTATGAACCAACTGAAACTTGCCGTTTCCGGCGCGCAGATTTTATTGTGGCATTCCGGCGCAATGGTGCTGGTTCCTCCCTGCTGACCGGTCTGAATCCGGCTCTTTGCGCTTTTGGGCGCAGGCTTGGGAACGCTGCTGTTCCTCAATACACAAACGCAAGTACCGGATTTTCTCGGTTCTCGTTTGCTTTATCGCGCGGATATCTACTACCGTCCGCGAATGGGGGCTGCTTCCACCATGTCTCGGGCTGTTTGCCCGCGCTTTATGTATTTGTGTTTGCCCGCTCAGTCCGTTGGCGCGGACTGGCGGGGTACACAAACTGCTGCCGCGCGCTGTACACCGGCTTCATGTCTATGCTGCTGTCTGTCTGTTCCGCTGGCGGCAAGCAGCATGGCAATGGGTCAGTTCAGCGGCAACAGGTCACGACTACGAGTATCCCGATTCTTTCCTGCTTTCGCTTTGCGCTTACCGCCATCTGTATCGGTTTCCGACCTGATGAAAGCTGATTTCCCATCTGATCGGTGTGCTCTACGGGTTATGTTTGGACATGCTGATGGAGCTGCTGGACATGCAACACGCGCCCTGGTTCGCGCTTCCCATTTTGAAGACCGCTCAGGTCAACTGGCAGGCGGCACTGTTTATGCTGCCCGTTGCGCTGCGCCCCGCATCGAACCAATCAGGCGCATATGGCAATCGGCAATGTAAACGGGAAAGACTACACAAAGACCCGGGCTTGGACAAACCTTTGCGGGCGACGGCTTGGCGGTGCGGTTTGGGGTCTGATCGGGCGCCCGCGGTATACACCTACGGCGAAGTAACGGGTGCGGTGATGATTACCAAAAACGCAACCCCGCTCATCATGACTTTGGGCGGGCGTTTTCGCGCTCTGATAGGGGTTTTCGGCAAAATCAATGCGTTTTCGGCTTCCTATCCGATGCCCGTATGGCGGGCATTTATGCTGCTGCTGTTTCGGCACGATTGCTTCTTTAGGCATCAAAACCTTGATTGATGCCAAAGTCGATTTGATGCTGCCGAAAGCTCGGCTCATCGCTCAGCTCGGTATGACCAAGGCGCATCGCGGATGACATCTCAAAATGGGCAGTTCAGACTTTGTGCGCGTGGGCTTGTGCGCGCTACTCGCCATGTGTGTGAACAGCCTACTGCGGCATCCGGAAGATACC

SEQ ID 4076

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VTGPVIMVIGLSVAVAASSMAMQADGQVIDYDTSLLSGFTFAVTAIVSVFGSRMKLPIILIGVASGYVLALLMGLVDTTSLAHAPFWAFVPHFETPQVNWQAALFMLPVAVAPATEHT
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SEQ ID 4077

ATGGAGTATAATCCGACACTTTCATATTCAATCCGCAAGCCGTCOCGAACCCTTATTTTCAGACGGCATTTTCCGGTAATACGGCATGACAGAAAAATCCCA

SEQ ID 4078

MEYNPTLSIFNPOAVPNPYFRRHFPVIRHDRKIP

SEQ ID 4079

TTGTGCGCTTTCTTGTTGCGTGC GGACGTGTGGGACGGGGCTCCCGCCCTGCCTTTTGCTGTTTTTTATGGGATTTTCTGTCTATCCCGAAAAATGCCGTCTGAAATAAGGG
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SEQ ID 4080

LSAFLLRADVGDGLPALPFAVFLWDFSVMPYYRKMPSEIRVRDGLRIEYGKCRILHFSRHFHPATDRRCLSDGISLPDVCIFTOPGLGKPV

SEQ ID 4081

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SEQ ID 4082

SEQ ID 4082

MGLAATLTLYLAISLISIFDMGDPSPWSHSSPVEDAANWGGFLPGAYVADVGYTLFGWSFWWWIAAACVVLKYNFLHAKQTENEAYNHKIAAAALFVLTVFSPVLEYFVLGGKYADSLFVVGAGG
NVGIRVGAVFAMWLKGKSGSLILILVLLLSLSLIVQISWLEFLNLGAGRAVQNRILSALSGKVMALKKRRPPIITKTDGVDQNTNRMVKEAKNITAKPVALPEGSSNRSKVAVSVAPPPKIQP
SLFEDNEVQQNGEYHKPTLNLRLIPDESPVSNINPAELERTAEILTSLKLAEFIGIGVQVVSATSGPVITRYEIEPAQGVKGSQIVALSODLARSMSLSQSVRIVETIAGKNTWIGIELPNDKRQD
VMLSEILSSPFAEAKSKLTVALKGDIAGTPPVGDLAKRPHLLVAGHTSGSGKSVGVNGMTMSLFPKATPEEVRFIMIDPKMLELSYIDGIPHLLCPVWTDMREAGQALNWCVAEMEKRYRL
LSHAGVRNLEGFNQYKVEAKAGKPLINLPFSLNLDEPEPEKLPMTIVVVIDELADLMTTERKAVBQQIARLAKQARAAGIHMTVATQRPSPVDVVGTGLIKANIPTRNAPTQSKIDSRTILID
QMGADELLKYGDSLFLQPGSAEPTRLQGTFFVSDGEVHQVNVYKVSQAPADYITBGLLSCEAALETANIVNPNADSDELFDQAVAYVLESKRTSISSLQRLRLIGYRNAANLMEALENAGIVS
PSDLNGSRKILAHKDL

SEQ ID 4083

SEQ ID 4083

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SEQ ID 4084

SEQ ID 4084
MSTFFRQTAQAMTAKHIGFPLSELDQVIDWQPIEQYLIRQKTRYLRDRRGRPAHPLSSMFKAVLPGQWHSLSDPLEHSLITRIGFNLPCRFDGPGIPGCSTLCRYKRFYARAAYFGLL
KVGVSHLKAMCLNLLKAANRLSAPAAA

SEQ ID 4085

EQ ID 4085
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SEQ ID 4086

MRFKYRTVALFASPCREEGLSFYQH NKFKGL

SEQ ID 4087

SEQ ID 4087

ATGATGAGCGTAACTGTTGAAATTTTAGAAAACTGGAAACGCAAGATGTTGTGTCCTGCTTGGTGCCGAATCAACGCAGAAACCGATAAAAACTGAAACCAAAACCCACGCGTGCAA
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AAACTGAAGCCAGCTGAAGGGCAATCAAGCCGCTGTGCGCAACTTCGAGAAAGCTACGAAGATCCTCAAGAAAGTGAATTGACTGGTACTACCGAGATACTTCCCGCTGCAAGCCCGA
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SEQ ID 4088

SEQ ID 4088
 MMSVTEILELNLERKVVLSLFWSEINAETDKKLKQTRRAKIDGFRPGKAPLKMAIQMGASAQNDVINELVQRRFYDVAVAQELKVAGYPRFEGVEQDDKESFVAAIFEVFPSEVIGD
 LSAQEVEKVTASVGDAEVDQTVELLRQTRFRNHVDREARNGDRVIDFEGKIDGEEFAGGTSKNYAFVLGAGQMLPEFEAGVVGMGAGESKDVTVNFPREYHGKDVAGKTAVFTTITLNV
 SEPTLPEVDADFAKALGIADGDVAKMEFEVKNVSREVERRVNBQTKESVNALIKAVELKVPVALVNEEAARLANENKQNFVNQGMTDANLIDLPLDMFKEQABRRVSLGLILAKLVDE
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SEQ ID 4089

SEQ ID 4089
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SEQ ID 4090

SEQ ID 4090
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SEQ ID 4091

SEQ ID 4091
ATGACGCACACCGCATCGAAAAACCCAAACTCTGGGCGGTCAATTGCCGCGCCCGCATTCATCTCTGCTGATTACCATCGGCATGAGGATGACGCTCGGACTGTTCGTCCAACCCGTCGTCA
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SEQ ID 4092

SEQ ID 4092
MHTTASKEPKLNAVIAAAAFILLITIGMRMTLGLFVQPVVNTTELNTAQPSLIITVQPLNMGVLQPLSGALADRFGAFVLSGGALLVCACLIASNIPTTWGLMTAVGLLLAPGTGSGGF
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SEQ ID 4093

SEQ ID 4093

ATGGCTAAAAATGGGGGATTTTCTTTGTTTCGAAAGAAAGAAAAACGCTTATCTTTGAAGGCAGGCATTCGCTCCGACAAACTGGTCAACGGCGAAGTATCCGCGTTTACCGAAGAAG
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SEQ ID 4094

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FLKLKARSIKIQRMDAILRMPITGDIVRKGFIARWGRTTATLFAAGVPLVDVLSTAGAAGNLIYERATREIRTRVIGLSMTSGHRA TELFPNMHLQMSSTIGEESGSLDDMLNKAAP
YEDEVNNAVGRLSAMMEPIIIVILGLVIGTLLVANYLPLFNLGNVVA

SEQ ID 4095

ATCCGGAAACACCTTCATTTTTTGGGAAATCCGGCTCATGAAAGAGTCCAGCAGTATGGTTACCGGCCGCTGTTGCAGAGCGACACCTGCATATGGGTGCGGAAACGCCCTGTTTGGACA
TGAATCCCGTGTCGCGGTAAACAGCTCCGCCGCTTCGAGGTAAAGCCGTTCCGCGCTGTCTGCCGGCGCGCTTGGGAAACGAAGGCCGCCGCCGCTTCCGCGCTGGCATAAAGCGGTAA
ACTGCGACACCAGCAGCACCGCGCCGCGACATCTTTCAAAGACAGGTTACAGCTTGCCCGCTTCGCTCTCAAACACGCGCAAAATGTGCGATTTTGTGCGCGATATAGCGTGCATCTTTTTC
TGTGTCGCTATGCGTTACACCGAGTAACACGACAAACCCGCGCTGATTTTGGCCGAGGTTTCGTCGCGGCTTCGGACACGACATCCACCTTTGCACCTACCGCTTTTCTGTATGACCGCA
CGCAT

SEQ ID 4096

IRNNLHFVGNPRHERVQVGYRPVVAERHLHRAETPCPTMNPVSA*QLRRSQVKPLRLFCRRGLGKRPPPCRVGIKKRLRHQFRAADIFQRQVQLARFVFKHQMCDPFGDLACTFF
CVAMRYTF*HDKPAVDFAAGFRAGFGHDIHLCTYRFLYDRTH

SEQ ID 4097

ATGATAAAACCGAACCTGAGGCCGGAAGCTCGGCTCTCCGCGCTGATGCGCTTCTTTCCCTGTATCTTCGCTGGTATTGAATTACGCCCTTTTTCGCAAAGTTGTCGAACCTCGCCCTT
TTAACGACACCGGGGCGGACATCTTCTCTATACGATGCCGGTGGTGCTGTTTTTTT

SEQ ID 4098

MIKPNLRPKLGSSALIAFLSLYSSLVLNYAFFAKVVELRPFNDTGADIFLYTEIPVVLFF

SEQ ID 4099

ATGAAGATACACACACTGCAAAATTAAGAAAGAAAGTACAAAAAGAACCGCTCCGTCTCTTTGTACCGGAAGTTACCGCCCGTCTTCGCGCGGATATTTTGGGTATTCATCCCGATTTCGGCGG
CACTGTTTTTACCGTAAATCCGCACGGTTACCAATCATCTGTTTGGCCTTGGCTGCGGATGAGGTTTTCGAGGGGCCCGCGGGGCCGGGCGCAAGCTGTTTTCGGCGGACGGCTAAAGGCAG
ACGCGGTTCGCGGC CGGTAGGAAAGCGGTGTGTCTTCGGCATTCGGAACGCAACGGCGGGCGGCTATACCGTTTCGCGAGGACAATTCGCAACCGCTGAAACGCTGCTCCCTGCCGCTCAAAAAA
AAATCATCCCGGACGGGTATTGTTTATGCGGATAGCCCGGGCAGCCCGCGGCAATCGGCAGCTCGGACCGGGCGGTTTACCCGTTTGCCTGATCAACGGTTTCCAAGGAATTTTCAGACCGCTCGGAACCA
CATTAATCGCGCATTTGGGAATCTTTTGGAAATCAGGCAAAACCGCGCTTCGCGAAAAACACAAACGGAATTCGCGGCTCGCAAAACCTTTTCCCGCGCTCTCT

SEQ ID 4100

MKI THCKLKKEVQKEPLRSFVPEVTARSAADILGHPDAAALPYRKIRTVTNHRLLAAAEVFECPGAGPASC FGGRRKGRGRGAVGKAVVFGIPKRNGRAYTVVAEDNAEPTLLFAVK
 KSCRTVLMPFIARAAAASRTAVLPAVAESTVPRNLQTVGTTLTAIGTTFGIRONAPCENTTESTANLSRRS

SEQ ID 4101

ATGAACA CACTCCAACGCCGAAGACGCACTAAGTCTCATCGATCATATCACCGTCGGTFCAGAAGCACCGTCGTTATCCAATCTATGACCAACACCGACACTGCCGATGCAAAAGCCA
CCGCATTGCGAGATTAAAGGAATTAGCGATGCCGGCTCGGAAATGGTGGCGGATTACCGCTCAACAGCCCCGAAGCCGCGTCCAAAGTTGCCGAAATCGCGCCCGCTTGGACGATATGGGCTA
TGCACACCACTGATTGGCGATTTCATATTTAAACGGCGAACGCCGTGTTGGCGGAATTTCCCGGAATGCGCGCAAGCAATGTGCCAAATACCGCATCAATCCCGGCAATGTTCGGCAAAAGCGCTA
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ACCTCGTTCTCTCCCGCGGCAAAACGCCCGGAAGCTGATGAAGAAGCACTGATGTCTCCGTTTGGAAATCTGCCGCAAAAGCGCTTATTTGGAGTACCCCGAAGACAAATCATCTCT
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AATGTCTATATGGCTACCTTTTATCCCGGGGTGAACTGCTGAAACGTTGCCGTAAATGGGCTGCGTTGTCAATGGCCCCGGAGAAAGCAATTTGGCGACATCGGAATCAGCCTTCCCGGT
ACGGGGGAAACACCCCTCGCATCTTGTATGAGTAGTCCCGGAGCGCAAGCTCACTGAAAGGTAATAATATTGCAAGCGAATTCCTAGCTATTTGATAGGAATATGTTAAAAACCAATTATG
CGAAAAACAGTTCTAAACCGCAATAAAGGATAGCATCCCGATCAAGTCTCTA

SEQ ID 4102

MNTLQRRKTHQVLJDHITVGSEAPVVIQSMVTDADAKATALQIKELSDAGSEMVRTIVTNSPEAAKVAEIRRLDDMGYATPLIGDFHFNGERLLAEFPEGCKALKSYRINPGNVGKGV
KGDSEKPAFMIRTAANDKAVRIGVNWGSLDQSLAKRMDANLVSSAPKPPPEEVMKEALIVSALESAEKAVLGLPEDKIILSCKSVSAVHDLIQVYRELGRSCVYPLHLGLTEAGMSKGIV
ASTAALSVLQLQEGIGDTRISLTPEPGSPRTQEVVVGQEIQLTQGLRSFTPMVTACPGCGRTTSTVQELAQDVQNYLRQKMSIWRTLYPGVESLNAVVMGCVVNGPGESKLADIGISLFG
TGETPVAPVYVDGERKVTLKGNNAISEFLAIVEEYKTVNGYKNSKRNGKVIPIQSL

SEQ ID 4103

ATGGCAGCAGATTTTAATCGGACAACAGGGGTAATTATGCTCTTTAAGCCATCCAAACGAATCTCTTTATTACTTGTCTTGGCTTGGGGCGGTGCAGCACTTCCACGCGCCCTCGGGG
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CGAATCTGGCTGGCTGGTCCGTGCCGAAATCTATCAATACCTGAAAGTTAAGCAGCAAGGCGCAGGAAAGTTTCGCGCAAGCCCTCTCCATCAACCCGACAGTGGCGAAATCAACAACAC
TACGGCTGGTTCTGTGCGGCAGGCTCAACCGCCCTGCCGAATCTATGGCATATTTTCGACAAAGCCCTGGCGGACCCACCTACCCGACCCCTTATATTGCGAACCTGAAATAAGGTATAT
GTGCGCGCAAAACAGGGGCAATTCGGAATTCGGCGGAAGCTATTTGAAACGTTCCCTTCGCGCGCCAGCGCGGATTTCCCAACCCGCAATTTAAAGAACTGGCGCGCACCAAAATGCTGGCGGGCA
CTTGGCGGATGCGCAATCTACTACTTTTAAAAAATCAACAGCAGGTAGAAAGTTCTTCAGCGCGGATGATTTCGTCGTAGGCTGGAATAATTCGCAAGCCCTTCGGCAAGGTGCAGGCGGCATAC
GAATATGAAGCAAAATTCGAGGCAAAATTTCCCTCTCGGAGAAATTCGCAACCCGCTCTCACCGGTCAA

SEQ ID 4104

MAADFNRTTGVIMPPFKSKRI SLLVLVALGACSTSYRPSRAEKANQVSNIKTQLAMEYMRGQDYRQATASIEDALKSNPKNELAWLVRABTYQYLKVNDKQAESFRQALSTIKPDSAKINNN
YGFWLCGRNLNRPASMAFYFDKALADPTYPTPYIANLNKGICSAKQGQFGLAEAYLKRSLAAQPQFPAPKELARTMLAGQLGDADYYFKYQSRVEVLQADDLLLGWIKIARLGNVQAA
EYEAQLQANFPYSELOTVLQ

SEQ ID 4105

ATGAAAACCAATCTGCTCAACTACGACCTCTCAAGGGCTAACCCGACATTTTGC CGATATGGGTGAAAAACCATTCGCGCGCAAAACAGGTATGCGTGGATGCAACCAATCCGGCGCGCAAA
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CGGCAGGGCTTCAACCGCAATTTAAACCGCTCGCGAAATCATCGGACAGTTGTGTGGGCAAAACAAGCGATGGGCGTTACACCGAAAAACGAGCGTGTGATTTCCAAACGTCGTCTGATGG
GCATGGGCGAGCCGATGGCGAATCTCGACAAATGTCGTTACCGCCTTGAGCATCATGCTGGACGACCAACGGCTACCGTTTGAGCCGCGCGCGGTAAACGTTTCCACTTCGGGTATGGTTC
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ATGGCCGCGATGCCAACGCTATCTGGTCAAAGCGCCAGGGATTTTCATCACTTTTCAGGATATGTGATGCTGGACGGTGTCAACGATAAGGCACAACATGCATACGAACTTATTGAACTGGTCA
AAGATGTTCCCTGCAAAATCAATTTAACTCCGTTTAACTCCTTTCCCTAATTCGGGATATGAACGTTCAAGTAAACGAAAAACATCCGTATTTTCAGAGATATCCTGCAACAAAGCCGAATTTGT
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GGG

SEQ ID 4106

SEQ ID 4106
 MKTNLLNLYDQLGRHFDADMGKEKPFRAKQVMMWMMHQSQAQNFDMETDLAKSLRHLKLNQASIEIPKLLMSQESSDGRKWLDDVGTGNGVETVFIPESDRGTLICISSQVGCALCEKTFPCSTG
 RQGFNRNLTAABIEIGQLWANKAMGVTPKNERVINSVMMGCGEPMANFNDVVTALSTMLDDHGYGLSRRRVTVSTSGNVPMQDLRDVMPFALVALVSLHASNDEVNRQIVPLANKYPLFKEL
 MAACQRYLVKAPRDFITFEYVNLGVDNKAQHAYELIELVKDVPCKFNLIPFPNPNNGYERSSNENIRIPRDLQQAEPVTVVRKTRGDDIDACGQLAGQVQDKTRRQKWKQQLIGQQ
 G

SEQ ID 4107

SEQ ID 4107
TTGATACATACACCGCCCAATTCCTATTTCAGACGGCATAAAATATATCCATGCCCTCGAAAACTCTGTTGCAAAAGACTTCAATCAAACTTGCCTGCCCTGCAATTTTTATTGGAAG
CCTTAATT

SEQ ID 4108

LIQYTAQFLFRRHKIYPCRLKTLLOKTSNQTCLPCNFLFEALI

SEQ ID 4109

SEQ ID 4109
ATGGCGATTGAACGTACCATATCCATCATCAAACCCGATGCCGTCGGCAAAAACGTTATCGGCAAAATATACAGCCGCTTGAGGAGAACGGTCTGAAATCGTTCGCCGCCAAATGAAGC
AGCTTACCCTCAAAGAGCCCAAGAATTTATGCGGTTTATAAAGACCGCCCTTCTATGCCGGATTGGTTGAATTTATGACCGCGGTCGCGTTATGATCAAGTACTGGAAGGCGAAAA
CGCCGTTCTGAAAAAACCGGAACTGATGGGGGCGACCAATCCACCGAAGCCGCAGAAGGCACGATACGCGCGGACTTTGCCACTTCGGTCAGCATTAAACCGGTACACGGTTCGGACAGT
CTGGAAAAATGCCGCTTTGGAAATTGCCCTACTTTTCAGCCAAACCGAAATCTGCCCCCGT

SEQ ID 4110

SEQ ID 4110
MAIERTISIIKPDVGKNVIGIKIYSRFEENGLKIVAANKQLTLKEAQEYAVHKDRPFYAGLVFMTGGPVMIQVLEGENAVLKNRELMGATNPTEAAESTIRADFATSVSINAVHGSDS
VENAALEIAYFFSQTICPR

SEQ ID 4111

SEQ ID 4111
TTGGCTGAAAAGATAGGCAATTTCCAAAGCGGCATTTCCACACTGTGCGAACCCTGTACGGCGTAAATGCTGACCGAAGTGGCAAAGTCCGCGCGTATCGTGCCCTCTGCGGGTTCGGTG
GGATTGGTCGCCCCATCAGTTTCGCGGTTTTCAGAACCGCGTTTTCGCCCTTCACGACTTGTAATCATATACCGGACCGCGCGTCATAAATTCACCAATCCGCGCATAGAGGGGCGGTCTT
TATGAACCGCATAAAAATCTTGGGCTCTTTGAGGGTAAGTCGCTCATTTTTCGCGGCAACGATTTTCAGACCGTTCCTCTCAAAGCGGCTGTATATTTTGGCGATAACGTTTTCGCGAC
CGGACCGCGCTTCACGACGACATATGCTACGTTTAACTCGGCATGCTATATCTCTTAATTTTACTTAAGAAGAATCAAAATCGGTATTCTACCAAAAAAA

SEQ ID 4112

SEQ ID 4112
LAEKVGNQSGGIFHTVGTVYGVNADRSGKVRAIRAFCCPGGIGRPHQFAVFPQNGVFAQYILNHNRTAGHKFNQSGIEGAVFMNRIKFLGFFEGKLLHFGNDPQTVLLKAAVYFADNVFAD
GIGFDDGYGTFFNRHAISLFLKKQNGIGILPKK

SEQ ID 4113

SEQ ID 4113
TGGTGGCTTGGCGGCGCAACAACGGCGGCAACAACGGCGCCACACCCCAAGCCACACAGGACAAGCCCTCGGAGAAGCAGTCAAAACCGCCTTCAAAACCCCAAGCTACA
TCCTGCTGCACCTGAGCTTTTTCGCTGCGGCTTCCACATCGCCTTTCGTAACCCAC

SEQ ID 4114

WNLAGNNNGNNAAHTOHTQATHGQSLGEAVKTAFKTPSYILLHLSFFACGFHIAFLVTH

SEQ ID 4115

EQ ID 4115

ATGAAGAAACCTCGTTGGCAATTGTTGCCGTTTTCGCTTAAGTGCCTGCCGGCAGCGGAAGAGGCACCGCCGCTTTACCCCGGCAGATTAGCGACCGTTCCGGTGGGACACTATTGCA
GTATGAACTCGACGGAACACAACGGCCCCAAAGCCGAGATTTTTTGAACGGCAAAACCGCATCAGCCCGTTTGGTCTCCACCGTCAAGCAGATGTTCCGCGTATACCAAGCTGCCCGAAGA
GCCCAAAGGCATCCGGGTGATTACGTTACCGGATATGGGCAATGTTACCGATTGGACGAATCTTAATGCCGACACGGAGTGGATAGATCGCAAAAAGCGCTTTTACGTCATCGCACAGCGCG
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TTTTTCAAG

SEQ ID 4116

SEQ ID 4116
MKKTLIAIVAVFALSACRQAEAPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKPDQPVWFSTVKQMFGYTKLPEEPKGRIRVIYVDTMGNVVTWTWNPADTETWIDAKKAFYVIDS
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SEQ ID 4117

EQ ID 4117

ATGATATATAGAGACCAACTTTTAAAGCCCGCGGTTTGAAAAACCACAGCCCGTGACTGTGATCAGGCTGCCTCACAACTGCCCAACTTCATCCGCGACGACGCACAGGCGGCCGCA
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CGGACCGCGCAAGAGCTTTCTGATGAGACGCTTTTTTCGGCTGCCCTCCCTTACCGCGCAAAACGCGCGTCCACTTTTCATGCTTTATGCGGGAATCCACCGCGCGCTGAAAGCCCTGAAA
AGCGAAAGCAACCGTTGAAATCCGTTGCGCGGAGATTACCAAAGAAACCGAGTATTGTGTTTGACGAAATTCATGTCAGCGATATTGCGGATGCAATGATTTTAGGCGCTGTGTGG
AAAACCTGCTTAACGAGGGCGTTGTTTTGTTGGCGACTTCAAATACCGCGCTTCCGAACCTCTACCCGCAAGTCAAACCAGGAGCGGTTTTCTTCCACAATCCGCGCTCATCGATCCAG
TCTGACCGTCTTTAAACGTTGACGGAAGGGGAAGATACCGCGCTGCCGTACCTCCGCCCCGCGCCAGGATTTCTTTACGCTGCGCAATGAAGAAATGAGGCAAAACTGTTCAA
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CCGCTCACAGTCCGACATCTGTATTTGGCGCAACATTATGAAATGTTTATTTTCAGTGTGGAACAACTCTCACCGCAAGAAAGGCGGAGGCGCAGCGCTGACTTGGCTGATTGA
CGTACTCTACGATTTCCGGGTCAAACCTGTGTGCCACGCGCGGTAGATGTCAACCATATCTACACGGAAGCGATTTTGCGGAAGAAATTTACCCGACCGCCAGCCGATGTGTCGAAATG
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SEQ ID 4118

SEQ ID 4118
MNNRDLQFKAPPFENHSPLTWYQAAASQLPNFIRDDAQAAAEHLDRLWTELMFPRKRNRNPLGRSLRSPQVFKGLYFYGGVGRGKSLFMDAFFGCLPYRRKRNRVHFAPMAEIHRRLLKALK
SESNPILKSVAARIKTETRVLCFDEPHVSDIADAMILGRLEENLLENGVVWAFSPNYAPSELYPQGQNRSGFLPTIALIESSLTVLNVDDGEDYRLRLTRPAEIPPTPANEENEAKLAKLFPK
EETGITLDNPGISTITHGRRIIPKHAESGRITWFDRLALCFSPRSQSDYLYLAEHYEMVFI SGLEQLSPOEKAEARRLTLIDVLYDFRVKLCTGAVDVNHLYTEGDFAEFFTRTASRMVEM
QSEVYLEQPHLTLSPKASGG

SEQ ID 4119

SEQ ID 4119

SEQ ID 4120

LAFFVEKNNDAAHKGGISKGGVLIWCRYEPKCLLFQAAF

SEQ ID 4121

SEQ ID 4121
TTGTCTCTCTCAATATTAAAAACGACGCTGAAATAAAGGCATTTTGGCTCATCTGACCATATTTAAACGCGCGCTTGGCTTATACCCCTTTGTGCGCGTCATTATCTTTTCAC
GGGAAACGCCAAGTTTGAAGGAAATCATTTATAATACCAGCGGTAAAGCATTTTCTTTCT

SEQ ID 4122

SEQ ID 4122

ISSFNIKTOPEIKGILAHICTILKRRLCLYPLCARHYSFPRETPSLKEITYNTSGKHFLS

SEQ ID 4123

SEQ ID 4123
TTGGAGGGGGCCGAAACACACACGGAACAGGTTGCTTATGCAAAATTCGGCAACGAATAATACGAAGCCCAGAAAGTGAAGTAGGAAATACGGGGGATTTTAAATGTT

SEQ ID 4124

LEGAKTQOEQVAYANSATNNTKPESEVGNTGDFNV

SEQ ID 4125

ATGAATAATTGGCGTCTATTTGCCGGATAATCCGGAATAATCAACCGCTTGGTGTGATTTATTTGGCTTTCCGGCTTGACGTGTACGGGAACAAATTTACATACCAAAATCGAGCTTCCGGCGTT
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CACGGCGCATTTGGTATTGGCACTACGGAATCCGGGAATCATCAAAATGTGTTCTGCCTTTTCCTGCTTATTTATCGCAACGCTCTGTAACCGTGGGGAGAAAAGCCTTTACTGCTTATTTAG
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TACCAAAAGATTTTATCGAAACCTGTCTGCGGCAATCAGCAATCGATGTGCGTTTCCATAAAGGATACGATCAGAGCTATTACTTTCATCGCCAGTTTTATTGGTGAGCATATCGCTTAT
CACCGCGCATTTTGAAG

SEQ ID 4126

MKFAVYLPNDPNEPQPLGVYIWSGLTCTEQNFITKSSFRRYAAEHQVVVAPDTPGRGEQVPNGAAYDLGQAGFYLNATEQPAANYQMYDYILLNELPLRIEHPPTNGKRSIMCHSDG
 HGALVLALRNRREHYQSVSAPSPILSPSLVPWGEKAFTAYLGKDREKQQYDANSLIQQGYKVQGMRIDQGLEDFLPTQLRTKDFIETCRAANQPIDWRFHKGYDHSYTFIASFYIGEHYAY
 HAAFLK

SEQ ID 4127

TTGAGCCCGAAAGATTACGATAAAACCAATCAAGATGTGTTGTAGACATCAACAAATGGGGCATTGACCAACCCTTTGAATGTATCGGCAATGTAAACGTAATGCGTCAGGCATTAGAAA
GTGCACACCGAGGTGTGGGACAATCCATCATCATCGCGTAGCGGATGCAGGACAAGAAATTTCAACCGGTCCTGTTCCAATCGGTAAACAGGCCGTGTTTGGAAAGGCTCGGCATTTTGGTGG
TGTAAAGGCCGCTCCGAGCTTCCGAAAAATGGTGGAGGATTCAATGAAAGGCGATATCCAATTAGAACCAATTTGTGACCCATGCAATGACCCCTTGATCAAATCAATGAAGCCCTTGAAGTTA
ATGCACGAAGGTAATCGATCCGCGCTGTTATTCAATTAC

SEQ ID 4128

LSPKDYDKPIKIDVLLDINKGIDHTFECIGNVNVMRQALSAHRGNGQSIIIGVADAGQEI STRPQSVTGRVKGSAFGGVKGRSELPMWVDSNKGDIQLEPFFVTHAMTLDQINEAFEL
MHEGKSIRAVIHY

SEQ ID 4129

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SEQ ID 4130

MLLRQGYFVNELRGKTMEMQTDSTLKSRAAVAFAPNQPLQIVEIDVEMPRKDEVLIRNTHTGVCHTDAFTLSGSDPEGVFVVLVGHGAGVVAVAVGEGVSSVKPGNHVPLPYTAECECE
FCLSGKTNLCVSVRDTQKGLMPDGTTRFSYQGQPIYHYEGCSTFSEYSVVAEVS LAKINPKANHEQVCLLCGVTTGIGAVHNHTAKVQEGDSVAVFGLGAIGLAVVQGARQAKAGRITAI
DTNPAKFLAKQWCN

SEQ ID 4131

ATGACTTATACCACTGCCAAGCTGCCGAAAAATAGGCATCTCCGCCACACCTTACGCTTTTACGACAAAGAGCGTTGTGTGCTTAATATCGGACGTCATGAATACGGTAACCGTGTGT
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TCGGTAAAGCTGTAAATTTGCGCGCAAAATTCCTGAAACGGCT

SEQ ID 4132

MTYTTAKAAEKIGISAHTLRFYDKEGLLPNIGRDEYGNCRFTDNDLQWLYLLQCLKNTGASLKDIKRPAECTVIGDDTIEERLSLFENQIENVKQIAELKRYLDLLEYKLAFYQAKALG
SVKAVNLPOIPETA

SEQ ID 4133

TTGGCAGAAGTATTTCGCCGCAAAAACGGCAGCATCTTCTGGCAAAAGACGTAGAGTACAGCGCTAAAGCTTGGTTGACACCATGACCCGATCGCTGCCCGAGGTCACGCGATCGAAA
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ATTGCCCGAGCGGGTCGACTTGGCTTTAAAAGAAAAATGCCAAT

SEQ ID 4134

LAEVFAAKNGTHLLAKDVEYSVKVLVDTMTRSLARGQRIIRGFGSPDLNHRPARIGRNPKTGERVEVPEKHVPHFKPGKELRERVDLALKENAN

SEQ ID 4135

TTGGCGGCAAACTACTTCTGCAAGCGAACATTAACTCAGACTTTGTGATGTCGCAACCTTATTCTTGTTGGCGGGAGAGTTTGGCTTTTCAGCAGGTGCGCCAAAGCTGATGGTACCGGCA
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AATAACGACGGCTTCGCACTTCTTCTCTCTTTTGTATTTGCGTACGCGTTCTTTCGCCGGATTTCGGTCCAAGACAGTTCGACAGGTTGAACGACAGCCGTCGATGCCCGGGCAGGCGGACGA
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CCTTGTCGATTTTCGACAGATGCCCGTAGTCGGTTCAGGTTGGATATCTTGCCAAACAGCGGGTGCTTTCGCGGATATCGGCGATGCGGTCAGACCGTTCAAGAGTCTTTGCCCGAGTTGTTTCA
TACCCAGGAAGAACACCGTGTTTCTTGTGGTGCGGATTTCAATATCTTTGGCTTCAACATCTCGACGACTTCCAAGACTTCGCTCGGGTGTTCACGCGACGCCATGCCAAATCGGTGATGTG
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AGCGATCCAAATCGGCTGCGCTTTGCGCTTTTTCGCGGACAGTTCGTTTTCGCCGAAGCGTTTTCGACGGATTTCGATGTTAACGGTTACGAAGTGCGCCGATCTTTAACTTCAATTTCCGCT
TGACGCTTTTGAATTCAGCTACATTCGATCAGGAGATC

SEQ ID 4136

LAAMTSKRRTINSDFVMSATLFLFAGEFGFQQVAGGFGIRIGGGIDGVQCFAAFFGIFGPNKGFDAAVFAVNGNDGPNFVAFPFQFGQVFNAGVKFGFSROVAFYFVRQGDNSAFGVM
RFHGTNPQRTFVVAHDEAVERIAFLQFDTQGDAPFFHIDCYDGFDFPSSFFVAYGPFAGFGPRQVGVNQTVDAAGQADEYAEIENGFNRTGDFVSFVVVGKFPFPRIGLALFHTQRDTA
AAYFDONHDFDFTVLYDFARVYVVPVGVHFGDVVYTFDALFDPECAVVGQGVYFBAQAGGLRITAGOTAPRIFAQLFHTQGNLFLFLVERQYFGNFLLTFQDFARFVHAFFPQIGDV

QQAVIDAAQVNECAVVGDIFFDDAFDDGAFLOVFOQGFAPFTQSGFQNGAAGNNDVVAFVQDFHFDLFAFKMGSVFNSTYVDQRTQECADAADHNGQAADFPTVDDAGQDVAVFHGFFQ
SDPIGCAFQGFAGQFGFAEAVFDGFDGNGNEVADFNFNFALSVPFESYIDQGF

SEQ ID 4137

SEQ ID 4137

GTGGGGCGGATATTGCAACCAATTGTGCGGGCGCGCTTGCCGACCGTTTTCGGCGCGGTTACGGGTATTAAAGCGGGGTGCCCTCTGCTCGTCTGCGCTGCCCTGATTGTCCTCCAACATCCCGACT
TATTGGGGCGCTGATGATTGCGCGTGGGGCTGCTGCTCGCAATTTCGGACCCGGTTCGCGGGGTTTTCATCATATTATGGACAGGTGCGCGCCCAAGTCCCCACACAAACCGCGGCTTGGCAT
CCGGACTGGTCAACCGCAGGCGGTTTCGGCAGGACAATTCTCTGTCGACACCGTGTGTCAAGAGCTCAAGAGCTCTGCTGCTCTGCCCGAAGTCGGCTGGACGGGTACATTTTACGTTTGGGG
GCAATCGCCCTCTGATTCTGCGCGCTCTCAATGGTGGCTTTCGGCGGGCAACAACGGCGGCAACAACGCCGCCACACCAACCAACCAAGCTCACACGCGGACAAAGCTCTGGAGAGCAG
TCAAAACCGCCTTCAAAACCCCAAGCTACATCTGCTGCTGCACTGAGCTTTTTCGCTCGGGCTGCTCAACATCGCCTTTCTGTTAACCAACCCACCTACCCACCGAAGTCGCGCTGTGCGGACTGCC
GCCACCGCTGCCCTGACATCCCTGACATCTATCGGACTGGCAAAACATCGCCGGTTGCGTGTCTCAAGC

SEQ ID 4138

SEQ ID 4138
VGRIATTVRRACRPFRRVQGIKRRCPPARLRLPCLQHPDLLGADDCRRAAARIRHRFRRVFHHYGTGRRPSPHQTQLGIRTGQRRRFGRTIPVETAGSKTQGLVVLFEVGTGFTFYWG
AIALLLIPVSWHLAGGNNGGNNAHTQHTQATHGQSLGEAVKTAFTKTPSYILLHLSPFACGPHIALVTHLPTFEVALCGLPATVASTSIALIGLANIAGCVFSG

SEQ ID 4139

EQ ID 4139
 ATGTCGTGATTTTGCTGTGATTGTGCGCGGTTTGCCGTGCTTTGGCAGCAGTTTGGGGCTGCTGGTCGGCAGCTTCCTGAATGTCGTCAATTACC GCGTACCCGTTATGATGGAACGCGGCT
 GACCGGTATTTGCCAAAGAACATTTAACACTGCGCGTGACCGACGATGAAAGCCGTACCTTCAACTGATGAAGCCGGATTCCGCTGTCCTCCAAATGCGGTGTGCCGATACGGCGGTGGCA
 GGACATCCCGATTGTGCAGTTACCTGCTCCTGCGCGGCAAAATGCGCTTCCTGCCAAACCAAATCAGCATACGTTATCCCTTAATCGAGCTGCTGACCGGGGTATTGTTCCGGGCTGGTGGCC
 TGGCAATACGCGTGGTCTTGGATTACCTGGCGGTGTGATCTGACCGCGTCTCTGATTTCCTGACCTTTATCTGATGCGGACACCCAAATACCTGCCCGACTCGATGACATTACCCTTGA
 TCTGGCTGGGGCTGATATTAAATTGGACGGCGGCTTCGTGCCATTGCAAGTCTGCGGTTCTAGGTGCGGTTGCCCGGCTTAATGTCCTTATATGCACTGTATAAATGCTGAC
 AGGAAAAACCGGTATGGGCAACGGAGATTTCAAACTGATTGGCGCATTTGGCGCGTGGCTCGGCATATCCGATTCGCGGTGCTGATTATTGTTTCTCTCTGATCGGTTTGGTGGCGGCA
 ATCGTTATGCGCTGCCAAGGGCGGCATTTCGCTTCGGCCCCGCACTGACAGTTTCGGGCTGGATAATTTTACGGCAAACGATTCCGTATGGCGGGCGGTCACTGGTGGCTGACCC
 ATCCGGTGAGA

SEQ ID 4140

SEQ ID 4140
MSDLSVLSPFAVPLAAVLGLLVGSFLNVVTVYRVPMMERGVTVFAKEHLNLPITDDESRTFNLMPDSCCPKCRVPIRANQNIPIVSYLLLRGKCASCQTKISIRYPLIELLITGVLFGLVA
WQYGSWITLGLLITLAPLISLTPTIDADTQYLPDSMTLPLINLGLIFNLDDGGFVPLQSAVLGAVAGYSSMLLCVAVYKLTGKTGMGNGDFKLIALAGMLGISALPVLIIVSSLIGLVAA
IVMRVAKGRHFAFGPALTVSGWIIFTANDESVNRVAVNNWLTHTPVR

SEQ ID 4141

SEQ ID 4141

TTTGAAGAAAGCTTTACACCTGCAAGAAATGAACCCGGGTGAGGTGATTACCGTGAAGTAGTGGCAATCGACCAAAACTTCGTACCGTAAACAGCGAGTCTGAAATCAGAATCCCTGATCG
CTGTAGCTGAATTTAAAACCGCTCAAGCGGAAATTAAGATTAAAGTCGGGACTTCGTTACCGTTACCATCGAATCCGTCGAAACCGGCTTCGGCGAAACCAAACTGTCCCGCGAAAAAGC
AATACGCGCAGCCGATTTGATCGCTTTTGGAGAAGCCATTGGAAAAACCGCAACATCCTGTCGGCATCATCAACGCTAAAGTCAAAGCGGGCTGACCGTTATGATCAGCAGCATCCGCGCA
TTCCTGCCGGGTCTTTTGGTCGACGTACGTCCTGTTAAAGACACTTCOCATTTTGAAGGCAAGAGATCGAATTCAAAGTGATCAAACCTGGACAAAAACCGCAACACGTCGTTGTTCCTCC
GCCGCGCGCTTTTGAAGCCACTTTGGGTGAAGAACGCAAGACCCCTGCTGGAAACCTGCAAGAAGGCTCCGTCATCAAAAGCCATCGTCAAATAATACCCGACTACGGCGACTTCGTTGA
CCTGGCGGCATCGACGGCCTGCTGCACATCACCGATTGGCATGGCGTGCGGTGAACCAACCCGACGAAGTCTTGGAAAGTCGTGAGGCAAGTTCGTAATTTGAAATTCGACCAA
GAAAAACAACGGTTTTCCTTGGGTATGAAACAACCTGGCGGAAGATCTTGGAGAGCTCTGACCGCGCTTATCGCGAAGCCACCGCGCTGTCGGCAAGATATCCAACCTGACCGACTACG
GGCGATCTGCTGAAATCGAACAAGCATCGAAGGTTTGGTATACGCTCGGAAATGGACTGGACCAACAAAAACGTAACCCCGAGCAAGTCGTACAACTGGGTGACGAAGTCGAAGTCAT
GATCTTTGGAAATCGACGAAGGCCCGCGCGTATCTCTTTGGGTATGAACAATGCCAAGCCAATCTTTGGGAAGAAATTTGCGCGCAACCAACAAGAGAGACAAATCTCCGGTCCGGTT
AAATCCATTACCGATTTCGCGCTATTCGTGCGGCTGCGCGCGGCGCATCGACGGTCTGGTTCACCTGTCCGACCTGTCTTGGACCGAATCCGGCGAAGAACCGGTACGCAAAATACAAAAAG
GAGAAGAAATCGAAGCCGTCGTATTCGCAATTCGATGTGAAAAAGAACGCAATCTTCCTTGGGTATCAACCAAGTGAAGCGCATCTTTCGCGCAACTTCATCAGCGTGAACGAAGAGTTC
TTTGGTTAAAGGTTCCGTGAAATCTGTTGACGCAAGAGCGCTGTTATGCGGCTCTCTGTGACGAAGTGAAGAGCTACGCTGCTGTTCCGAATTTGACGCGACCGCGTTGAAGACTTGACC
ACCAACTGAAAGAAGGCGACGAAGTTGACGCGCATCTGTTACCGCTGACGCGCAAAACCCGACGATCAAACCTTTCCGTTTAAAGCCAAAGATGCCAAAGAAAGCCGGAAGCACTGAACT
CGGTCAATGCGCCCGCAATTCGGAATGCCAATGCCGTACCCAGCTTTGGGCGACCTGCTGAAAGCCAAACTCTCCGGCGAACAAGAA

SEQ ID 4142

[illegible]

SEQ ID 4143

EQ ID 4143
GTGCGCTGTGAAACCTTATTACCCGCCGTGCCGTGCCAAGGACTGCAGACACCCACCAACCCACCCGACCCCTTGCGCGTGTACCGAAAGAGTTATATATGTCCTATGGAAAAATTTGC
TCAGCTGTTGGGAAGAAAGCTTTACCCGTGCAAGAAA

SEQ ID 4144

VPSETLPTRI PCOGLQPTNPTRTPWRCTEKS YICLNKILLSCHWKALPCKK

SEQ ID 4145

SEQ ID 4145
GTGGGTCTCTGCAGTCTTGGCACGGCAGCGGGTAAATAAGGTTTCAGACGGCACAATGGAAATTCATGCTGTCTGAAGCGCAATCGGGCGATTATACCTGAAAAATT

SEQ ID 4146

VGVCSPWEGRRVNKVS DGTWKFMLSEAQCGRLYLKI

SEQ ID 4147

SEQ ID 4147

ATGCCGCTCGAAGGTCATACCTCTTTTCAGACGGCATTTGCATTGATGCCGCCACGCCGGAATCCGAACCGGCTTGCCGGCTTTCGTGCGGACGCTTTCGGGCGAGCGCGCTTCGGTCTGCT
TAGACAATCGCTCTTTAAACAGGTAGAAATTCGCCCCAAACGGGAAACACACCTTCAGACGGCAAAACCCATACCCCAAACATCAGGAATCCCCCTTATGAACAGACAAAAAGTCATCGC
CATCGACGGTCCGGGCGCATCGGGCAAAGGCACGGTCGCGCGCCGGCTTGCCGCGCATTTGGGATACGATTATCTCGATACCGCGCGCTTACCGGCTGACCGCCCTATATGCACAAAA
CAAGGCGTGGAAATGGCAGATGAAGAAAACGTTTCCGCACCTGCCAAAAAATGCCCCCGCTATTTTCAGGCAACCGCATCTCTACTTGTATGGCGAAGACGTTTCAGACGGCATCCGGACAC
AAGCCATCGGTATGGGCGCATCCGCAGTTGCGCAATGGCCAAAGTCCGCGCGCACTGCTGCAACCGCACCGCGGATTTCTTACGCCGAAAAAAGGACTGGTGGCGAAGCGGACACCGG
ATCGGTCTGCTTCCCCAAGCCGAAGTCAAAATTTTCTGACAGCCGAATCTAAATTCGTGCGGAAACGCCCGCAATTAACGATCGCGCATTTCCCTGCGAAGGTTTCACATTCGAGCGCATC
CTGTCCGACATCGAGACCAGAGACGAAGCAGACCGAAACCGCAAGTTGCCCCCTGAAACAACAGCCCGATGCCCTGCTTTTGGATACGAGCCGCTTAACATAGAAGAACTGTAAAAA
AAGTGTCTGATTGGTATTCGTAAGTT

SEQ ID 4148

SEQ ID 4148
MPSEGHSTFRRHCIDARHAGITGLPASVGRFPGRRRSVCLDNRLKQVESAPTGMTFFRRQNFYKPKSGIPLMNRQKVIATDGPASGKGTVAAARVAALGYDYLDTGALYRLTALYAQK
QGVENHDEENVSAKAKLPAPVPSGNRIILDGEDVSDGIRTRAIAGMCAVAQWPKVRAALLQRQDRFLTEKGLVADGRDTSVVPQAEKIKFLTAESKIRAEKRAKQIGIPCEGFTFERI
LSDIETREADRNRRKVAPLKQQPDALLDLSRLTIEETVKKVLWYRKV

SEQ ID 4149

ATGTCTTCCCTTCAAATACCAACCGTCAAACTGGTCAGCCGTTTGACTTTATATCCTTACCGTGTGCCGGCGCAGCTGTCCGTTTCGGCGCAGCTGGCGTTTCDCGTATTTCGTCCGTG
AAAACGGCGCGCGCGCGTATGTGTTTTTATCTGTATCCGAGTGTCTGGTTATCGGCATCCCGATGATTTTGGTGGAAAAACGTCATCGGACGGCGCAAAGCGGTGAACCGCGTGGATGCGTT
CGCGCGCCGATGAACGGCAAACCTGTTGCCAAAATTGTGAAATCTGGTCGGCCGGATGGGGCTGCTCGCGCGGTTTCGGCATCATGGCTTATTATATGTTACTCGGTGGCTGGGTAATCAGC
TATATCTGTTAATATTATTGGAGGAAATTTGAATATTTCAGCCCCGTGCAGCGTGTGGTTACAAAAGGCTTCTTTACCGAACAACATTGAAAACAGCCCTTGGGAAATTCGCTCTTATACGC
TGTCTTTTGTGCGCGTGAACCAATGAATTTTGTGTCAAAGCGGTTCTCGGCGGATTCGCGGAAATACCTTGATGCTCTCTGCTGTTTTTGTTCGTTAATCCGAGTGCTGCTCGCGAA
CGCTACCTCTCCGGGCGCAATGGAAGGGTGTCTCTTCTCTGAAACTGATTTACGAGAAATACCGCCGCACTGTCTGCTTTTTTGGGACAGTAATTTTTTGGCTCATCGCTGGCTGGGT
TTCGGCGTGATGATTACCTTATCCAGCTATCTGGATAAAAAAGAAAATCTGGTTACAGCGGCAGTTATCACGGCAATTACCAATACCATCATCGCTGACTTTCGGGCTTTATGATTTTCC
CGTCGCTCTTCAGCTTTCGGCGTTCGCCCAATTCGGCCCCGACTTTTGGTGTTCAAAGTTTACCAGATTGTGTTCTCACAATGTGGGAGGACCTGTGTTCCGCGCTATTTTCTTCTCTCT
GCTCTGATGTCGCCGCTGACAACCTCGCTGACGATTATGAAAGTGTGTGATTACGACATTACGAAAAAACCAAAATCCGCCGTCACGCCGAATACAGATTGTATTGTCCGTCACTCTC
GTTTTCGGCAACATCCCGCTATTATTGAGCTATGGCCCGTGGAAAGACGTTTTCGTGTTTCGGCAAAAATATTTTCGATGCTTCGACTACATCAGCGCAACATCTTGTGTTATGCTGACCG
CGCTCGGTTTCGCACTGTTTGTGCGTTTGTGATGAGGACCAAGCGAAGGAAGAAATGCTTTATAAAGGCAACCATACGACGGTCAATATTTGTTTGGCTTATGTGAAATACCTTGTGCG
GCTGTGATTCTGCTGATTGTTGCTTCAGTCAAGGATATTC

SEQ ID 4150

MSSPSMTRQWSSRLFYILTVAGATVFGATWRFPYVLVGENGGGAYVFLPCIAMLVIGIPMILVENVIGRRKGVALDAPGGPMNGKPVAKINKLVGRGSLGAPGIMAYHVMVLGGWVIS
 YVINIIGGNLNISSPDVGVTGKPFTEHIENSPWEIASYTLTLFVAVNQWLKVGVIIGIEKTAKYLMPLLLFLFLIAMVVENVTLPGAMEGVAPYLPKPFKSTAEIFVFPVLQVFPFALSIG
 PGVMITLSSYLDKNENLVQTAIVITAITNTIIAVLAGPMIFPSLFSFGVAPNSGPTLVPQSLPVPFSHMMAGPVFAVIFPSELLLAALTTSLTIYEVLTITIQEKTIRRTAAITIVLSVIP
 VFGNIPISILSYGPNKDVSVFGKNIFDAFDYISGNILFMLTALGSALFVGVPKDEAKRELLYKGNHTVNTINFAVYKYLVPVLVILLIPVSNLF

SEQ ID 4151

ATGATGATGAAAGAGAGGGAATTTGAAATAGAAAACCATCTATACAAGGGGAGAGTATAGATGGCAAAACACATTTATGGGGAAACGCTCTTGCTCATAATCCCTTGAAACAGGCGTTAC
TTAGACAAGCGGATTATATCGTAAAC

SEQ ID 4152

MMKEREFEIENHLYKGRSIDGKTHYGENVLLIILLBOALLROADYTWN

SEQ ID 4153

ATGTGCGAATACGCCGGGTGAAGGTGTTGCACGCGGTTCGCCGGGCAGCAACCATGCGTTTGACTTGGTGGTATTTCCTTCGGTAATGGTCAGCAGCAGGGGTGGTCGGATTTCACAA
ACGGCATCGGCCGCACAAACGGTTTCGTTTCGTCGTGGAGCGGCACGCCCTTTTCAAGTTTCGCAGAGCGTTTCCTTCGTAGGGTGTTCGAGGGTACTTCGTA

SEQ ID 4154

MCESPAVKVLHAVAGGSNHAFDLVVFSFGNGDOOGGRIFONGIGGTNGFVVFVERHAVFOSPAERFSCRVFERYFV

SEQ ID 4155

TTGGAAGCTGATTTCGGATACGGGCACATGACAGGACTTCTCAGTCCCTGCTCTTTTTCATCCACATTTCCCATACCATCATGAAACTCATCAAATACCTGCAATATCAAGGCATAGGAAGCC
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AGTAACCTGTCGTTCCCGAACCCCTATTCTCATCTCTGCTCAACAGCCTGGAAGATTACGAAATCTTCGACACAAACGCAACCATACCGCAGCGTATTTCAGTCTGTTCCCGCAGCATATATGCGGTA
AAGTATGATGTACGAGCGCGTCCGAGCGCTGGATGTCGGGATACGACCGGCTGATTTCGTGATTACCAACAGCAGCGGCAATCGAACCAACCTGACTTCGCGCGGACAGAAAAATCCCAAGCTGAT
ACGAAGTAACGCTCAAAACCCCTACAGGAGAAACGCTCTCGGAACTTTGAAAAAGCGGCTGCGCTCCACGACGAAAAAGAAACCGTTTGTGCGCCGATGCGGTTTGGAAAAATCCGAC
CACCTGCTGCTGACCATTACCGAAGGAAAAATACCACCAAGTCAAAACGATGTTGTGCGCGCGGCAACCGCTGCAACCACTTCACCGCGCGGATTCGCATATTGGAAACAGAAAC
CTCAAAACCGGGGAATGGAAATTTATCGAATGTCGGAATTC

SEQ ID 4156

LEADSTDAIDRTTFSVLSFSSHSHTFMKLKLYQYQGIGSRKQQLIRGGYVSINGTCMDTADIDSSYVETLIDIDGEAVTVVPEPYFYILLNKPDEYETSHRKPHYRSVPSLFPDNNR
NIDMQAVGRLDADTTGVLITNDGKLNHNLTSPSRKIPKLYEVTLKHPTGETLCETLKNGVFLHDENETVCAADAVLENPTILLTITTEGKYHQVKRWVAAAGNRVQHLHRRRPAHLETEN
LPGKPKTIECPKF

SEQ ID 4157

[illegible]

SEQ ID 4158

MNFWIITGKARDSLNRNRWVLAAVLLLAALALSGLFGSSPTGSKVDPLTVTVVSLSSLSIFLIPLIAMLLSYDALIGEIERGTHALLLSYPIWRNQILAGKVGHLLIILALATTAGY
 LAGITLQLANGGFDAIAWKPFALLIAASVILGAAPLSMGYILISAKVKERGTAAGISIGVWLFFVVIFDMALLGLVADSKQVITAPVTVETVLLFNPDIYRLLNLTGYENTAMVAGMAGLS
 GOIGLTPVPLIAOVLVWVLIPLVLAAGIFKKRI

SEQ ID 4159

ATGTGCAAACACTCAAACCATCGCCCTGACGCGATCAGGTCGTGCGGTTTGTGCGGGTTTCTATATATGCCAAAACACTCATCACACCAAGTCGSGTTTAGCGAATATGCGGTTAAACCTTT
CAATACCTCGACCTGCGCAACGACAAAACAATATTTCCAAATCGCGGACGCTGTGGGACBAGCTGCGCCAAAGGCTTCCGGATGGCGGAAGTCAATCCCGAAGCTGGTAGCGCGCCACGAAAGCAA
ATTCTATCGCAGCGCGCAGCTATTTTCGACAGGGTCGTCACCGGAGCGACCCCTATATGTACCATATCGTCGCAACGAGTCAAAAAACGCAATATGCGCGCGGAAGCGCGCCCTGCTTCCCTTC
ATCGAAAGCGCGTCGCTGCTCAACAAAGCGCAATCACTACGCTCGGCGCATCGGGCTGTGCGAGTTTCATGCCCGCTACCGGACGCGATTACGGCTTGGAAAAACAGCGGTTTACGCGCGGAGG
ACGACGCTTTAGCAGCTACCGATACCGCATCGCCGACTCAACATCTGCGATATCTCTATGGAGCTGTGCGGACGCGCGCTGCGCTTTTGGCGCTCAACTGAGGAGGAGGCAAGCTCGACGCGCGCG
CGTCAACCGCGCCCGCGACCAAGGGCTCGAACCGACCTACGAAAACTGCGTATGCCAACGAAACGCGCAACTATGTGCCCAAGCTGCTGCGCGTGGCGAACATTATTTGCCACCCCCAA
TCTTTGCGCATGAATATCAGCGCATAGACAAACAACCTATTTTCAGGCGAGTGGAAACGGGCGTGTGCGCTGACAAAGCAAGCATTCGCGCGGCTTGGCGGTCATCAGCGAAAGCGAGCTGTG
TCGCGCTGAATCCCTGCATTCAACGTCGCCCGCTCATCCCCAAAACAAACGCAAACTGCTGCTTCTGTGCGGTCCGACCACTTCCAAAGCAACTACCTCAACGCGCGCACCGGACAG
ACCTGTATTATCATGGGCTCTATACGCTGCGCGCGCAAAACGCGGCTTCCGACATCTCGACGGCAACCGGCATGAGCATTCGCGACATCAAAACGCTCAACAACTGAACCGCAACCTTGTG
CAGCGTTGACGAGTACCTTGTGCGCAAGAACCGCGCAAGCCCTTCATACGCGATCGGAATCCGCTGTTCATCGATCATGCGACATCGCCCGACACTACCGCTCCGAATATCGCGGCA
GCACGTTGAACGTGAGCATTTGCCGGAATCCAACCCGCGCGCGCACAGACAGCGGACATTCACGTCGCACTTTGCGCGCAAGAAACGTCGTCGACGAAACCGCATCCCTTGTGTCGCGATTAC
CGAACCGCGCTTGCACACGCGCAGCGCAACCTCAAAACGAAAAACAGACATGCGATGCGCTGTGAACACCGCAACCGCAACACTCGCGCAGGTCATCCCCCCCCAAACGACATCGACGGCGCA
GACGAACATCATGCAGCTTGTGCGCGAAACAACTGCGCGCGGACGCTGAAGAAACAATCTCCGCGCTCATCGGCACGCTGACACAGTGTGCCGAACAACAATTTCTCTATCTCCGCAAC
ATACCGTTGTCGCGCGGCGCAACCGCGGCGCACTTTGGAACAGCGCGTAGCCAAAGCTGCCGACGCGGAAGCGCAACCTCCCGCTCATTCGCGAGCATCCACCGCTGTAGAACGCG
CACCGCTTTCAACATTTGCCAAACGCTCAACGCTGACGCTGAGCGGACCTATTTGTGCGCAACAACATCAAGAGCAACACCATTCGCAAAAGGACAGGATTGTCGCGCTGCGGCTGAGGACGCCCT

GCCTAAACCCGATTATGAAAAGTATCTACACCGCGCGCAAAGGCGACACCTTCAAAGATATCGCGCGCTTCAATATCCATATCGACGACATCCGCGGGCTCAATCCCAACTGAACA
CCATCAATCCGGGACAGAGGCTCAAACGTATGGAAGC

SEQ ID 4160

MSKLTFTIALTSAGLSVCPFLYAQNTSSHQVGLAIMRLNSSILDLPPTKYTFQSGSLWDELRLQGRFMGEVNPENELVRRHESKPLASRSYFDRVNVNRSRPTMYHIANEVKKRNNMPAEAAALFF
TESAFPYTKAKSHVSGAGSLWQPMFATGRHYGLEKTPYVDGRHDVYAATAALNYQLYLGLPGDWPLAFAAYNVGEGNVGRAVNRARDQGLEPTYENLRMPNENTRNVKPLALVRNI LAPPO
SFGMNISSIDNKPYPQAVEPGRPLDNEAIALRAGITQSELLALMPAFNVPAPI PKNKRKLLPLVASVQTFQSNYLNAAPDLSFWESVYTPAAKTSLSIDISTATQIDIKRLNPNGLNV
NAGRSTLIVAKNGKTLHTASESVSSVIDNTDPDYRNSMPAGTVNVSIARIQAPAAQATDITVAPLQETVTRTEPLDPLVRI TEPAALATAAQQTKEQTAMPSETQSIATLQAQVILPMDQAA
DELMQVLVARNRLRRQAEEFISAVIGTPTVAEHNISSSPQHTVAADGKKRARLETSPHSAKAADGEAETSPHSAKHIDRVVEGDTFLNLAKRYNVSVADLIVANNIKGNPTIQGOVRLRLQAAP
ATRIEIKVTAARGKDTSLASARFNHIDDIRLNPFLNLTNPNGQVRKLIGS

SEQ ID 4161

SEQ ID 4161
ATGCATCCATATTGCGTCCGTTTCAACAGATTGCCTGCCGATATTTATTCCAAACAGGATTTCTGTCAAAAACACATCGGCCGCCCATTTCCGAATCCGCATAAAGTTCCTGTAAAC
TTGACGCTTTTTCAGTCAACAGTACCATCGGACGATAAAATATGTTTATTCGCCGAGTATAATCATGTCCAAACTCAAAACCATCGCCC

SEQ ID 4162

SEQ ID 4162
MHPYCVRFKOLACRYFIPNRI SVKKHIGRPFNPHKVPVKLDAFSVKQYHRTIKYVYSAEYKSCPNKSPSP

SEQ ID 4163

SEQ ID 4163

ATGCGATGATCGTTTGAAGATACGCGGATGGGGCGGTATGTTGCAAAATTGGAACAGGACTTCTTTAATCGGTATGTGGCGTCATACCGTTTTTCGGGAATGTGTGCGGTTCAAGTGGGCG
TFCAGTGGCTGAGCCTGTCTGAAGACATTTGTCTGTGTGCCCGAGATATGTTCGATGTGCGGCGGAGAAATATGCTTTTGGCGGATGTTTTTTCGGGATATGCTGCTTTTGGCCGCATACGCTGGA
ATGCGCGGTACCTTGCAGAAATCTGTGCGAAGCGCACCGGATATTGAAACCGTCCGAGCGTTTGATGCTGACGGGTTTCAATCCGTTATCTCGCTTTGGGGAATCTGCCGCTTTGACCGGT
GTCCGCTTGC CGGAAAAACGGTTTGTCTGCCGCTGCCGAGTTGAAAAAGCGAGCTTCCGATGCCGGTTTGATATTTGAATTTGGGAAATCATGAGTTATCTCGCTCCGCTTCCGCTTTCGTCGC
TCGGGCAAAATACGCTTTTGGCGGTTTATGGAAGAAGCGGGCGCACCGTTGTTGGCCGCAATGTGTGCCGAGTGTACCGTTTGGTTTGGTCAAAAAGGGCGGGCGGCGTAAACCCCTGCCCGC
TGGCGCAGGATTTGGGGCGGCAAAAGCCCTTGC GCGGGTTCGGCAAGGGTTGCGGAT

SEQ ID 4164

SEQ ID 4164

MDAWFEDTAMGRVTVAKLEQDFNRYVASYRPSGMCAYVGGQWLSLSEDTVCVPRDMSMAENMALADVADMLLLPHTLECGVPSQILSEAHRIIKPSGRIMLTGFNPYSLWGPCRWFDG
VRLPEKRFCLPLPELKRQLADAGFDIEPKGFVYVLPVSSLSQIRFWFMEKAGDRWNPQCAAYGLVLVKRAAGVTPLPAWDGTWGGKALAAGAARVAD

SEQ ID 4165

SEQ ID 4165

GTGCGGCAATAGGATTCGCGATTAAAGGACGCGCCTCTTTTCAGACGGCATCTGTCAAGAAGAAATGTCGGGAGGGGTTATGCCGGAATTGCCGGAATGGAACACAGCTTCGCGCGGCATCGCCCGCATATTTGAAGAAAAACCGTGGGAAGCCGPGATATTGCGCCAACTAAGCTGCGCTGGCGAGATCAATCCCGATTTCGGGGAGATTTCGTGCGGCGCGCAGGTTTGTCTTCGCGCAGGCGTGCCAAATATCTGATTGTCCGTTTCCAAACGGGAGTTTGTGTAATTCACTTGGGGATGTCTGGCGAGCTTCGCGGATCTTTACGCCCTCGGACCGAGCATATCGGCAGGCGCGGACAGACAGATCACGTCGATATTGTGTTTTCAGACGCGCAGCGTCATCGGTTACCGCGATCCGAGAAAGTTCGGCGCGATACTTTGGTATGAGGGAATCGAAGAACGTCATCCGCTGTGTGGAATAACTTCGGCGCGGAGCCCTTGTGCGGAGGCATTTTGCACGGATTATCTGTATGCGGGGCTGAAGCCGCAAGAACCGCGCGCTCAAACTCCTCTGTGATGGAACAATACCGCTGTGTCGCGCTGGGGCAATATTTATGCCAACAGAGAGTCTGTTTCAGGCGCGGCATTTTCGCCCCACCGCTCTGCCCAACCGCTTAAAGAAAGAGAGTTCGCGGCTTTGTTGGTAAACCGTCAAAAGCGGTGTTCGACGCGGCCATTGAAACGGGCGGCAGTACGCTGAGGGATTTCGTGGACAGCGCAAGCGCGCTACTTTCAACAGGAATATACGGTGTACGGGCGGCACAATACGCGTGCCTCCGCTGCGCGGTTTGTGTTGTGAAAGAAACTTTGGGGCAGCGCGGCAGCTTTTATTCACGAACTGTCAAGAA

SEQ ID 4166

SEQ ID 4166
VRQGLRIKGRPSFRRHLSBEMSGGVMPFLPEVETTLRGIAPHIEGKTEVAIVLRQLKLRWQINPDLGEILSGRQVLSGRRRAKYLVIRFQTGILLIHLGMSGSLRITPTPSDGRIGRDPDRHD
HVDIVPSDGTVMRIRDPKRFGAILWYEGIEERHPLLEKLGPEPLSEAFCTDYLAYGLAKQKRAVKLALMDNTVVVGVGNVIYANESLFRAGISPHRPNANRLKKKECAVLVETVVKAVLQRAIE
TGGGTLRLDFVSDSGKSGYFQOEYTVYGRHNPCLRCGGLVVKETLGRGTFFYCTNCOX

SEQ ID 4167

SEQ ID 4167
GTGCTTCCGGTGCGCCGGTTTGGTTGTGAAAGAAACTTTGGGGCAGCGCGGCACGTTTATTCACGAACGTCTCAGAAATAGGGCGGAAAAACGGTTCTCGACGGCAATTTTATCGGTATGCC
GTC CGAAACGTTTCAACAAACAAACACCGATTATCGGGAAGAANTGCCCATGCTCTTCAAA

SEQ ID 4168

PPVRRFGCERNFGAARHVLLHELSEIGRKTVSDGILSVCRPNVSTNTDYRERIAHVFK

SEQ ID 4169

[illegible]

SEQ ID 4170

SEQ ID 4170
LPMSSNKASFFTLRLRLCRLTVNLFPTGKNLRGIDGGCPKSRNRAVIALGKGALAAALDILEVGRPAPEHPNGVLVAANHVSMLDIFAMSAVYPSSTIAKQEIKSWPVLGKMGQNACTVFI
NRNSRRDIEPIINRAVCETLQRQGNVSFPPEARTSSGLGLLPPKAAFLQSAIDAGAKVLAVALRYDETGKRTARPSYADVGLPTCLWRIVSMKKLTIKVPVFCVADAASEEDRYALKDRIE
ESTRAVVAGDADVAV

SEQ ID 4171

SEQ ID 4171

TTGCCGTCCGGCTGCTGCTCGCATTCGCGACCGGTTCCGGCGGTTTTCATCATATGAGGACAGGTCCGCCGCCAAGTCCCCACACACAAACGCGGCTGGCATCCGGACTGGTCAACGC
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TTCTGCCCGTCTCATGGTGGCTTGCCGGCGGCAACAACGGCGGCAACAACGCCGCCACACCCAACACACCCAAAGCCACACACGGGAAGAGCTCAAAACCCGCCCTTCAA
AACCCCAAGCTACATCTGCTGCACTGAGCTTTTTCGCTCGCGCTTCCACATCGCCTTCTCTGTAACCCACTACCCACGGAAGTTCGCCCTGCGGACTCCGCGCCGCTGCGCTCG
ACATCCATCGCCATCATCGGACTGGCAAACTCGCCGGTTTCGCTGATCTCAGGCTGATGCACCGGACCTCTAAAGGAAACACACATCTCTTGTGGAGCTTACGCCTCACGCGTCGCCATGG
TGCCTGATTACATCTTCCACCAAAACGACCTCAACTTTTTCGATTTTCGCCCGCGCACTCGGATTACATGGCTGCCACCGTGCGCCCGACCGCCGCTTACCGGCAAACTCTTCGG
CAGCGCTACCTGCCACCCCTGTTGGAGACTGGTGTGCTCACCCACCAAAATCGCGCGATTCTCTCGCTCGTACATCGCGGCATCTGTGATTACACAAATTCGG

SEQ ID 4172

SEQ ID 4172
LPGGCCSHSAFVPAGFPLWDRSPPKSPHTNAAMHPDWSTQAVRQDNCSHRWFKDSRTRRPARSRLDGYILLRLGNRPAD SARLMAVACRRQQRQRRPHPTPHSHTRTKPRSSQNRLO
NPKLHPAAPELFLRLPLPRLSRNPPTGSRFVRTARHRRLDIHRHRTGKHRLLVLLRMHRTLQRKTHPVRTLRLTRRHGADLHLLTQNRPLLHFRRTTRTHMARHRRPDRRYRQTLR
HALPRHPVRTGDAHPPNRRIRPLVHRHRDYTIR

SEQ ID 4173

ATGCGCGCGGTCACCTGGTGGCTGACCCATCCGGTGAGATGACAGCATGGGTGCGACTGACCGCGGAATCGGCAGCGGCAATTCGGCAGCGCGCAATATTTTGGCGGATTTGGCGGTGC
CGCGCATCGATGCGGACGCGCGCGCGCACTCGCTGACGGCTTCAGACGGCATCGCCCTCCGGAATCAGGCGGCTGTCGGCGACACCGCTTTTCGACACACAGGGTTTGTTCGCGCGGA
CATATTGCGTAAGAAATCTTTGCCCTCCCATCGCCAAAGCCTTGCTCGAATCCGTGATGTTGCCGCTGATTTTCTCAGAAATCAAAAACAGCAAGAAACCTTTACCGATGCGGTTTAC
GGCATTTGCGAAATTCGCTGCTGACGGAAGCGTCAATTTATCAGCTGATACGGCGTCTGACCATAGCGCACCTTTGGAAAAACGATTCGCGAGGGTAATGGCAGCGAGCGGC
TGACGCGCGCGAGGTGGCGGACATCATGCCATCAGGCATCCGAATCCGAACGCGCTGCTGCTTGACAGCATGTACTGCTCAATGACGGCAGCGCTCAAAAGCCTACGTGAGAAACAAT
GCTCTGACGCGCTTTTATTCAGGATTTTCCCTCAAAACCAACAAAGGAAACACAATGGC

SEQ ID 4174

MAGQQLVADPSGEWTAVGLTGGIGSGKSAAYFADLGVPRIDADAAHSLTASDGIALPEIRRLFGDTVFDQGLLRDILRKEIFASPSRKALLESVNLPLIFSEIKKQOETPTDAVY
GIVRIPLLTREKQFISLIRRVLTISAPLEKRIGRVMARSGLTRGEVADIISHQASESERILLADDVLLNDGSLKSLREKTHLHAFYSGIFASKPTQGHNG

SEQ ID 4175

TTGTCGGAATGTCGCGGTATGATTCGCTTTTGGCGGATGCCCTTAAGCGTCCGGTAACGGGAGTACCTCAAAAGAAATGCCGTAAGGATAGTTGTGTATAGTGGATTAAATTTAAATCAGG
ACAAGCGCGGCAAGCCGAGACAGTACAAATAGCAGCGCAAGCGGAGGCAACGCCGTACCGGTCTAAATTTAATCCACTATATCTATGGAATGCAATCT

SEQ ID 4176

LSECGGMRPCCGLKAAVTGVPQKKCRKDSLLYSGLNLNQDKAAKPQTVOIARQGEATPYRSKFNPLYLWKHPS

SEQ ID 4177

ATGCTTGCCATACTGTTGCTGCAATACTGGGACTGGTATCAACAACCTGCCGTGCCGTGCTCAGAACCCGCCACCGACATACCAAACTATCAGCAAGGCAACCAAGCAGATGCTGC
ACCCGCAATGACGAAATATTTGGAACGCCGTGCCGCTGGTACCGATCGCAAGGCAACGTCAGGAAATGCGCGAAACAAAAAGCGCGCAAGCATTCGCCACCGCTGCTTATGCGGA
ACAGAAATCCAATGCCGGCGGCTTATGAGGCTTTCGATGATTTCGACGGCGCGAGGTTCCGCCGT

SEQ ID 4178

NLAILLAILGLVSTTAAAGTSEPAHRHTKHLISKANKQMLHPECKRYLERRAAWYRSQGNVQELRENNKARKAFETLFLYAEQKIQCRAAEAFDDPDGGRFR

SEQ ID 4179

ATGAGTCTGAAACTGCCGACAGTTTCCCGCTTCCATCTTCCATCTTATCTGGAAGGAATACAAACTGAAAGGATCGTCATGTCCTCAATAAGATGCTTGCCATACTGTTGCTGCA
ATACTGGGACTGGTATCAACAACCTGCCGCTGCCGCTGCTCAGAACCCGCCACCGACATACCAAACTATCAGCAAGGCAACCAAGCAGATGCTGCAACCCGGAATGCAAGAAATATTTGG
AACGCCGTGCCGCTGGTACCGATCGCAAGGCAACGTCAGGAATTTGCCGAAACAAAAAGCGCGCAAGCATTCGCCACCGTCTTATGCGGAACAGAAATCCAAATGCCGGCGGC
TTA

SEQ ID 4180

MSLKLPTVCPFHPSILYKELQTERIVMSVNDACHTVVCTGTGINNCRCRYVRTPPTYQTYQGGQADAAPRMQRIFGTPCRVPVPIARQRAGIARKQKAQSIHPALCGTENPHPGG
L

SEQ ID 4181

TTGTTAAATTTTGCAAGTATGATTTTGGCAGCGCGCGCCGACAAATTCATTTTCTTACCGATTGGAATTTATTTATGAGATTATATGTTATTTGAATTTGCATATCAACCGCAAG
TTTTGTCGGCTGAA

SEQ ID 4182

LLNFAKYDFCHAAADKFHFLTDWNLRLRLICVNLHLIKRQVLSAE

SEQ ID 4183

TTGCAAAATTTAACAATTCGACGGGCGGAAAAACCGAAGTTTTCCTTTTTCGTCGGAATTCCTTATTTTCATCGCCTTGTAGCCGGAGCGGTCAAAAGGCAAAAAATTTACCGTTTTT
TATCGGTAAAGAATATCAGATAAAACAATGTTA

SEQ ID 4184

LQNLTIIRGGKPEVFLFRKILISSPCSRSRSGKKPFRFLSVKNVQIKQHL

SEQ ID 4185

ATGAATACACCGACTGATTTAAAGTAACCAACGAGACGGAAGATTGGAAGCCATGATTTGGATAGATTCAACCGTGTCTTACTTTGGCGCGCGGAAGGATTGGAATATGTTCCGTGT
CGCAGGTCGAGTTGAAATCGCATATCCAGTTTCACAAACCGCATCCGACCCGACGACATCCAGCAAAACCATCATCAAAAGCGCTGCGAGATTAAATTTGGAAGATACCCCGGACATCAATA
CCTTGCCGACGCTTTGGCGATTTTCCATCTTCGTAAATAGCCTACGGCGAATACGAGCCGCGCACCTTTACAAACCATGTTAAAGGCTCACCGATGCCGGAATACGACAGGCATATC
CTTGAGGATTACAGCCCGGAAGAAATTTGACGAACCTGAACGCTATATCGCAACGACGATATGTCCTTTTCTATGCGCGCGTCAAAACAGCTCGAAGGCAAAATATCTGTCAGAAAC
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TCTTTAAGATGTTTACGCGCGCGGTCAAATCTTGTTCGCAAGGTGGCGTGGCGCGCGCGGCAACCTTGTTCACCCCTTGTGGCATTTGAAGCGCAAGCCGTGCTGGTGTGAAAA
CAACCGGGCGGTGAAGACACCGTATCCGCCAGCTTGATTATGGCGTGAATCAACCGCTGCTGTACACCCCGCTGATTAAAGGCGGCAACATTACCGCTGTTTTCGCCCAACGAGGTT
TCGGGGTTGTACGAAGCGTTTTCGCCGACCAAGCAATTTGAGCGGCTCTATACGAATACGAGCAAGACCCGAACATACGCAAGCGTATCAITTCGGCTGCCGACCTGTTTTCACGC
TGATGACGAGGCTGCCGGACCGCGCATCTACATTCAAAACGTCGATCACTGCAATACGACACCGCGTTCGATCCGCGGTGCGCTGTTTCATCAGTCCAACCTTGTGTATGGAAT
CGCCCTTCCGACCAACCGCTGGACAACATCAACGACCTGACGGGAAATAGCCCTGTGTACACTGTGCGCTTCAACTTGGGTGCATTAAACAGCTTGGACGAATTTGAAGGCTTGGC
GATTTGACCGTGCAGCACTCGATGCACTTTAGATTATCAGGATATCCCGTAGAAGCGCGCGTACCTTACTATGACCGCGCTTCGCTCGCATCGGTGTCATCACTACGCTACT
ATCTGGCGAAACCGGTGTCGCTACAGCAGCGGTTCGCGCTCGGTCTGACCCACCGTACCTTTGAAGCCATACAGTATTACCTGCTCAAGCATCGGCAACCTTGGCAAGAAATACGG
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AATGCAAAATTCGTGATCAGGCGATTTCGCCCAACCTGCTTACGACCGCGGCAATTCGAAGGTAACAAAGTTTCTATGAAACAAATGCTCAAGACCTGCTGACTGCCATCAAAATAC
GGCGTCAAAACCTGCTACTACCAACACCCGCGAGCGCGGACGACACGACAGCGATTTCAAGATGACGCTGCGCTGCTGGGCTTGTAAAGATT

SEQ ID 4186

MNPTDLKVKRDLGRLEADLDKIHVVWAAEGLNVSVQVELKSHIQFYNGIRTDIHETIKAADLISEDPDYQYLAARLAIPLHRLKIAYGEYEPHLYNHVKLLTDAGKYDRHI
LEDYSREEFDELNAVYDHERDMFSYAAVKLEGKYLQNEVTRQIYETPQFLVLVWAMCLFSKYPKEARLDYVKRFYDASTFKVSLPTPIMSGVETPTQFSSCVLIECDDSLDINAT
TSAIVKYVSQRAGIGINAGRIGLDSEIRGGEARHTGCIPIFFKMFQAAVSCSGGVRGGAATFLFYPLHIEAESLLVLKNNRGVEDNRIQLDYGVQINRLLYTRLLIKGNITLFSFNEV
SGLYEAPFADQDEFERLYTYEQDPNIRKRIIPADLFSTLMQERAGTGRYIYNVDHCNTHSPFDPVAVPVQSNLCMEALPTKPLDNINDPDGEIALCTLSAPNLGALNSLDELEGLA
DLTVRALDALLDYQGYVPVEARTSTDRRLSIGVINAYYLAKNVRSYDGSALGLTHRTPEAIQYLLKASANLAKEYGACTLFNQTVYSQGLPIDTYKKDLDAVCGEPLHYDWESLR
ADIVKYGLRNLSTALMPSETSSQIANATNGIEPPGLVTVKASKDILKQVPEFTLKNAYETLWQLPGNEGVLKLVGMQKFPVQAI SANPAYDPKGFEGNKVSMQMLKDLIPAYKY
GVKTLYYHNRDGDADTQTDIQDDGAGGACKI

SEQ ID 4187

ATGGTGTGATTTACATCTTCTCAACCAAAACCGACCTCAACTTTTACATTTTCGCGCGGCACTCGGATTCACATGGCTGCCACCGTCGCCCCGACCGCGCGTTACCGGCAAACTCT
TCGGCAGCGCTACCTCGCCACCTCTGTCGACTGGTGTATGCTCACCACCAAAATCGCGGATTCCTCGGCTCGTACATCGCGGCACTCGTGATTACAAATTCGTGACTACGGCTGGAT
GTGGTACGCGGATGCGCTACTCGCCGGCAGCGGACCTGCTGTCTGCGCGTCCGCGCAACCCGAAACCGCGCA

SEQ ID 4188

NVLITYIPSPKTDLPFYIFAAALGFTWLATVAPTAAVTGKLFSTRYLATFLGLVMLTHQIGGFLGSYIGGIVITQFGDYGMWYADAVLAGTAALLVLPVREPRTAA

SEQ ID 4189

ATGGCTGAATCGCGGCAACACGCGCTTCAAGTCAAATGTCCGACCTGTCAAACCGCAGTAGTATGGAACCGGAAACCGCATTCCGCGCGTTCTGTTCGCAACGCTGCAAACTGATCGACT
TGGCGGATGGGACAGCGGAAATATACGGTTTCCGGTCAAACGAAAGTTTGCCGGAATATCGAAACCGGACGGGCAACCGC

SEQ ID 4190

MAESRQTRLQVKPCPTCYAVVWKPENAFRPFCSQRCKLIDLGGWADGKYTVSGQTESLPELSEPDGAYR

SEQ ID 4191

ATGCCGCTGAAAAACAAAGGAACAACCATGACCAACATCATGTCGAATAGGAAAGTAACAAACGGTTCCGGCGCAAAAGCCGTCAGCAAGTCGATTTGGTTTGAAGCCAG
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CAAAGCGGGGCGCGCTTCGAGCCAAATCGGCTACCTGCCGAAACCGTTGCGCTGCAACCTTCGCTGACCGGCATCGAAACGCTGGATTTTATGCCAACTTAAAAAACAGCGCTC
ACGAGAACCGGGGCTGCTTGAGCGCTCGGCAATTCGCCAGACCGCACACCGCGCTCGGCACTTATCTAAAGGATGCGCAACGCTTGGCTTGGCACAAGCCCTGCTGGCGAGC
CCAAAGTCTGCTGTTTGACGAACCGCAACCGGCGCGACCTGCAATCAGCAAAATGTTTACGAAGTCTGCGCGAATCAACGGGCGCGGCGGCAACCATATTGCTCAGTACCCACG
CCTTGGCAGTGGACGACAGCGGACCGCATTTGCTGATGAAAAACCGCGTTAAGTTGCGGACGCGAGTATGACGAATTCGACGTCGCAAGCGGCTGCCGCTGACCTCAATATC
CGCTCAATGCGCGCGCACCTCAGCAGCGCTGGCAGCGCTTTCAGACGCGATTTCTTACCGCGCAATGTCAGCGCGAAGAACGTATGGAAGTCTTGGCGCAATTTGGCGACCGCTGT
CCGACCTTGCCTATTTCAGATCCACAGCGCGCTTGACGAATGTCAGCAGCTTCTTGAAGGAGGAGCGTA

SEQ ID 4192

MPSENTGCTMTTHHVELRKVTRFQAQKAVSQVDLVKAGESVGLAGHNGAGKSTINKLILGLITPTEGEVMLLGERTGSKAGARLRSQIGYLPETVALHPSLTGIEFLDFYAKLKKQFL
TQNRGLLERVIGISQTAHRRVGTYSKMRQRLALQALLGEPKVLLEDEPTGPDPAQRQMFYEVVRELNGRGATILLSTHALAELDGHADRIIVMKNKGKVDAGSMDELHVQSGLPLTVNI
RLNAPRTLSSRWQPLSDGISYRAQCQABERNMELGELSLDLAYFDIHTPTLDEMYARFLKREDV

SEQ ID 4193

ATGGATGTCATTTCGGCTATTCTAGTTGAATATAAATTTATATATTTATAGTGTCTTTTAGTATTGCTATTTTAGGATGGCACTTTATGATAGAATTCAACATGTTTATATGGTG
AATTAATAATTATAGAAAATCGAC

SEQ ID 4194

MDVIRSFLEYKFIIFISVLVFAILGWHFIDRIQHVLYGELKINRKVD

SEQ ID 4195

ATGTTTTCGGTCAAGCGGTAATGTCGCGCTTATGACAGCAGAAATACGAGGTATTGAAAACTGATTGAAAAACAATTTGCTGTTTTCGGCGCGCGAAGAAATCGACGCTGTCG
GCGACCGTATCGACTACGCCAACCTGCCGCAACGAAAAACATATTTTCATCAGCAATCTGAAATATCAAACTGCTCGATTCCATCAAGGGCGAGTCCGAATGTTGCTTGTGCTG
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CGGAAAAACCGTTACTGCTCTTTCGCGCGGTGAAAGAAAACTCTATCTCTGCTGCTGATGTGCTGCTCAATGTTTGAAGCCATCCGTTTCTACGTTTCAATTTGCTGCTGCTT
TGCTGAGCTGAGTTGATGGAAGGCAACGCCAAATCATCAAACTGATTGCCCGCGATGAAGCCCTGCACCTGACCGCGCAGCAGCATATGCTTAACTGATGCGTTGCGGTGTTGATGAT
CCGGAATGCGGGAATTTGCCCGGAGTTGCAGGACGAATGTTTCCAACTCTTCAAAAAGCGCGGCAAGCAAAAAAAGATGGCGGCAATTTGTTTAAAGACGGTTTCGATGATCGGTT
TGAACAAAGAAATCTTATCCCAATACGTGAATATATATACCAATCTGCGTATGACAGCGGTTGGGCTGCCGCGCGGATTGAAAGCGCAATCAAAACCGGATTCCTGTTGATTAATGCGTG
GCTGCTGCTCGCAACGTCAGGTCGCGCGCGAGGAGTGAATATCTCTTATTGATTGGTCAATCGATTCTGAAGTGAATACGGATGACTTGGCGGATTTTGAAGTTG

SEQ ID 4196

MFFGQPVNVARYDQKYEVEFKLIEKQLSPFFWRPEEIDVSRDRIDYANLPEHEKHIFLSNLKYQLLDSIQGRSPNVALLPLVSIPELETWVETWFSFSETHSRYSYTHIRNIVNDPSVVF
DDIVENEYITARAEDIACTYDLEIYTYQYINLGEVHNVGGKPTVSLRGLKKLYLCLMNVNLEAIRFYVSPACSPAFABERLEMEGNAKIILKLIARDEALHLGTQHMLNLMRSVDD
PEMAETAAELQDECFQLFKAAEQEKWAAYLFDGSMIGLNKEILSQYVEYITNLNRQAVGLPAGFEGANQNPFPWINAWLSSDNVQVAPQEVEISSYLIQIDSEVNTDLDGDFEL

SEQ ID 4197

ATGGCGCGCATTTGGTACGAATAAGGGCTTTTGGAGCTCTTGGAGGGTGAGACCTGTTGGAAGGCTTGAACGACGCGGCGATATGGTGAATATCAGTCCGCAAGCGGATATTGCGGAT
CGTGCCGGGTAAAGATTTTGGAGGGAAGCGTTACTTATCGGGAGCGGCTTTGCTTTTGGGGCGGACGAGATATGCGCGTCTGCTGTTGCTGCGAGGGGATGTCAGCGTGAATG
CGGTTTGGCGGGGAGGATGAGGGCTGCTGACAGTTTGTGAAA

SEQ ID 4198

MARIGTNKGLFELLEGETLLEGLERTGHMVEYQCRSGYCGSCRVKILBGSVTRYREPFLAFLGRDEILPCCCVGEGDVRILDCGLAGEDEGLSDSLX

SEQ ID 4199

TTGATGAAGTGGGTAACTGCTGTTTATCTTCGCACTTGTCTGTTGCCAATACAGCTGTGTTTCGGCAAAGGCAGCATCGGACGCAACAGCAGCTGAGAGAACAGATTGCCGTTCAAG
AAGAAAAAACAGACACTGCGCTACGCAATCATTCCTTGCCTCGGAGGCTATGATTTGGAAGAACGCTCAAGAACCATTTTCGGAATCGCCCGGTAGAACTGGGTTATATCAAGA
CGCGAAACCTTTTACCACTCATCAGGCATAACCGG

SEQ ID 4200

LMKWTVVLSFALVCCQYSWPGKSGISGRNSSLREQIAYQEEKQTLALRNHSLAAEVYDLENGQEAISEIARVELGYIQDGETTFYRLIRHR

SEQ ID 4201

ATGGACGTCGCGCGCTACCGAGCGCGCATCCACCGGTGAGAAAGAGCTTTGGAACCTTCGCGACGCGGACAAATCCCGCTATTCCGCGCAAAGCGCTATTGAAGCGCTCGAACACGCTCA
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GGCGAAGACGCTATTATTCGATTGACTGCGCGCTCCAGCAGTTCTACAAGACGCGCAAAATACCACTTGAAGCGGAGGCGCGCTCTACACCAACCGGAAATTTGCCGAATCTTGAA
GGCTTGGTTAACGAATTTCCGATTTTCCATTGAAGACGGGATGAGCAAAAAAGCTAGCAAAACGCTTGGTCAAGTCAAGTCAACCAATCGGTACTTTAAGCGAAACCTGAAAGCGCTGATCTGGC
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AAATGCAACCGCTACGCCAGCGTGATGAGCCACCGCTCCGCGGAAACGGAAGCAGTACCATTTGCGGCACTTGGCAGTCCGCAACCACTGTATGACAGTTAAACCGGTTCTTTGACCGCT
TCGACCGCATGGCGAAATACAACCACTGCTGCGTATCGAGGAAGAAATGGCGGAAGCGCGCTACTACCGCGCAAGCGGCTTCTACCACTGGGCAAA

SEQ ID 4202

MGRAAVPSGASTGQKEALELRDGDKSRYSGKVLKAVEHVNQIAQALIGIDANEOSYIDQIMIELDGTENKGNLGNATLAVSMVARAAAEADSGLEPLRYLGGAGPMSLPVPMNVING
GEHANNSLNIQEFMIMFVGAISPREALRCGAELPHALKKLCDSKGFPTTVGDEGGFAPNLNSHKEALQLMVEAAEAAGYKAGREVLFDALDCASSEFYKDGKYLHAEGRSYTNAEFAEYLE
GLVNEPFIISIEDGMDENDWEGWKLITKLGKKVQLVGGDLFVTPNPKILAEIGKGVANALLVKVNIQIGTLESLKAVDLAKCNRYASVMSHRSGETEDSTIADLAVATNCMQIKTGSLSR
SDRMAYNQLLRIEELAEAAAYPGKAAPYQLGR

SEQ ID 4203

ATGATGCAGACTTTCCGAAAAATCAGCCTGTATGCCGCAACCTTGTGGCTCGGTATGCAGATTATGCCAGGTTATATCGCCGACCGGCTGCTGTTCAAAATGCTGCCAAAAATGCAGCGG
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ATTGTCGCCCTTTCGCCCAACCAATTTTGGTTACACCCGTTATCGAGGCATGAAATACGGCATGAAATTTGCTGTTGTCGGTTGCAGGCGGATCTTCGGAATGTGGCAGCGTATT
TCCAGCATGACTTTCATGGCAACCGCCTACTTTCAGCAGTTTAAAGTTGGCGCTTTCGCCGCAAGAGGCGCTC

SEQ ID 4204

MMQTFRKISLYAATLWLMQIMAGYIAAPVLPKMLPKMAGEIAGVLPDILSWGLAVWGTVLAAPAAALTRRQTALLFLLSALANQFLVTPVIRALKYGHENWLLSVAGGSFGMHGI
SSMFFHATALLSAVLSWRLSGKEAV

SEQ ID 4205

CCCAAAACCGACTCACTTTTACATTTTCGCCCGCGCACTCGGATTCACATGGCTCGCGACCGTTCGCCCGGACCGCGCGCTTACCGGCAAACTCTTCGGCAGCGCTTACCTCGCACCC
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CGGCACGGCAGCCCTGCTTGTCTTCCGCTCGCGAACCCTGAAACCGCGCATGACAGAATGCCGTCTGAAACCTTCAGACGGCATTTTCCAAACACCCCGCGCTTTCGCCGACTGCACGG
CACGCAATCAGCCTTATCAACCGCAATTAACCGCGCATTAACCGCCATTCAAATAGCCCGCTTTTCCTTCGGGTGTAAATCATCAC

SEQ ID 4206

PKTDINFIYFAAALGFTWLATVAPTAATVTKLPTRYLATLFGVLMLTHQIGGLGSIYIGIVITQPGDYHMYADAVLAGTAALLVLPVREPRTA*QNAV*NLQTAFSKHPARCFRAR
HANQPYQTANNRRD*TAIQISPSFLRV*NHH

SEQ ID 4207

ATGGATATTAAATCAACGACATCACCTCGGCAACAAATTCGCTTTCGCTTATTCGGCGCATCAACGTTTATAGAGATTGGATTCCACCTCCAACTCTGCGCATTACGTGGAAG
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CAAAGCAGAGTTCGGCATCCCGCTCATTTACCGACGTACACGAACCCCATCAATGCCAACCGCTCGCGCAAGTGTGCGATGTCAATCCAGCTTCGCCCTTCTTCGCCGCGCAGACCGATTG
GTGGCGCAATGGCGGAAACGGGCAATGTTATCAACATCAAAAACCCAGTTCCTCAGCCCTTCGCAAAATGAAAAACATCGTGAAAAATTCGCCGAAGCGGCAACGGGAAGCTGATT
TATGCGAAGCGCGCAGCAGCTTCGGCTACGACAACCTCGTGTGATATGCTCGGTTTCGGCGTGATGAAACAAACCTTCGCCGCAACCTTCGCCGCTTATTTTCGAGCTTACCCATTCCTGCA
AACCCGCGATGCGCGTTCTGCGCGATCGCGCGTCTGTCGCGCACAGCTTTGGATTGGGCACTTCGAGGATGGCAACCCGCTTCGCCGCTGTTCTTCGAATCGCACCCCGATCCGAAA
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SEQ ID 4208

MDIKINDITLGNNSPFVLFGGINVLDDSTLQTCARHYVEVTRKLGIPYIFKASFDKANRSSIHSYRGVLEGLKIFKVKAEFGIPVITDVHEPHQCPVAEVCVDVQLPAPLARQTDL
VAAMAEATGNVINIKPQLSPSQMKNIVEKPREAGNGLILCERSSFGYDNLVDMLGPGVMKQTCGNLPIVFDVTHSLQTRDAGSAAAGGRRRAQALDLALAGMATRLAGFLBSHDFPK
LAKCDGPSALPLHLEWFLIRIKALDDLIKSPILIFIE

SEQ ID 4209

ATGTTCCGTACTATATCTGGCGGAAAAATCCACCGCCACCGTAACCGAAGCCGATTAACTACGTTCGCGCAGCATACCGTCGATCAAGACCTGTTAGACGCGGCAAGGCATTCGCCCCA
ACGAAAAAGTCGCGCATCGTCAACAAACAAACGCGCAACGTTTGAACCTATACCATTCGAGGAAACCGCGCAGCGCGCTGATTGCTGAAACGGTGCTGACGCCAGGCTGTACAGAA
AGGCGACATCGTCATCATTTATGTCTTATATCAACTTTCGGAACCGGAAATCGCGCACAGCAACCAAGTCTGCTTAGTGGACGGAACAATAAATCCCGACATCATCTCTACGAG
CCGCCGCACACCTACTG

SEQ ID 4210

MFRTILGGKIHRAITVTEADLNVGSITVDQDLLDAAGICPNEKVAIVNNNGERPEYTTIAGKRSGSVICLNGAAARLVQKGDIVIMSYIQLSEPIAAHEPKVVLVDGNNKIRDIISYE
PPHTVL

SEQ ID 4211

TGGATGCAATTTCGCCCTTCTGTGCGAATTGGAAGCCGACGATGCTGCACGCGCGCACTGACGGAATATTGAAACGGGACAGCCGCTATATGACTTTTACACCGAAGATACCC
AAACAAGCCGTGATGCGGCAAAATTTGTCCGCACTATGCACTTATATCGACTTATGGGCAAAATCCGGCTTTTCCGCTTATGATTATATGCCCCCAATATAGAAAGCGACGA
AATCTTTCGCGTCAAACTCGATTTCGACGCGCAGCATTTCTCAATCGATTGGGAGAGT

SEQ ID 4212

LDAAFAPLSELEKADDAARAALTEYLKRSRYIDFHTEDTQTSRDAKFVRTMQLIYISLWAKNPAPAVMDYMPANIESDEILAVKLHLHDSIFSIDSSES

SEQ ID 4213

TGGGTATCTTCGGTGTGAAATCGATATAGCGCTGTCCCGTTTCAAATATTCGCTCAGTGGCGCGTGCAGCATCGTGGCTTTTCCAAATTCGACAGGAAGCGGCAAAATGCATCC
AATGTTTCGGTTGCGAGCGCTTTTCAATTTCTGCTACAGGAATACCTCGACAGATATGCTTTGACGGTCAGCTCGTCTTCCAGAGGACATCTTCTCTCGTCAAAACCTTCGGTGG
ACAGTGTGGAATAGGGGTGAAAAATCGACATGATTGTTCTTTTGG

SEQ ID 4214

LGIFGVKVDIAAVFPQIFRQCAGSIVGTFQFGQEGGKICQCFGWQAVFIFCLQEYLDKIAFDGQLVFPEDIFFSVKTFGGQLLEIGVKRRHDCSFH

SEQ ID 4215

ATGTCGATTTTACCCCTATTTCACAACTGTCCACCGAAGGTTTTCAGCGAGAAGAAGATGCTCTTGGGAAGACGAGCTGACCGTCAAAGCAATCTTGTGAGGATATCTCTG

SEQ ID 4216

MSIFHPYFQQLSTFEGFDGEDVLWEDELTVKGNLVEVFL

SEQ ID 4217

GTGGCCCCGCAAAACCGCACGGGCGGCAGCTTCTGCATCGCGTGGCAACCGGTACGAACAACAGTCCGCCGCGCGCTTTTAACTGCGCAACCGCGACAGCGCTCCGACACCA
AATCC

SEQ ID 4218

VRPAKNGTGSFCAIVATGTNNTSAAPLLICHNADSRSDTKS

SEQ ID 4219

ATGGCGCGCGCTTGGCAAGGTTTGCCTCGCGCGCGCGTATCGGCATTTTCATCAATGCAGACCGCATTTCCAACTATATTCAGGTGTCCGCTTATGAAAAATCGTTTTATCACAA
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AATGGGGGTACACCCGTTACCTACCGGTCAACCGCAGCGGGTAAACCGGTTTTCGGATATAAATCCACCTTCTCTCATATTTAAAGCACTCAAAAAATATCGCGGATTGTTTTC
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CGTAAAAACAAAAATAAAGGGCATTTTGAATGCCCTGTACCGCATTGCCCTGCGCATGTTGGAAGGCTGATCGTATTAACCCCGACGACAAAGACGAGCTGCTGCATCAATACGG

CATCAAAATAAAAACATTTCATATTTTGGCGGAATCGGTCGGATTTCGGCGAATATCCTTATTCGAGGCGGATATTCGGATGAAAAAGAACCCGTAATAATTTCTCTTTATCGGCAGA
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 ATCTTGGCCGAAAAATGATTTATTTATCGAATAACAGGGCTGCCGCTCGATGGCGAATGCAAGTTATGCGAATGGCCAAGATAAATTCGATGCCGAAAAAGTCGATTTGAAATTTT
 TCGATATTTGAAGCG

SEQ ID 4220

SEQ ID 4220

MRRAWQRFARRAPPYPAFHQCRPHQSYIQGVRLMKIVFITTVASSIYGFRAPIVLKLGKNHQQYVAFVSEFSDNEOLDIREMGVTPVTTYRNSRSGVNPFSIDKSTFLIFKALKKISPDLVF
PYFAKVPVIGTFAAKLAGVPRIVGMLEGLGFAFTPOPEGISPLKTKIITKIGILIALYRIALPMLESLIVLNPDDKDELLHQYGIKIKNTHILGGIGLDLRQYTPYEADIPDEKEPVKFLFTGR
PLKEKGIDDFIRAAEQVKGKYPDTVPVTALGAIDKSRGGGGDLERFIARDIRFPGFVNNVSEVIKAHHTFVLPSYTYREGVPRSTQEMAAVGRAVITTDVPGCRETVAQKVNGLIEFVNP
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SEQ ID 4221

SEQ ID 4221

ATGTCCTCAACTATGTCAACTATTTCGATATTACAGCAAAATTATCAACAAGCGGGCAAGTGCCTTTTTCGCTACAATGCCAATACGATAAACTGTCGGCCAAATCATTTTGAAAACTGCC
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ACACGGCAACTACTCGAGCGCAACAACGCCCGCTTCGATTTCGTAACGGCGCAGCGCTTCGGAGACAGCGCGTACCGTCCCGCAGGCATCATCGACAAATCTTCGCGCGCGCGCCGTATCTCGCG
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AAACCGGTATTACAGCGCATGAGAAGCAGAGTGTCTCAAAGAAAGCCGAAACGCGGCAGTGCAGAACGGGGCAGGGCGGAAAAACGGTCTCTTGAAC

SEQ ID 4222

EQ ID 4222

MLNYVNSDSDIHDNIIINKAGKCVFAYNANYDKLSANHFENCQIGMHPATAAIEGTSLEHDNSFINNGSVQYVSTRFLDWSEGGHGNYNSDNSPFDLWGDGFGDSATRPDGIIDQI1WRAPVSR

LLHNSPATSIVKWAQAQPPAVLPGGVVDSKPLMKPYAPKIQTRYQAMKDELLKEATROQSERGRAENGSLN

SEQ ID 4223

ATGACCTGCGCCCATCCCAAAACCCCGTGAAAAATCCCGTTGGTTCAATCTTTTCGCAAGCTCGCTGCCCTTGGCTTTGGCGCGTTATTTTGCCGCAACAAGCGCTCAAAGCCGTCGTACACC
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 ATCGAGTTCAGGATCAATACCGTCAAAACCGTACTAAAAACCTGCAAGGCAACCGCTGCCCAAGAGAAAT

SEQ ID 4224

SEQ ID 4224

HTCP1PKPREKSRWFNLSCGSLPLALARYLPHKRLKAVITQDAEQALRLQTAWRFFRPHDTAVFLPDWETLPHYERFSPHQDLVSRRLSALWQIKSGAADVLFPVATAMQKLPVPVFLAGE
TFWLKGTQPTLDIGRLKTLVDVAGYHNHSHVVAAGEFAVRGGIVDLFPWGSFTPYRIDLFDDEIDISIKTPTDTQRTISPVSEIRLLPAHEFTDSEAKIFRFSRFRBEVDGNPNDAAYKA
VSNHGFGAGVEYVILPLPFENELETLFDYITGEDALFVSLGDVHAERANRPWNDVKSRYAMAQGDETYPPLLPQHLYSADVAGRLKNYGQVLPDVGSKAHSPLDPAVNRQSDPLQALKDFQ
TAPDGRITLLCAESLGRRETMGLGLFQQNGLKAKPVSDWQGLSAHEPLMITVAPLAYGFKLGGQSSSQQTVPASEGEGKAVTDQTEFSASATNPLPSPLPQERBQSAAAVSDGLKAAAVS
TESSLYLVASDLHGQTRQQSAPSPVGEWGEKGVAQAISAVITESDLYQVARSVRHNRKKRAAVSDGLLRDLAEINIGDPVVHEEHGIGRYTGLVIMDLGGETNEMMLLEYAGEAQL
YVPVSQHLILISRYSGQAHESVALHKLGSAGWNKAKRKAEEKARDTAARLNLNYAQAASGCHKFEINESDYQAFADGPGYEETDQAAAJAAVIKDLQAKPMDRILVCGDVGGFKTFVALR
AAFVAVWGGKGQVAVLAPTTLLVEQHAQNFAFRADFPPVKVASLSRPNKSKATKATLEGMADGTVDIVGTHKLQVQDILKPNLGLLIDEEHRFPVGROKEQLKRLRANVDILMTATPIPR
TILMALEGLRDFSLLTTAPSRRLAVTKFVKPKVSGREAVILRELKRGQGVFLFNEVETIENMRKERLETLPEARIQVAGHQLRERELQVMRDFLQORFNVLLCSTIIETGIDIPNANT
IIRNADKFGLAQLHLQGRKVGSRSHQAYAYLLTPEYITKDEKRLDAIAADELIGAGFTLAMQDLETRGAETILGEGQSGEMQVGFPTLYTEMLQAVRDLKKGRQDPLADPLGITTEIK
LESFALLPEDYCPDPIHERLVLKYKLAVCEVTQVKINATHEELVDRFGLTEQPVKTLTESHHLRLAAKELGIDATDATSEAVTVTFGRHECIDPTGILLIQTDKKYRLAGADKLRFAAEMEN
IEVRINPVKTVLTKLQKRLPKGN

SEQ ID 4225

SEQ ID 4225
ATGTGCTTTAAAAAGCAGCCGTGCCATGGTTGACGGCTCCGCGCTCGGTTCCGTTGTATCATCGGCTTCCCTGTGTCGGTTCCCATTAATCGCGCGCGGTCAAACCGCCTGCCACAGT
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GTAAATCATGCGCCCGGCGCCGCGCTCCGCGCTTACATCCACAAACACACGCTCGCTGGTGGCACTTCATCTTCGGAATGCTCTTGGGTATGACCGGCTATTTGGGACA
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SEQ ID 4238

NADMKKITPQNLRLSLSLGHDTDFVNVNLALIKFLRRGGKKCAGERFDLIIDTFKQDRELLSRFSRCFYIWLAIHTYALIKLIGFSRHSFAREMGIRIYERPMPSYKDFANLGEVFLY
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RKGAGSGSSSVKVAHLERLRQTVGRKLKLLTDIQTGAGNSRLTIALMNSLIYAEEQYSTRHLRRSSIRMLARSITENKSHGHEHYITRNKKEYFKMPSAAGGGGIALMALLKIRIG
TLDLSPFLASLSAGFYIGFMIHMLHCTVATKQPMATAASFABQVDLNEGGKAVDNLSKLLIDVCRSQSVAVFVGNVSIALLACAIISFGYAHLYRLPILDAHTAAYQFKSIDLINHPT
LWYAAIAGLWLPSCGIIAGFPDMRADYINLRQLRPFNPLRLKIRMPRRVLAAYIHKHYSLVGNFIPGMILLGHTGYFGHLLGLPLDIRHVFSSANLGYAAVSGNVGFTFVLGIFSVL
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SEQ ID 4239

ATGAAGATAACACTCGAAATTAAGAAAGAAAGTACAGAAAGAACCGCTCCGTTCTTTGTACCGGAAGTTACCGCCGCTTCTGCGCGCATATTTGGGTATCCATCCCGATTCCGCGG
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SEQ ID 4240

MKITHCKLKKEVQKEPLRSFVPEVTARSAADIIGIHPDAAALFYRKIRTVANHRLAALADGVFEGPAGPGSGYFGRRRGRGRGAAGKAVVFGPIKRNGRAYTVAADNAEPETLPPAVK
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SEQ ID 4241

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SEQ ID 4242

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TGRGRVIRGKTHIEPIKNGEREIVIDEIPYQVNKALVEKIGDLVREKTLEGISELRDESDBKSGMRVVIKLRNENAEVVLNQLYKLTPLQDSFGINMVVLVDGQPRLLNLKQILSEF
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SEQ ID 4243

GTGGCGATGGTTGCGTGGCTCATGTTTCAATGTTTCGTATGCGCAAAAAATGTTGCTTATTTTAGCATATTTGACATGAAACGGTGCGCGGTTATGCCGCTC

SEQ ID 4244

VADGCVGHGFNVSYGKLLLLILAYFDMKRCGGYAV

SEQ ID 4245

TTCGCTGCGTCACTGTTTCAATGTTTCGTATGCGCAAAAAATGTTGCTTATTTTAGCATATTTGACATGAAACGGTGCGCGGTTATGCCGCTGAAACACGGTCCGGATTATAATGCGG
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GCGGATTTCGTATCAGATTTTCAAGGATCAAGTTGTTGCTGCGCGCTCCATCAGCGTTTCGCGGCAATTCATTGCTGATGAGGAAGTGGGGGCAAGAGGATATGTTCC
GCGCATCGCATCGATACCGGATGTTTTCAGCAGGTACCGCGCGGCTGATGGGATTTTCAAGGTTGCGG

SEQ ID 4246

LRRSNQCFVWQKIVAYFSIFRHETVRLCRLKHGADYNAEKISWRSLSRNLPMWTCAAVQSWRANDCFRPNQSFCSARISLSRPFKDSRLLPARASISVSRHSICMRKSGAKEVCS
GASASIPDVFSRYAARSMGFFKVR

SEQ ID 4247

ATGATGTCTCCACCATCAACGATGCTTACCGCACCTTGAATAATCCCATCGACCGCGCGGTACCTGCTGAAACATCGGGTATCGATCGCGATGCGCGGAAACATACCTCTTTCCGCC
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CTGCGGTCTGAAACAGTCACTCGCGCGCAAGACTCGACACCGCGCACAAAGTCCGCCAAGGAGGTCTTCGACAACTCCGCCACGAAATTTCTCCGCATTA

SEQ ID 4248

MMSSTINDAYRTLNKPIIDRAAYLLKTSIDADAPHTSFAPDFLMQMEWRETLMEARAGNNLESKNLNEIRAEQKLPGLKQSFARQDCDTAAQVVRQGRFLDKLRHEISSAL

SEQ ID 4249

ATGGAACCGGCGGCAAGGCGCGTAGGTTTGTTCACAGTTTTCGGTGCCGATATCGAAAGCGGTTCAATCCGGAAGAGGTGAAATATTGGGACATAGTAGGATGATAAATGTAAGAT
TTTGGCAGAAACTGTTTTCCTTA

SEQ ID 4250

MTGGGAGVGLPVFVADIESGFNPREBEILGHSRMINVRFQKTFVPL

SEQ ID 4251

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TACCGCCCGGAGCGATCCGAAGCGCGCGGTTCGAGCGCATTTGTTGGACGATCGCTCTGAAGGGCTTTATCTGTTTCC

SEQ ID 4252

LILSRFYALNVEALAAAAGVFDIGVFKFETFLQIFPGVIDCAVQINQAFRVDINARAVSFENQVAVGFIDKFVVRHPRAAAGFTQAYAQAFAPGEIVIDVFGILGKNHISLL
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SEQ ID 4253

ATGACGGGATCAGGTTTCCGCGCGGACGATTCGGCATTCCCGCTTTCGCAAAATGTCGGCTTTTGGTTTGTCTTTATAAGATTATTCGGTAATTTATTCGCGTTTTCGGTTTGT
GTGTCGCCGGAATCTCAAGGATTTCTGTATTTGGCAACGCTGCGCGGGAACCTCTATACCGCGGAAGCCAGCAGGTTGGCGAGTGCTCTGTCAGAA

SEQ ID 4254

MTGCRFPGRIRHRSRFRNVGFVVFIRLFGNYSALRLCAAGISRDSLILYATVRETSIPKASRLASASSE

SEQ ID 4255

GTGAATATCGGAATAGTTGACATAGTTGAGCATGATGCCCTAATCGCGGCTGCCGACGGCGATATTGTCGAACACTTTGAGCCGTTCCGAAACATCAGCACATAGCCCATATTTGTTGCC
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CTCATACCGGAACGGGTAAACGCTCAGGTTGCGGAGCGTTACGTCGCGCGCTGTACGGCTATGGTACGCCGCTCTTGTCCCTTCGATGTTGCGGAACGCTCGGCAGGCCCTTCAATCG
TAATCGGTTTTCGATATAAAGTTTGGTTTGTATATACGCCGAAGCCAGTTTGTATCGTATCGCCGCGCGCGCGGCAAAATTTCCGCAAGGTTGCTTTCGCGGGAACCGTGGACGAC
GGCTGCCGATGCCGTCTGAAATAATGCTGCCGCGCGCAAGTATCAGCAGCGCTTCAGCCATATACGAGCGCGGATGTGTGCATAGTGTCCCTCTGTTCTGTTTCGGTATGGCCGAACAAA
TAAAGCATCATTTAAATGTCCTGTTTATATAGCGAAACGCTGAAACGGTACCGCAAGCGTTTGCTTA

SEQ ID 4256

VNIIGVIVHEDIALAAADGIVERFEPFKHQHIAHIVAHGNIAADFVAVGVHIVDGTQVAEAVVFIGVVRAGIGKNAVPPFNVVADDLRAGRVFNGNIAALIIHAQRIADDFILAH
HRIGRTMKVYERILKNIIVFNQARGGPFPEINTGICWQAHGTGNGQVAERYVRVYGTGTPALVPPFDGCTVGRPFNRNRFVDIKFGLIYAGSQFDRIARPGAGNFKGVVLGRNVDD
GCRCLKNAAGKYQHGLQPYTTERGCVHSVPLFRSVWPNKIKHNSNVFVFIAPKETVRQAVHL

SEQ ID 4257

ATGAGCGTAGGTTTCTGAGGATTTCTGTTCAAACAGGTGCTTACTGTTGAGCGGGCGAGCATTTACTACAAATGAGTCGACGCGGGTAAGGAAGTGTTCGCGATGCTGTTTTCAGAG
GTGTCATTTCCGCCCAAGTCGCTTTCGCGCATTTGATTCGAGGGGTTCAGTTTATTCGATTTCTGATTTTCGCTCATTTATCCGCCCAACAGGTCGTGATGGGGGTGTGACGGAGGAGCAGAT
GGTGGAGTTCCTACTGTGTGCGGTTTTCGCTCGGGCGCAAAAGTATTTTTCGCGTTTTCGATTCGACCCAGATGCCGCAAAATCAGAAAACCGTTTCTGCCCGAGGATTCGGTTGAG
TTGGTCAATTTGAGGATGACCACTTGGCGGTTTTCGCTGATTTGGTGGGTTCGCTTTCGACATCGCTGCTTCAGGAGCTTGGGAGGGGCAAGAGGAAGAGGAAGCCACACCTGTATA
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CAGGACGGTAGGATGACGCTGACCTTTCAAAGGGCGGCAAGCTGTCGATTTCCGTGTCAGCACATTTCCGACGCTGTTTGGCGAAAAGGTGCTGATGCGGATTTTGAATTTCCGATGCGG
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GTCGCTCTATACTGTTGAATATTTGAATACGAGTCCGTAATATTTGCAACCGCGGAAGACCTTCCGAGATTAACCTGCCGGCATCAATCAGGTTAACGTCAATGATAAGCAGGCT
CTGACTTTTCCCGCTGCTTTGAAGTCTTTCTGCGTCAGGACCGGACATCATTTATGCTGCTGAGATTCGATTTGGAAGTCCGATATTTCGAGTTAAGCGCGCACAAACAGGCGATA
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SEQ ID 4258

MSVGLLRILVQNVVTVERAHYINESQAGKEVLPHLSDGVISPKSLAALIARVFSYSTLDLRHYPRHRLMGVLTPEEQVVEFHCVPVFRRGDVPVFAVSDPTQMPQIQKTVSANGIAVE
LVIVEDDLQAGLLDWGSRSTSLQLGEGQEEESHTLYIDNEEAEDGPVFRPIHKTLSDALRSGASDIHFEPYEHNARIFRVDGQLREVVPPIAVRGQLASRIKVMRLDISEKRIP
QDGRMQLTFQKGKQVDFRSTLPTLFGEKVMRIILNSDAASLNDQLGPEFFQKLLLEAHRPYGMVLVGTPTGSGKTVSLYTLNLTATESVNIAETAPAEINLPGINQVNVNDKQ
LTPAALKSLFRQDPDIHVGEIRDLETADIAIKAAQTGHNVSTLHTNNPATLSRLAMGVAFNNIASSVSLIMAQRLRLRLCSSCKQEVERPSASALKEVGFTEDELAQWKLVRAGV
CDRCRGGQYKGRAGVYVEMPISSEMRVIMNNGTEVGLLDVAYKEGVLDLRAGILKIMQGTTSLEEVNTAMD

SEQ ID 4259

ATCGCGTCCGAACCGCGCGCTTCGGATCCGTCGCGGGCGGTACAACAAGGAAGAAATATGATTACCTTTACCGAGAAATGCGCAAAACACATCAATGACTATCTCCGCAACCGCGGCA
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TTATATCGACCCGAAAGCTTGTGTTATCTGGACGGCACACAAGTCGATTACCAACAAGAGATTTTCAGGAAGGTTTCAAATTTGAAACCCCAATGTCAAAGACTCTCTCGCGCTCGCGC
GAGAGCTTCCACGTT

SEQ ID 4260

MPSEPPAASDPGAVQQRNMITLTENAAKHINDYLAKRGKGLGVRLGVKTSGCSGMAYNLEFVDRANGDDLIIFBHGARIYIDPKSLVYLDGTQVDYTKEDLQEGFKFENPNVKDCGCG
ESFHV

SEQ ID 4261

ATGGCATACAGCGATAAAGTAATCGACCACTACGAAAAATCCCGCAACGTCGGCACTTTGACAAAAACGACGAGTCGTCGGCACCAGGATGGTCGGCGCGCCCGCTGCGGCGACGCTGA
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TCTGGATGACGCGCTGGCAATCAAAAACAGCGAAATCGCGAAGAACTGGAATTCGCCCGGTAAAAATCCACTGCTCCATCTTGGCTGAAGATGCGGTAAAGCGCGCGTTGCCGACTAC
CGCAACCTCAGGAAACAGA

SEQ ID 4262

MAYSDKVIDHYENPRNVGTFDKNDSVGTGMVAPACGDVWRLQLKVNDEGIIEDAKFKTYGCGSAIASSSLITEWVKGSLD DALAIKINSEIAEELPPVKIHCSILAEDAVKAAVADY
RKRQENR

SEQ ID 4263

GTGGATTTTACCGCGCGCAATTCAGTCTTCGGCGATTTCGCTGTTTTGATTGCCAGCGCGTCATCCAGACTTTTGCTTTGACCCACTCGGTAATCAGGCTGGACGAAGCGATGGCG
GAACCGCAGCGTAAGTTTGAATTCGCATCTTCGATGATGCTTCATCGTTTCACTTTGATTGACGGCGCATCACGTGCGCGCAGGCGCGCGCCGACCATGCCGTGCGGACGGACT
CGTGGTTTTTTCGAAAGTCCCGACGTTTCGGGGATTTCGTAGTGGTCGATTACTTTATCGCTGTATGCCATGATGTTGTTTCTTAAATATCTGGTTTGTGTTGATGTTT

SEQ ID 4264

VDFYRRQFQFFGDFAVFDCQRVITQFAFDPLGNQAGRSDDGTAASVFEPRIFDFAFIVHFDLQAHVVAAGGRADHAGDGLVVFVESADVAGIFVVDVTFIACHDVVSLKYRGLIMP

SEQ ID 4265

TTGGAGAAGCTGAAAAACGAAAACTATTTCGGGGTGTGGATAAAGATAAAATTCGCCGAGCGTGCAGCCTATTATTGACGAGTTGAACGCTCTACATCTTTTCGTGAAGAAACGGCA
GAACATTCGCCCTGTTTATGACACAATTCGCAATAAAAAACGGTTTTTCAGATACATTGGCAAAATATCTTCGCCGAACAAATGATTCAAGCCTGTATTGAGGCATACCATGCGGATAGCAG
CTTATTGGCAGCCCTAATATTAGACAATTAGACAATCGTCTTTTCAGACGACTAAAACATCAACAAACACGATATT

SEQ ID 4266

LEKLNENYLRLVDKDKFAERAAAYLDELNVLPFFREGNGRLRLFMTQLAKNGPQIHWQNI SAEQMIQACIQAYHADSSLLARLIIRQFRTIVFPRILKHQQTTF

SEQ ID 4267

ATGAGTAAATACGGTGGTGAAGACGTAATCTATATGAATGATGGTGTATTAGAAATAAATTAGCCATTCAAGATCCACTTAAATTTAAAAAAGGTGGAAGAGACATTTCTGCTATTTC
GCCAAAATCTGCTTTTGCAACCCATTACAGGCAATTCGATTTCGGCGCATTTACAGACCATTCATCGCAACTGTTTGGCAATGTTTA

SEQ ID 4268

MSKYGGEDVIYMNQVFRNKLAIQDPLKFKGRKRHFYFRPKSAFATHYRQFRFGAFTDHSRTVWQCL

SEQ ID 4269

ATGGAGAATTTAGAAATAGCCGACAACTCAATATGCAATGCAACTTCTAAAGATTGGTAAACAAATATTGAGAAAGAAATAAGAAAAATTAACAAAGGTTT

SEQ ID 4270

MENLEISRTQYAMQLLKIGKTNIEKEIRKIKQRF

SEQ ID 4271

ATGGCGCGCGCATTAAAGATTGATGTCACAAAGAGCTGTCTGAGAAAGAATACCATGAAAGTTAAATTTAATTTGCCAAATGGTTATAAACGTATTNTTATGAAAAATATTTTGAAC
AATTTGACTTAGATTATGAACAAGATTAGACGTATTAAAAAAGATATTGAATTTGCTTTATCTGTTATTGAATACAAATCGATCTATATTCAAAAAATCTCTTCTCTATTGAGAAATA
AATCATTTTGTATTATCAAGGAGGACATCATCTGATATTATTGATCGTATAAGGAAGTTTGAA

SEQ ID 4272

MGGALRLMSNKGCLRRKNTMKVKIINLPNGYKRIIYGYFEQDLDDYEQDLVLLKKDIEFALSVEYNSIFKKFSSLFENKIIFVYQGGHLDIIDRDKGSLX

SEQ ID 4273

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CAGCGGATCCGCTGCACTCTCGCTCGTCAACCCAGCTACGCTCGCGCGCTTGGCGCGCAACGACGAACTGGCGCACTACCTTCGCGCATCACTTCGCGCGCATGACACCGAA
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AT

SEQ ID 4274

MTVKTPVYLDYAATTPVDKRVAEKMI PYL FETFGNPASN SHAFGWTAEAEVEKARADIAALINADPKIIVTSGATESDNLAIKGAANFYKTKGKHLITVKTEHKAVLDTMRELERQGFV
TYLGVQENGLIDLEELKAAIRDITILISIMVWNIEIGVQNI PAIGEICRERKLAFHVDAAQACGKVPVDVEAAKIDLLSMSAHKVGYPKGIGALYVRRKPRVRLAQMHHGGHGERGFRSG
TLPTHQIVGMGEAFRIAKEELAQDTAHYLLKLRDIFLKGIGIEEVIYINGDLEHRAPNLNVSFNPVEGESLIMAVKELAVSSGSACTSASLEPSVILRALGRNDELHSLRLITPRMTTE
EEVQFAELIKSKIGKLRKLSPLMEMFDGIDLNSIEWAAH

SEQ ID 4275

ATGCAAAACCGTCAAACTCGCCAACAGGAATCGAACCTGTATTTACGCTTAGGAGGCATACGTTCTATCCGTTGAACTATGGCGAGCCGAAA

SEQ ID 4276

MTVKPRQESNLYPTLRRHTFYPLNYGEPK

SEQ ID 4277

ATGGCGTCTGAAGGCAACAGGCTCTCAGACGGCATTTATAGCCAAACCGCTTCGCGTACCGTTTCAGGCGGTTTCGCTATAAAAACAGGCACATTGAA

SEQ ID 4278

MASEGNRSSDGIYSQTACRTVSGGFAIKTGTFE

SEQ ID 4279

GTGTCGGATAAGGTTGGAAAAGACATCCGGAATCCGGATTATTGAAAAAGATCTTAATTATAAGGCAACGAGCAAGCAGGGCAAGAAAACGAGTAGGCGGCGCGGGGTTTCGCGCC
GCCATTCAAACGTCCGCGAGACA

SEQ ID 4280

VSDKGWKRHPESGLLKKILNYKATEQSRARKRVGGAGVSARHSNVROT

SEQ ID 4281

CGGTTTGACACCGTTTCTTCCAAAAGGCGCATGATTTCAGCGGGCTTTTCTCGCTCAAACTTGTTCCAACTGGTTTCTGACCAACTCGAAAGGCTGCGCGTGGGGTTTTTCCG
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TTAAAGCGGTTTGGACATCTTATCTTATCCAACTTCCTTCAATGCCCTGTTTTCAAACCTCCAAAGTTTCAGCGCGCGGACGCGCATCTGTTGCGATTGCTGCGCGTCCGCTC
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SEQ ID 4282

RPTVFPQKIDFPAGFLPQLVSDQLERLVRGVFPDRAEFQVIAQFDRIAGNVATVHTGKLRSQRLKILRHNETVERLLVVRITLHQPFRRQPFQELRLRLRLFLGCEADL
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NCGSGLFLPHGIPCPARRQ

SEQ ID 4283

TTGGCGATGAACGCGCAACCGGCGCGCTCAAACCTCAGTGCCATCAGCGAAGCCAAAATATATCCCTCTCTATCTCGAGCAATGTTTCGGCAAACTCCGCGCGCGGACTGGTTGAAA
GCTTGGCGCGCGCGCGCGCGCTACATCTCGCGCGCGCTCCGCGCAAAATCAACATCGCCAAATCATTTCCGCGCGGAGACCGGCTGGAGCGCAACATGCGCGCAGCAAGCCAA
CTGCCACCAACGCGCGCGCTGCTGACGCGACGACTTTGGGAGAAATTAACAAACCAATCAACGACTATCTCGGAGCGTTACCTCGAAAGCATCATCGAACAGAAAACACGCGGAC
GGCAGCGCGCTGCTCAATTTACACACATCCAT

SEQ ID 4284

LAHNAQTGAVKLSAISERQNI SL SYLEQLFGKLRAGLVESLRPGGYYILAAPQINIAQII SAAEDRLDATQCGSKANCHGAPCLTHDLWENLNTINDYLSVTLQSIIBQKNNGD
GSRVQVFTHH

SEQ ID 4285

TTGGTGGTCACTCTCATGGTGGTGGTGGCTGCTGCGCTTTTTATAGTGGCGGAATGTCCAATATCTGAGTGTTCAGTCAAGTATGGGGAGCTGTTGCCGATTGTTGTTTAAAT
GGCGGTATAGTCTGATTTCCTTATTTGTTGGTTTTTGAATCAGTTAGTTATGTTTTGAGGAGCGCGGTTGGGCGTTTTGCGCGCAAGCGTTTCAAACGATTGATTATTT
T

SEQ ID 4286

LVSILMVVVARVGVFFIVGGIVQYLSVSVKYGAVADCLFKWRYSLILLYLFGFLNLQVMPFERRLGRFAGKRFQNDLIYF

SEQ ID 4287

ATGAAACGTGATTGAGCAAAATGACCTGCAATTGAAGACTTGCACCGCGTTGCCAAGCGCAAAATGCCGCTATGTTTTACGATTACATCGATTTCGGGTTCTGTCGACGGAACGACTTATA
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GAACACGGAACCGCGCAGTTCCGCAATATCTGTCGACACGCGCAAAACGTCGCGGATTGTCTTCTCTCTGTCGACGCGCGAACAGTTGACCGCGCTTAAGCTGGGACGAGCTG
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GTGGCTTTGGTGGCAAGGACGATGATAGTTCGCGCTTCTGTATGTTTGGTGGCTATGGCAAGAGCGGTAACGCGCGCGCTGAGATTTGTACAAGGAATGGAATGTCG
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SEQ ID 4288

MKRDLSKMTCTIEDLRVAKRMPFYDYIDSGSWTEFTYRENTSDFDKIRFQKVLVMEGRSLETKMIGGDVMPVALIAPTGTMAHADGEILAAARAEKPGIPTSTMSICSIEDV
AENVSAPPFWFLYVMDREFMENLIRKADAKSALVLTADLQVLGQRHDKINGLSAPPKPTIANLINLATKPEWCMKMLNTERRTFRNIVGHAKNVGDLSSLSSTABQDPRLSHDDV
ARIKDLWGGKLIIGIMEPEDAEAKASGADALVVSNHGRLDQTVSAIKALPDIVSAVSGSDIEWMDSGIRSGQDILKAWLAGKTMIGRAPLYLGLAYGEBGVTRALEILYKHEHVS
NAPTGHREDIQDVASILRSKDWGRETV

SEQ ID 4289

ATGGCGAATAATAAACCGTTGTTGATTGGGTGGAAGACCGCAAAATCAATGCTGGAAGAAATGGAACAGACGGAATTTTTGCGCGTCCCTGAATTTGTTTCCAATAATTTAAATATCCGT
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SEQ ID 4290

MANNKTLDFWVEDRKSMLLEMEQTDFFALPEFVSNNLKYPPFEWQKSALENFVIFDRTSKLKDFDPIKRNPHLLFNMATGAGTKMMIALILYYPEKGYRHLFFVNKNNIVYKTEHNP
DPHFKPLFTFKLQGDVFIPIRKVETFSQVSDGIEIKFPTSQKLYNDIHTERENQTTADLHMLNLVILGDEAHHLNAQTKGKQGLDLBKEMNERTSDAEIERKWEHMLLELLLNKH
GNPQGNVLEPTATLPENAEVQKQYADKIITKFLKEFLQKGYTEINLVSGTLNKKERVLEHLLFMYRHQIALKYGLANFKPVLFRSKTIDESKADYSAPLWVENVQADDFSFITTF
STSLSDSNWANEQKTRTEQALFKPMQENKFEFVHLANWVKQYQKHNVLIITNSETNKTTEKTDSETEKLLANLEADNPRAIFTVDRLTBGNDVILNFDIVRLYEQNGGGSNNKSGKT

AAATVSEKQLIGRGVRYPPFAPECKQPNKRFPNDHQHELRIILELFYYTHDEQSRYYITELKNELRKDGYPKEDDDKVLITPFLKSEFADNKDFRELLIWANKKIPNPNKSNNSNADSLQA
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EKHLNESDIPFIGTKFTPPKKLWEIPGTQKQWKKDDIKTALATQNDWYVMDNFAGTGLEBALIQIISARIGDLKSQYDVHLIRNEEVFLNNFADGEGFPDPFVLLKKQKQSSSDSDV
DFLHYQIPIEPKGGLHVENDSWKEAFLKSTVETGRDKLQKNTPHYRLIGLPFTTDHQKQGFTELFLPGAASLEK

SEQ ID 4291

[illegible]

SEQ ID 4292

SEQ ID 4292

LLNNDELKRHFVVEVNGVLVFLKDFRFFDLKHSINNSYTKYANRIGLTDGNRFLKONSDIVLDFPFKDCVLNGGQSTEEGEETYFKRNSQPASQPASQPASQPASQPASQPASQPASQPASQPASQPASQPLYTKLTRKRQEIFFNQTLAFDEIDRLFDAKAFSKFSRHTADGKQVGEIKRRSDGTPAENLITKGNLITAMHSLAQFGKGVKLVIYIDFPYNTETDSFAYN
DKFSHSTWLTFTMKNRLEIAKELIKDDGLFVQCDDKREQALVILVLDISTFTRENFLNCIAVOMSEPSGNKMAHFSHREKEIKKEYILTYVKNKKNLKNIPREQKSEMDNEYNITLENFTQDEYK
FIDLIVNSQTEKNKEINGFLKEIDILLKKISPISVNQKALQWIKNDNEVIKWLDNAYRIVRTAASSVKVLKADDEKICQOOFVSVSKRDKLITVYKSDSKADKAPRYQVLFAEDYK
ISLCLDWTNINTTGLEAEGNVELKNGKFKPSLIETIILKATNNDIVLHYLGSSTAAVAHKNNRQYIGEDMYETIETLAVERMKKVIDGEQGGISKAVNWQGGGEFYIARLSFFNETAK
QOTLACENSQDGITKTFEGLCERHFLKYNVSVNEFSQIIEEPFQSLALDBQKQMLEMLDLNQMYISLSEMDDEQFACCLNDDKALSRAPYQSVKHQAEEKDGE

SEQ ID 4293

SEQ ID 4293

TACCCGCGGAAGACCCAGCAGGTTGGCGAGTGCCTCGTCAGAAATAGGACTTGGCGCTGGACGAGGCAAAACCGCGCGCGGGAAGAGGGTTGAGCGAAGCAATGAGGCCGAGTGCGGGCTTCGAG
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SEQ ID 4294

SEQ ID 4294
YRGKPGWVRVPRQNRWAWTRQNRRRERG*AKQ*GVRLRVRCRPGAGVFYSRRGLAAVAVNAVEGVSDDMGGGFGSTFARSFYLYQYRFGHIGGGHACRIEFQCGQGLFHQCFIQHP
LQGRNVQDVPDVGQVALLVKEIDKDVDAGGFLVGKGVFARLRVQVLLLEIFPDAGVQGHIAPFVSADLTRGRGVMAEFGIGK*IRFFAFEGQVVRVPVDFLAFKFDTRHLYAQRLQLPLV
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SEQ ID 4295

SEQ ID 4295

TTGGAACAGCGGAAAAAGACGGTGTGCGAGCTGGAAAAAGCCGCCAAAGCCGTACGCGAAGGCAACAAAGTACGCGTGTATATGACGGCCGTCGCCCTGCTTACAGTATCCCGCAGTTTG
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SEQ ID 4296

SEQ ID 4296
 I EAAKDCVLEKAAKAVREGNKVRVYMTAVAPAYSTPOFEVNOGDEVTVYVTNVTIEDLTHGFTLEGCGIAMEIGPQATSSVTFKAVRPGVHWYYQWPFCHALHMEMSGQMTVHPK

SEQ ID 4297

SEQ ID 4297
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TTGGTGGAAAAAACCGACCCGTCATTATCGGTTTGTATTGAA

SEQ ID 4298

MRITYNDEDRHSNRISPSPAITRKNMGERRKNHFGQKHPVGFGGKNRPVHYRFTIE

SEQ ID 4299

SEQ ID 4299
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SEQ ID 4300

INNM LIPPNPD AFGHPRLSQR CERPRKQQRQ RIDFI IYL

SEQ ID 4301

SEQ ID 4301
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SEQ ID 4302

LRKYQHIIQTQPVFLTAAQAEDAAVFIRRKAFIRHISF

SEQ ID 4303

SEQ ID 4303
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CGCGCAACCGCACAGCAGCGGCGATGCGCGAAGGAGAAATCATTTGCCCGCGCCGCGCGCATATTTCTTAGCGGAATTTTCAGACGGCCGTCCAAAGCACTGACAGGCAACATCCGCCAAGTG
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ACCGTTTAAACGATTATGCCGTCCATATGCTCAATGCGGGCAACGCGCGGTTTCGAGGAAGACCTGCCCTCCGATACGCGGTACGCGTTTACACGAAACGCGCCCTTTGTCGGTT
TGGCGGAATATCAAAAGGAAATATGCCGTATGAAGCCCTTGCCTGTATGAACACGCGGCATCTCCCGCC

SEQ ID 4304

MTNKAIRKPVNGVLLDKPEGLSNTALQKARRLFHAERAGHTGVLDPLATGLIPVCFGEAAKFAQVLLDADKAYTATLKLGEASSTGDAEGRIIAARADISLAEFQTACQALTGNIRQV
PPMPSALKHGBKPLIEYARKGIVIERKPRDITVYSIDIAEFDAKAVISVRCSTGYTIRLSEGLAKHIGTFAHLTALRRFTAGTFTIAQSHTLBALANINETERDGLLLPCDVLVSHFPQ
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SEQ ID 4305

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SEQ ID 4306

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SEQ ID 4307

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ATTGTCCAAACGCATCAAGCTGTTCAAAATCCCGAAGTGCATTTCAATACGACGAATCTTTGAACGCGGTATGAGCTGTCCGCCCTTATCGATCAAGTGGCGCGGAAAAACCGGT
GAAGAC

SEQ ID 4308

MKRPQRGYARQDRVKEQIMRELAELVRTGLKDPFRAGFITINEVEITRDYSHATVYTVLNQDREITTEEVLEHARGHLRSELSKRILFKIPRIHFKYDESLEGRMSLSALIDQVAEEKPV
ED

SEQ ID 4309

TTGTCATCTTCGCGAGTATCAGTCTTCAACCGGTTTTCCGCCGCCACTTGATCGATAAGGGCGGACAGGCTCATACCGGTTCCAAAGATTCTGTCGATTATGAAATGCAGTTCGGGGATT
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SEQ ID 4310

LFILAVSVFNRFFRRHLIDKGGQAFATFQRFVVFEMQFGDFQDLDAFGQFAAEVSARVQHFPRNFARILVQNGVEHGGVAVIAGNDFVDSDEAGARVFGSGTDEFGKLAHMLFFDTVLA
GVAALGFFHEYPQHQWTAFLPPGRLRKGV

SEQ ID 4311

AATCAATTTCTATAGTTTAAATACGAAATCTTGGCGTATAATCGCATCCATAGTTTTTCAAAAGGAAATAAATATGTCGATTCAAGAAATTTATTAATCAAGAAACCGGTACGAAT
ACGCTTTCGCGCAATCTGACTGTAAAGCGTTTGCCTCCCACTTGACCAACCTGAGAAAAGGAACAAGAGCGATGACTACCTCCAAATGCCCGTAACCATCTGACCAT

SEQ ID 4312

NQPHSFNNENLGV*SHP*FLQKENKMSIQEIYMQETGYEYAFRQIVL*AVCPFPDQPEKRNKSDDYLMQPRNPSDH

SEQ ID 4313

GTGTGCGTTGCAGAAACGCGCATGCGCGTTTCGGGTTGCCAAGTATAATACTATATCCGTGCTTATCAACGTATTACCTTAAAAATCCCGCGGATTTCGGCTATAATACGCCCTTTCGCAACC
GCCCCGCGCGCAGAAATGCCGTC

SEQ ID 4314

VCVAETACAVRVAKYNNYIRAYQRI TLKSRRFYNTPPFRNRPGRNAV

SEQ ID 4315

ATGTCCAACGAAAAACCGTACCTGTTCTTTTTCGCGAAAAATCCAAATCACACGCCAAACACCTGATTGAGGGCAAAAAACGCTATATCTGCGACGAATGCGTGCAGAACTGCCTCGAAATAT
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GGGCGAGGCGAAAAAGCGCTGCGGTTTCAACCATTAACAACGCTGCGCCACCGGAAAGCGGCGGTTGCAATTTGCGAAATCCAACATCTGCTTTATCGGCGGACG
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TATTTTAAACGAGCGGAAAAACGCTTTGGTCAAGCAGTATCAAGCCTTGTTCGGCATAGAAAAAGTTCGGGTTTGAATTTGAAGAAGGCGCATTCGCTTCATCGCGCGGACGCAATGGAA
CGCAAAACCGCGCGCGCGCTGCGTTCCATCGTCGAACGCTGCTGCTGATACGATGACCGCTGCCGATTTGCAAGGCTTGAAAAAAGTGGTGGTGGCAAGGCGATCATCGAAG
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SEQ ID 4316

MSNENRTCSFGKSKSHAKHLIEGKNAYICDECVANCLEILYEGDNGGTPPENAGGEPESGLPTPAEIVANLDDYVIGQQAQKALAVAVYNHYKRLRHPKADGGVELSKSNILLIGPT
GSGKTLIAQSLARKLDVFPVMAATFLTEAGYVGEDVEQIIITLKGKCDFOVEKARHGIYVIDEIDKISRKSNPSITRUVSGEGVQALLKLIEGTVASVPPQGGKHPNQFIVNIZAN
ILPICGGAFAGLEKVRQTEKGGIGFASVHSDENAGITKLFIVGIEPDLIKPLIPELIGRLPVIAITLELDELDALINILTEPKNALVKQYQALFGIENVGLFEPEGALRSIARQAHE
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SEQ ID 4317

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GCTCATCCGAANTCGCCGCTACCTCTCTGAAACACGGCGTGATGATCTTAGTTGCGGGTGCGGAGTATGCGTTTCGCGCTTCGCTGCTGTGAACGATGAGGATATGCGGAAGGTTT
GCGCGGTTTGAACACGCTGCTGACGGAATTTGCCCGCCAAACCGCCCC

SEQ ID 4318
MHKLWHISNTYTRPAQELAQKLKHSFADKVFVFCNSGAEANEALKLARKYARDRFGSGKSEIVACINSFHGRITLFTVSVGGQPKYSKDYAPLPQGITVFPNDIAALEAAVGEYTCAVI
IEPIQGESGILPATAEYLAQARRLCDRHVALILIDVQVTGCMGHTGRFLPAYEHGVVPDILSSAKALCGGFPITGMLATEKIAAFAQPGTHGSTFGPNMACAVGSRAPDIINAPFELHNVR
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SEQ ID 4319
TTGAAATATTTAGGTTTATTTTACCCTGCCCCGATATTGTCGCAATTTCCCTTTATCCGCTTGAAGAACCGGTGCATAATCCCGAACAAACCGCAATCAGGAGCAATTTATGCAAAAC
TATCTGACCCCCAATTTCCGCTTTGCCCGGATGATTCGCGAACCGCTTCAGGACGCGCGTTTGGGATACGGAAGGGCG

SEQ ID 4320
LKIPRFIFTARYCRQFPFIRLEKRCIIPNKTAIRSNYAKLSDPQFRLCPDDSRTRFRQPRLYGYRA

SEQ ID 4321
ATGCTTGAGGCGCGCAGCGTTTGGATTAGAACTCTCCCAATATTTTATCTTCGGACGGCATTTTCATCATGCAAGCAAAACGTTTACAAACCGCTTACTGCTATTGGTACCACACAGAC
GTGCGGTGCTTTTTCGCTGTCT

SEQ ID 4322
MLEARQRFDLESQYVYFLRTAFHARQNVNRLILLIVHERRAVIFALA

SEQ ID 4323
GTGGTACCAATAGCAGTAAGCGGTTGTAACGTTTTCCTTGCATGATGAAATGCGCTCCGAAGATAAAATATTGGGGAGATTCTAAATCAAAACGCTGCGCGCTCAAGCATTATATCT
GAAATTTTTTTTGTTTTTTTCAGCTATCCGTTTGAATATTT

SEQ ID 4324
VVPIAVSGCKRFALHDEMPSEDKNIGELIQAANAAPQALYRNVFFFSYFVNTI

SEQ ID 4325
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SEQ ID 4326
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SEQ ID 4327
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GTGCTTC

SEQ ID 4328
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PKTYGVFANGEHITPVSGVGKLDLDAKTWNAVYTAIDGETMEIAWQVLVDGNLDNGDADYQGYSFATCYNSERALTIVQAGSSNEQDWCVPDLKATEBGIKAGDFKEVNGVRLMDGRAEAK
SKYTRYIIPVNSPHGCNASPDGYKIMPNGKLPPTVTVLVDVSKLDDLFAKIKERDVVVAEPQLGLGLPHLTAFDGGRNAYTTFLIDSQMVKNWIDDAIKAYKGEKIDPIKQKLDVHYQPGHN
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SEQ ID 4329
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GAATTTTAAATGATATCCGCGTTTTTATCGGTATTTTTCGCTGCTTGGCTGCGGCGATGCGCGCGCTTGTATGCGGACCGGAGCGGCTATTGGTAACGGCTTGTGATCGGTACGCTC
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SEQ ID 4330

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SEQ ID 4331

ATGGTCATTTTCCTGATTCTGTCTGTGTGTCGGAATCGGGCGACCTGTGTGAAGGTAAACAAAAAGCCGCCCTTTTCGAGCGGCTGTTCGTATGGGATGGATTTCAGCAAGCG
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SEQ ID 4332

MVIFLLILSCVAESGDLCEGNKKAAPFSSGLFCVNDGFQASAKSTARLCGTNSSKRL

SEQ ID 4333

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SEQ ID 4334

MTMDAMPQTAVQENLHTCSIIVDDAQDFSPMLLDAGRDITLISESMIPQIRTVAAALIAERHDFSRSSPAEFTDAADFPAARILVLGVRFRHLVSLLIQILKTANKRACRFAEKHRLFFT
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SEQ ID 4335

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CAGAAGCGG

SEQ ID 4336

HLAKIPDGTIPIPHFNTHMKIIASALINTFALTACQDDTQARLERQQKQIEALQQQLAQADDTVYQLTPRAVKDTI PAQQAANGNNGQPVTKDGGQYTYDQSTGSWLLQSLIGAA
AGAPIGNALANKPFRAGNQDSFVARRARAAYHQSARPNARTSRDLNTRSLRAKQQAQAQRYRPTTRPFVNYRRPAMRGFGRER

SEQ ID 4337

ATGCCCCAACAATAACAAAAATGCGCTCTGAAAGCCCTTCAGACGGCAITGACGCGCGGGTTTACCGCTTCTGCGGAAACCGCGCATAGCGGGACGGCGGTAAATTGACGGCGCGGCGC
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GACGGCGCAGCGGGCTGTCTGGTTGCCCGCGCGGTGTGAATTGTTTGCCAGCGGCTTGGCGATAAACCGCGCTGCCCGCCGCGCAATCAGGCTTTGACGACGCGCAGCTTCTGTGCTATTG
GTCGTAATATACCTGCGCGCTCTTTCGGGTAAACGGGCTGACCGTTGTTGCGGTTTGGCTGCGGCTGGGACGGAATGGTGTCTTTGACTGCTTCGGGAGTCAGTTGTAACCGGTATCG
TCTGCTGCTGTGCGAGCTGCTGTGTCAGGCTTCAATCTGTTTCTGTCGCGTTCGAGCGCGCGCTGCTGTGCTTGGCAGCGGGTGAAGTGAATGTCGATAAGCGCGGAGGCGA
TGATTTTTTTCATGTGTGCTGTTGCTGGGTGAAATCGGTTGATTGTATCGCGCTGGGAATTTTGGCAAGCATTCGCGCGCAATCG

SEQ ID 4338

MPLTNTKMPSESPDGIDAPGLPSPAETHSGTAVIDGRACRAVTLRLRLFLTEAARVQIPAGARIGACGLMVGSTRATGDAVLVARPCFVQVRADKACRRANQALQQPASCR
VVNILLVPVAGNLTVVAVCLRLGRNGVDFCGSQLVNRIVCLLCELLQGFNLFLPPEPRRLRVVLAGECECCDKRGDDFFHVCVVRVENRLYCIAGVNGFKHSAGKS

SEQ ID 4339

GTGCAAAACACAGCGCGCGCAGGCGCAGCGTTACCGCCGACACAGCGCGCGCGCTCAATTACCGCGCTCCCGCTATGCGCGGTTTCGGCAGAAAGCGGTAAACCGCGCGCTCAATGC
CGTCGAAAGGCTTTCAGACGGCATTTTGTATTGTGTTAGGGCATTTGATTGTTCGCGTTGATTTCAGACGGCATTTTGTTCACAGCGTTTGTATGTCGGGATGCAATTTCTGATCTA
CGTCGCTTGGCAGGCGGCATTGTCTATACGCCGCTGGGTTTTCAGACGGCATCATATCGAACCGTCAAGCG

SEQ ID 4340

VQNNRRRRSVTARQARPSITAVPLCAVSAEGKPGASMPSEGLSDGIFVVRGIVMLPFDQTAFQAFDVGMAILIYVRWQGGIVIPPLGFQTASYRTVKP

SEQ ID 4341

TTGGCAACGATTGAAAATTTCCGTAAATTCAAATATCTAGATTCTTCTCGTGGGAATGACGCGAAGGGTTTCAGATGCAGGATGGACATTCTGCTACCCAATCTGCCCTACCGC
TTGACCGTTTCGATA

SEQ ID 4342

LATIENTFRKFKYLSFLRGNDAGFQMDGHSCLPNLALRLDGTI

SEQ ID 4343

ATGTCGGCGCAATCAGCGCGCGCAGGATACCGCCATAAATGCCACCCGATGACCGTACCGATCAGCAAGCCGTTACCAATACCGGCTGCGCTCCATCAAGGACCGCGCATC
CCGCCAGCAAGCCAGAAAATACCGATAAAACGGCGGATATCATTTTAAAAATTCAAAAATTCGGCAACAGGAGAACTGCGCTTTCCTGAAACCAACGGACTCAAAACCCCTATGGT
CAAAAGATGATACCGAGGTTCAACCCGTGCTTCTGACCAACGGGACAAACTGTACCAATGCGCTGCTGTCATCAGCAGCAATATGTTGCGGAGAGCGTAAATGTAATGTTGTCG
ACCAACCCCAACAGAAATCAGCGTAACCGAAGACAGGGGAACAAACTGAAATTCATCGGTTACGACACCTGACCAAGATTCTTCGCGCAG

SEQ ID 4344

MSAALSGPTGIPPINATPMTVPIISKVPTWTCGRPIKGTPHPASQATKIPIKTADIILKFKNSATGGTCAPPETNGLKTPHVKRMIPRPNPCFSTNGTCTNAVCCISSNVAETVIELLLL
TTPNRI SVTNRGTGLKFI GYDFTLKDSFAS

SEQ ID 4345

ATAACGAAAATCTGGCGTATAATCGCATCCATAGTTTTCGCAAAAGGAAAATAAATGTCGATTCAAGAAATTTATTACAATCAAGAAACCGGTACGAATACGCTTTCGCCAAATCGT
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CTACGAACCCACAGCTTCGGCCAATGGCAGCAACACCGACTTCGCCGAACCGCTTTGAAATCAACGGCGACGCGGCACACTGGGACTACCGCAAGACGATGACGACTTCTCAGC
CAACCGCGCGCTTGTTCACACTGATGAACGACGCGCAGAACAGGCTTTGTTGACAACACCGCGCAGCCATGGGCGATGCGCCGACTTCATCAATACCGCCATATCCGCAACTGCT
ACCGTTGCGACCGCGCATACGCTGAAGCGGTAGCAGGCTTCGGAGTACCGCTGAGAGCAGCACAACCGCTCCGCGCAGCCGATCCGCGACTGGGTGAGCGCGTTTGTGTAAGGGGG
CATATGTGTGATGGAATGAAGAAATCTGTCCCGCGCTCCGATACCGGAATACCGGGCATAAATGCGCTGAAACGCTGTTGACCGTTTCAGACGCGCAT

SEQ ID 4346

ITKILAYNRHSFCKRKIKCRPKFITIKKPVNTLSAKSYCKPFAHLTLNRKGTTRAMTTSKCPVTHLTMNAGPVDNQNLSLTAGPRGPLLTQDLMLNEKLADFVREVI PERRMHAKGS
GAGGTFTVTHDITKYTRAKIFSEVGGKTEMPARFTTVAGERGAADAERDIRGFALKFYTEBGNWDVVGNNTPVFFLRDPKRPDLANKAVKRDPRTNMRSATNNWDFWTLPEALHQVTIVM
SDRGIPASYRHHMFGSHTYSPWNEAGERFWKPHFRSQOGIKNLITNEEAAKI IADRESHQRLDYEAIERGEFPKWTMYIQVPEADAEKVPYHPFDLTKVWPCKDYPLIEVGEFELMRN
PENFFADVEQSAFAPSNLVPGIGASPDKMLQARLFNYADAQRYRLGVNFRQIPVNRPRCPVHSNQRDGGRADGNYGSLPHYEPNSFGWQQQPDFAEPLKINGDAAHWDYRQDDDDYS
QPRALFNLMDAQKQALFDNTAAAGDAPDFIKYRHIRNCTRCDPAYGEGVAKALGIVTEDAQAVRATDPAIGQAGILL*GGIMMEIERILSRAVRYR*PGIKMPSETSPDRFRH

SEQ ID 4347

ATGCTATTAATAATTCGCGATTTGAACCTTGATAAAACATTTGTCCGCGCTCAGCAGCGAGGTTACGAAAGCCGACGCGGATTACGCGCAAGCTATTCGCTTTGCTTTGGAAGGCT
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GGCAGCAGCCGCGCAAGTGGCGCGCAAGTGGAGAAACGCACTGGCGTATGCCAAAATATGCGCTGTTCCGACCGCTCAGCATCTGCGCGGCACATGCTTCGGCTACCAAAACCGG
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GACCAAGACTCTGAAATTTATCGAAGTGAAGCGCTGGAGCGCAAGGCAAAATCGAAGAGCAGTTGTGTGATGCGACGATATGCGCCACAAAACCGGCTGCTGACCACTCTCGCG
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GGCGCGGATCATAAACCAGCGCAAGAGGCTTCCGCGCAAAACGCGCGCGGAGGTTTCAAGAAAGAGGCTTAAAGAAAGACGTTTCAAAACCAACCGCGGAGGCTTCAAGGCA
ACGCAAGCGCGGACTCTTTTTCAGGCAAAAGCGAAGCGGCTTCAAGAGCGC

SEQ ID 4348

MSIKFADILNLDKILSAVSEGYESPPIQAQIPFALBGCDIMASQTSKTAFFLLPTLQRLTKRSEKPGKPRALVLAAPTRELAAQVEKNALAYAKNRWFRIVSIVGGTSFGYQTR
ALSKPVDLIVATPGRILDLMOQSGKVDPERLEVLILDEADRLDMGFIIDIEITVEATPADRQTLTLLSATWDGAVGKLARKLTKDSEIIEVERVDGQKIEBOLLYCDMRHNRLLDHLR
DANIDQCVITFTSTKAMTEVIADLEYKGAANCLHGMPOGWRNRLTDLRKGKRLKILVATVAARGIDVPTITHVINYLDPKQAEYVHRIGRTGRAGRTGIAITFAEVNEYVKVHKIEK
YINRKLPELITTEGMEPARKRKSGAGKPKGKGWDRKSGRRGDHKGKPGKPGKTRGEGFKKPKKTSFKTGEFGKGRKAGDSFAGKSERYRDR

SEQ ID 4349

TTGATCTTGCAAGCGTATCTGTGCGAGTTGCGCTCGATGTAAACCAAGCAAGCGCTTCGCGACACCTGTAACTTCACATTCCTCCGATCTGTTACCTTCCCTGCTTCAGCGCGTC

SEQ ID 4350

LILQSVSVQVADVNVHKAACDNFVTSHPYRPSLLQAV

SEQ ID 4351

ATGGCTTCGTATGACGATATAAGCGGAGATGATAGGGTTTGGCCGAAAGGTCAGCAATCGGGCTTAATTACAGTAAATTTCCGTTTTCCTTTATCTGCTGAAATCAATGA
CCGACATCACACCGTTTCCCAACCGCTTGGGCAAAACATCAACACCTTATGAAATGGGCGAAACGCAACCGCATCGAAGCCTGGCGCATTTACGACCGGACATCCCCAAATTCCTTT
TGCGGTGATGTTTACGGCGATCGAATCCACTTCAGGAATACGATACCCGCTGGCTGATGCGGCGCGGAGAAATACGAAGCGTGGCTTGGCGAAGTATTTGAAGCGCGCTTCGTTTAC
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GGTCAACCTCGCAAAATCTCGACACCGGCTTCTTCTCGATCACCAGCAACCGCGCAAAAGTTCGCGGCAAGCGGCGGCGCAAGGTTTTCGATTTGCCGAAACCGCGCGCAAGTTT
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ACAATACCGCGTGAAGACATTTCCAAACATCCGTTCCGGAAGATTTTCGCAACAAAAATCCACCGGTTTGGGAAATCCGCGCAAAATCT

SEQ ID 4352

MASYDDISGEWYRVCPRSSNRALITVKFPSTFLCLKSMTDITPFANRLGKNIKHLMKMAKRNIEAWRIYDRDIPQFFAADVYGDRIHLQBYDFTGMLMRPGEYEAWLAEVLEAVPVT
GFPEQIRLKRERQKGLQYKRTGKAGDFVIAENGRKFWNLNLDKYLDTGFFLDHRNTRKKVGETAAGKRFNLNLSYTGSGFTVYAATGGAASSETVDSNTYLDWARRNFELNGIDMERH
KIVRADVPYQLTAYGEGQFDLIVMDPPSPNSKMPGILDIQRDHQKLIDGAVNLLASDGLILYPSNNLRSFVLDSVSEBYAVDKISKQSVPEDFRNKIHRCWEIRKHS

SEQ ID 4353

ATGCCCAAGCCCTACTCTGACGCTATCTGCGAATCCCAACCGAAAGGAAAAATATGAGCAGCGAATTAATCGTACACACCGGCGATGCGGCTTCGAGCAAGATGTTTGAATCCG
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CGACGCAACGAGCGCACCCGCTCCGTTTTCGCGTGGCGGCACTTCGACCTGATGCTGTTCAAAACCGCGAAGTCTGCGCACCAAGTCTCGCGCAATTTGCAAAAGGTCAGCTGACC
GCTTTGTCGAGGCTCCATCGCC

SEQ ID 4354

NFKPYPARYRANPRNKGKIMSSELIIVHTGDAFQDVLKSDLPVLLDFWAPWCGPCMKIAPILDDIAAEFEGRLKVKINIDNEATPSRFVGRGIPTLMVFKNGEVVATKVGALAKGQIT
APVEASTA

SEQ ID 4355

GTGGGCGGGCGGGAATAAGTTTTCGTGACGCGCCCAATCGCTTTGCAANTCTAAAAACCGGTCGACAGTATTTATTTTGAATAATTTACTTTATATCAAGTA

SEQ ID 4356

VGGDRNSFSPVPPQSLQILKNGSDSILFLKITPILKV

SEQ ID 4357

TTGGTTTGAACATTCATCTTAAAGATCTATTTAAACGGAGCATACACCGCGCGCGCTTCTGTACAGCCTCAAAACATTCCTTATACTTTGATAATAAAGTAATTTTCAAAAA
AAATACTGTCCGACCGGTTTGTAGAATTTGCAAGGCGATTTGGGCGGTACAGAAAAATATTATCCCGCGCGCCACT

SEQ ID 4358

LVLNHTLRIYINGAYTARAFYLSLKNIPYTLIKVIFKNILSEPPFRICKGDWGTETKLSRPPT

SEQ ID 4359

ATGACTGATTTTTCGTTTGGGAAGCTGCTCCCTTGGCGCAACCGTTGATCATATCTGCAACCGTACCAATGTCCACCGCGCACAAATTTGAAGAAATGCTGCCGCTGGCGCAGAAAG
TGGCCCAAGTCCATGCCGATACCTTTCCGCGGAAATTCGCGGCTGCTTGGCGATATGCGGGACGAGCTGCTGATGTCATATGATGAAGGAGAGCGGATGCTGTTTCCGATGATTAATCA
GGGTGTCGAGCGCGGTGCGCGATGCCATCAGCGTATGATGACAGCAATGAAGAACACGACCGCGCCATCGCACGGCTCAAGAGCTGACCGGTAATTTCCAGCAGCCCGGAGGGGCT
TGGCAAGTTGAGCGCGCTTACGCGCTGGCAAAAGAAATGGCGGAGATTGAACGACCAATTCATTGGAAGAACGATATTCGTTTGGCGCGGATCTGATTC

SEQ ID 4360

MTDFSVWEAAPFGATVDHILQRYHNHVHRAQFKEELVPLAQKVAVQHADTFPAETIAGLLADMRDELLMHMMKERMLFFMINQGVGRGAAMPISVMMHEHEEHDRATARLKELTGTFHAPEGA
CGSWTRLYALAKEMADDLNDHTLENDILFARVLDS

SEQ ID 4361

ATGCCGCTCGAAATACGGTFTTTCCGTTTTCAGACGGCAATTTTCATGTTTCAGCCAGCAANTTCGGGCGGAATCGGCACACAGGAANTCGGGTTGATTTTGTCTGCATCGCCGGTGAAGC
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TGGTTCGGTATGCCACAGGCCGTGGTTCGGGGGGTCTTTTGAATCGCCTGTGTACAGCCCAATGCTTCGGCAAGCCGGTAAACCTCGCTTTTGGTCAGGTCGGCAATCGGGCTGATGTC
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CGGCTTCTGGCGTTGGCGAGCGAAGCGGCTGATTGGCAATGCCGCTCGATGGAAGCCGCAAGGTTTGTTCAAAGGTCGTGAAGGTCGTGCATAGTTGGCGCTTCGCCGCTTACATGG
CATATTGCCCTTCGAGATTGCCGATGTGCGCGCTTCGCCGCTCAAGCTGCGCGAGGCTGTGGGTTATCGGCATATCCAGAACTCGGTCGGTTCGGCGCGGCGGAGCGCTTCGAGAC
GACGGCGGAATCGATGTCGCCCGGAACCGCTACGACAGATTCCTTTTGCATTTGCCTGAGCGGGCTATTCTGCCAACCATCGGACAATATGTGTGATAACTGCCTGCGTATCCATTTTTCCT
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SEQ ID 4362

MPEXIRFFRFRHFPVSAQQFGRNAHRNRKVFVLRHAVKPRIDQNPAPPSPFKIPGARAVAHACHPLQFGIACHLFLVGAFRIPQAVGRRGFLNRLVHAQCFPGKPNVLRFGQVGNADV
 HAAVAVFGKKTHARIFNLITCPRNQSVYLPVVVQGGHTQAASGVGERKRLIGKCRLMNADGLFKGLEGVQIGRLRATYIGILPLQIADVPPCFKLKLAGVLAYRHIQKQGAAGAGGERGD
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SEQ ID 4363

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GCCCGATTGCCGACTGACCAAAACG CAGGTTTACCGGCTTCCGAAGCATTGGCGGTGGACGAGCGGATTCAA AAAGCCCCCGCCAGCAGCGATCTGTGGGATACGGAACGACCCAGCA
GGAACAGATGGCGCAAGCTATTC CGAATCGGAGTGGGCAATGGCGGTGTACCGCAGCGCAAAACCCGAAGATTTTGAAGGACGGCGGCGGAAGTTCTTGGAATCTATACGCGCTTCAC
CGCGCGTACG CAGCAAAAATCAACCCGATTCTCTGTGCGCGCATTCGCGCCGAATTGCTGGGC

SEQ ID 4364

MDTQAVITHITVHWLEDEYAAQANAKGFVVGVSGGDISAVVSTLAA RTGRTTLLLDMP IROHPQGLERARRHRINLQGYANVSAQTANLTD TPTQTFEOTVGVHQTAFANQPLSLANARSRLR
MLTPLYVYGGIQIGLLVTCGKVKVEDFGVGFFTKYGDGGVDISPIADLT KTQVYRLAEALGVDEAIQKAPPTDGLNDTERTDEBQMGASYPELEWANGVYGRKPEDFEGRRREVLEITYRLH
RAMOHKINPIPVCRIPPELLG

SEQ ID 4365

TTGTTAATCCACTATAAACGCAAAATATCCCGTCATTCCCGCACCATCCCCACCGGTTCAAACCGGCACGAAAACCTTTTCCCGGTCATTCCCGCGAAAGTGGGAATCCGGAACG

SEQ ID 4366

LLIHYKRKISRHSRTIPTGSRHENFSASFPRKWSGT

SEQ ID 4367

TTGAAGCCC AAGGCGGCATCGTGGCGCCATAAATGTCAACAATATTATAACACGGGCCCATTTGCCGCCAGCCTTTTCCTATATGACTTTTATAAGCGGGGAATGGGAAAAATATTCATCA
ACCCGCCCTCAATCTATTCAAATGCAACGCCGCGCAGGCTA

SEQ ID 4368

LPKPAASCRLNCOQYYNTRHLAASLFLYDFFKRGMGKIFINPPSIYSNCTAGRL

SEQ ID 4369

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SEQ ID 4370

MPWAKKHIIHYPYTLIDMSDPFPHSDVLSVSLNFAFKSILEHNLAGLWLTAGEVSNLTRAASGHYFFSLKDSRAQVRCAPHKGAARLAQPLKEGDHIVAGKISITYEARGEFOITVNEVR
LKGLGQLYEAYERLKAQLQAEGAPAAERKKPLPVRPQCIGITVLSLAAALRDVVPTLKRRAPEIPVIVYPAAVQGAGSGFQIAQKATASQRAECDVLIVCRGGGGSTEDLRAFNEEPVWRA
IEACTIPFVSGVGHEHTDFTLADFDVADVRAPPTGAELVSPNRQESLHRLVQAQGLRLKTVLEQRYFDAQSKLDWLARQIRHPQKLBQEARISIGKLAQTLSTYNTQNLRAHTARFERQTQA
LOHCRPDSVYVRODIVELOTALPAAFSRLLARRROS/LTAQAALEAVSPHILRGERFSVVKNTFRGOVIRNADVLRKQGGKLHTTFSDGETDVRVSKBQGGQDLFDCL

SEQ ID 4371

TTGTTTATAAAATTTCTGTAACTTTGAATTTACAGCCATCTTCAATAAATTATCGAAACGTATCAATCGTCATTCCCGCGCAGCCGGGAATCCGTTTTTTGAGTTTCAGTCATTTTC

SEQ ID 4372

REF ID: A572
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SEQ ID 4373

TTGAAACCCGGCTTGGCAATGCTTGCTACAGGCTTAAAAATTCATAACATCTCTTTCTGTGAGTTGAAAAATAAAATTTTCATTGTGCCAATGGAACATTATTAATAATATATAAAAAA
TATCGGGTTGGGTTTATATACCGCCCCAAGATGCGCCGCTGAAACATTTCCGGGTGTGCGGAGAGGTTCTGTTTTTCGACAAATTCCTGCGGCTTTCCGCTTCGGATTCCCGCTTTT
AGGGACTGGATTCCCGTTTTCGCGGAA

SEQ ID 4374

1KPG LAM LASRSKNFITSSFCOLKNKISFAQWKLKKNYKKISGWVPTIRPKMRRLLKHFGCAERFLFFPTNSCGFPLPDSRFLGTGFPPSRE

SEQ ID 4375

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CGACGACGAAACCGCCATATCCGACGCTTACCTTGTGGGCGAAAAAGTTTCGCGCAGCGGCATATCGGCTCTGGTGGCGTTGGGCATTGGCCGCTCATACCGCTCGCTACGCGCTGGTGTATG
GTCCTTGTCAAAGCACTCGACCTTTTCTCC

SEQ ID 4376

EQ ID 4376
VPPAALAVHLAIGQIYYSVFNAPITKLIGITESAAGDWKLTIVGWIPSTIALANLGAASALPGTWMERVGPRKAIFAAACCSLGTFVSFAVGVRTHNLFLLYLGNVGIGVGLGLGYIGPV
STLKMFPDKPGMATGLAIMGFGGAGNLASPLSVSLNNAFSAASVGVBAETFAVLGLPYLALMFGAPTIRVPADGWKPEGYTVPKTKNQKPVSSNNHVNVSQAMKTPQFWLLFVVLCLNVT
GIGVLQASVMIQELFSETSAGRQAAYGGAAGFVSLLSLFLMGRFLWSSVSDKIRKNTYTTIPFVLGSLLYFAVPSIGEGGSKALPIGFCVIIISWYGGGFAAIIPAYLKDLFGTYQVG
AIIHGRILLAWSTAAVIGPVLVNYIRQSQIDSGIPAAQAYSVTMYIMAGLLTVGLLCLNAVKSVEHKKHEKDIKTAARSGNPDETAISDAYLVGEKVSQDGI5VWNRNALAVIPLAYGVVM
VFFKALDLFS

SEQ ID 4377

EQ ID 4377
TTGCACAACTTTGTCCCCAAAGCCGAGCGACGATTTCATCCGCAAAACCGCCGCATCAGGTACAATATCGAACCGTCCGACCGAGGACGGCATTTTATCAACCCGTCCTGCCGCACACG
CCGCAGAAGAACCCTTATCAGGCGAGT

SEQ ID 4378

LHKLCPQSRSDDFIRKTAASGTISNRPTEDGILSTRPAAHAAKEPPYQAS

SEQ ID 4379

EQ ID 4379

TTGATGGTTTCAGCGCGCTCTTGAGTGTGAACGATAAAGCCTTCGTTACCGCGGATTTGGATTACGAACTCGCCCAAGCTTATTACGTCGATGATCCTAAAGCGCGCGCCGTAGAAATCAGGG
CGCCTGTCGAAGCAGTACCTGCCGCAGCATCCGATACCGCTTCAGACGGCATTCGCCGAAGATGCGTCAGCTGAAAACGGTGATTCACCAACATTTATGGAACACAGATTTGGAAGCGGAACA
GGGGCAGATGTGTCGTCGTGGCAGTATGGCTTGACCATCTGCTGCTTTGGTATTCTCGTGTCCAAGATTGGATTGTGCGTTACGAAAAATGGTACGACCGCTCCCGCTTTGCTTTCCCTAACCTTTT
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TGTGAAACAGATTACCGTACCGCATATGCTGCATACCCGTTTGAACGTCATAAAATACCTGATTTTATTCGGTTTTTTGGCAAATTCGCTGTATGATTTGGGTACCGCGGAAAAAATTTGCC
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AATCGCGCCCGAGGGGCGACATCCATCCGAACGATGATACCTAGTCCCTGCATGCCAAGTGATGTACCAACACCATGACGCGCTGTCGCGAAGTTGTGGCGGAAAAATAGAAAAACAAAAA
CGCGCTCTCGGAAATCTGCAATATCTGCTTATGAGTCTGACGACGAGGACAGGCTCGTCCGTTTTTGTCAAACCCGAACCGCGCAATCTGAAAAA

SEQ ID 4380

SEQ ID 4380

LMVQRVLSVNDKAFVTADLDYELPQAYYVDDPKAPPVETISAPVEAPAAASDITASDGIADAASAENGVSQMLWKQIWKAKQGGIVVVGIALTILLLVLPQDWTIVRYEKWYDRFRFAFLTF
TLFYIGWYAQAQLSVVNTLT/PSAILTFPHWEFFLMDDPIVILMLPTAATHMLNWRGTFCGWLCPFGSLQELTNRIAKKLVGKQITVPHMLHTRIANVIKYLILPGFLAISLYLDLGTAEKFA
EVEPPKTAJILKFKMCDWFWFAVAVALLAGLPFERFFCRYLCPLGAGIALPGRFVFDWLRRYKMGCGNPQCITHECPVQAIAPBGDIHPNECIQLCHCQVMYHEDTRCPQVVAENKKKQK
QAAAKSGELENVSKQPOQBVVRFVKPETAQSEK

SEQ ID 4381

SEQ ID 4381

ATGCTCGAGAAATCTGCCCTATTTCACGCGACATCTGCCCTGAAGACCTTGCCTAAAGTCAATGAAGTCATCAACCGTCGGTGCAATCCGATGTCGCAGTATTTCGCAAAATCGGTACATATA
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CACACTCTCTCGACGACGATGCTGCTGATGAAGAAGCGATTTCGCGCGTGGCGGGGCAACGGCAAACTCTGTTCGGCAATCGCGCGCAGTGTGTGGTGGCGACTTTTATATACCCGTCGA
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AAGAACAATATATCCGAGTCATCCAAATATAAAACGCGCAAAATGTTTGAAGCTGCCGCTCAAGTCGGCGCAATTTTGGGCAAACTTCCCCCGGGCAGCAACAGCCCTTTGAAAGCATACGG
TATGTACGTCGGTACGGCAATCCAGATATTGACGATGTGCTGGATTATCTCGGGGAAACCCGAAGAAACAGGTAAAAAAGCTCGCGCAGCATTTTGGCGGAAGGAAAAACGACCCCTGCCCTTTG
ATTATTCTGATGCGTCAGGGTTCGGAACAGGTGCGCAACGATGTCGCTCGGCTTTGGAAATCGAGATCGGGCTATTTTGAAAAAATCCGCGATTATGTGTCGCTCGGTCGAGTGCCTTTGG
CATATTCGATAGGCGAGGCGCGCAAGCAGTCGATTGTGCCGTGCGCGCTGGATGCTCTGTCCGACAGCGAAGTGAAGGATGCTATGATTACAGTGGCGAAGGAATCTTTGTGTCAGGGT
GTCTG

SEQ ID 4382

SEQ ID 4382

MLENLPLYQRHLPEDLAKVNEVINRAVQSDVALISQIGTYYISAGGKRLRPIMTILAGKAVGYDDEKLYSLAAMVEFIHTSTLLHDDVVDESDLRRGRATANNLFGNAAAVLVGDFLYTRA
FQLMVASGSMRVLEVMDATNTNIIAEGEVMQLMNIQNTDITEEQYIRVVIQYTKAKLFEAAAQVGAAILGKASPGHEQALKDYGHYVGTAPQLIIDVLVDSGETEETGKNVGGDLAEGKPTLPL
IYLMHROGSEQVANDVRTALENADRGYPERKTRDYVVRSDALAYSIGEARKAVDCAVALDALSDSEVKDAMIQLAKESLVRVS

SEQ ID 4383

SEQ ID 4383

TTGTGCAAAATCCATTACCGCTCCTCTTATCATTTGAAAGATTCTACTCCCGCAGCAGCAAAACCGATTTCACCGTTGCAAAACTTTGTCCCAAAGCCGAGCGAGGATTTTCATCCGCAAA
ACCGCCGCATCAGGTACAATAATCGAACCGTCCGACCGAGGACGGCATTTTATCAAAACCGTCTGTCCGCACACGCCGCGAGAAGAACCGCCTTATCAGGCGAGTTAGGAAAAATGATGTCCAA
GCAACCCACAGCAAAAGCCCAATGTGGCGCGACGGCGGACGCCCTGTGCAAGAAAACGCCAAACCTTTCAAAGCAAAAGCCCGTCCCAAAGACGAAACGGCGCAAAACCGCCGCCCAAGCT
TACGGGACAAAAGTTCTCAGACGGCATCAAGTGTCAAAACGCCCAAAACAGCGCGCGCCGCAAGCCAAAAAAGCTCTGTCGTCGCAATCCCAACCAAAAAAATTATGGAACACGCGCGCGGATT
TGAAAGAACGCGCGCAGCGACCTGTGCGGTATGGAACCCGGAACGCCCTGTCAAAAAGTGCTTTGACGCTCCGGCGTGGCTCGCGCCGCGAAATGGAAGAATGGATCAACAACCGCTGGGTATC
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AAACAGAAGGCGGAATCGTTTCCCGCAGCAGCCCGCAAGCGCGGTACGATATTGACCGCTGCGCGAGCGCGTGGGTCGCCATCGCGCGCTGCGCATCAACACCA
GCGGACTCTGATTCTCTCACTACCTCCGCGAATCGTCTGCAAGCTTGTGCCCAACCCAGCTTTCGAAGTGTGAACGCGGAATACGCGCTGCGCGTACTGGGCGGGCTGACTACCGAACAATGG
CAGTCTCACCGAAGAAGGCGTGATGCTCGAAGCGCTTGGCAAAAGTCTGACAGCACTCTACGAACAAGGCGCGGAGGCGCAACAATGGTACAACATCGTGATTAAGAAGGCGCGCAAC
CGCGAAGTGTGGCGCGATATTCGAAGCCAGGCGCTCAGAGTCAGCGCGCTCGTGGCGTGGCTTGGGCCCATCGGACTGCCCAACCGCCTCAAAACGCGGACAGTTCTACGAACTCAAC
CGCGCGAAGTGCACCAATCTCAAATGGCGGATATGCTGCTGCCGGCGCAAGCGCGCGCAAAAAGCC

SEQ ID 4384

SEQ ID 4384
LCKSTYSSYHLKDDSTPARKPLSTVAQTLSPKPQRPHQNRIRIYNIEPSURGRHFINPSCRTRRRRTALSGELGKMMSKQPTSKRQWRDGAAPSAKKTAKPFTSKARPKDETRKTAQA
YGKASDGKIQONAPKORAAKAKKLVNPNWKIMEHARDLKERRSLSRMEPERLQKVLAAAGVGSRRMEEWINGNVTWNGKTAQLGDKVTPDQHTVKGSTIKLKWADRLPRIILYY

-337-

KQEGEIVSRDDPQGRVSIIDRLPQAASSRWVAIGRLDINTSGLLILITSGELVQRFAPSPFVEVEYAVRVLGGLTTEQMRSLTEBGMLEBDGLAKVERIYBQGGEGANKWYINIVIKEGRN
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SEQ ID 4385

ATGGAATTCACAAATATTCGGGAAGATTACAGCAAAACGGGAATTGTCGGAAGCCGATTGCGCCGATAATCCGATCGAGCAGTTCGAGCGGTGGTTGACGAGGCGGTACGCGCGGAGGTCA
ACGAGCCGACGGCGTCAATGTGGCGCGTTCGACGGGCGGGAGGCCAACAGCCGATATGTCGCTTTTGAAGGAGGTTAATTCAGAAAGGTTTGTGTTTTCACGAATTAACACAGCG
CAAGGGCGTTCGCTGGAACCAATCCGTTTCCGCGATGACGCTTTTTCGCGGAGCTGGAGCGTTCAGGTCGCGTGGAAAGGCGTGTCCGAAGGCTGGCGGAGAGTTGTCCGACGAA
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TGCACGTGCGCGCTCCCGCCATTGCGGCGGCTATATTTGATTCCCGATTGATTGAGTTTTCGCGAGGCGAGCGGAGCGGCTGCACGACCGCATCAATACCGTTTGTGATGCGCG
CTGGATACGCGAGCGGTTCGCGCT

SEQ ID 4386

MDLHNTREDYSKRELSEADCANPIEQFERWLEAVRAEVNEPTAVNVAVDGRGRPNRMVLKEVNSEGVFFVTNYHSRGRSLLELNPAAFTFPPELERQVRVBRVGRLEKLSDB
YFESRPYQSLRGAWSAQSEVIPNRAVLVAKAAVGLKHLVFRPPHGGYIVIPDLIEFWQGRPSRLHDRIQYRLLDGGWIRERLSP

SEQ ID 4387

TTGAACAGGAAAAACATATGCGCTGTAAGAACCGGAATCAGGTTTCAGACGGCATTTCACGCGGAAAAATACGGACGGGAAGTTTTCGTTTCCGAACGGAAGCCCGAATCCTCTT
TATACCGAGGAATTATGATCGGACGGG

SEQ ID 4388

LNKXKHPSENENQVSDGIFSRKYGREVFCVPNGKPESLYRGIMERTA

SEQ ID 4389

ATGAACACACCGTTACCTGCGCCGACCAACACCTTTGCGCGCGGCGACGGGAAACCGTTTTCGCGTTCGCGCCCGTCAAAACCTCAATCTGCCCCATTCTCGCAAAAAACCGTGTCT
GCGGACAAATGCAAGCGCAATGCGGACGCGCGGATATCAAAATGGCGGACACTCGGAACAGGCTTTATCCGAAGCAGAAAAAGCGCAAGGCAAGATTTCGATGTCGCGCACCAACCGCGCA
AAGCGATATCAATCAATCAATCCCGGCTGCAAGCGGATGCGCTACCGCTCCGACCTTCGCGCAGCATCGAAAGTATGTTTCAAAACAGGATGCGCTTCCTGAAACTTCGCGCTG
CCCAAGGCCCCCGCTTTGCTTACGCGCGCAATACATTTGATTTCCTGCTGCGGCAACGTCAGCGCGAGCTACTCCATCGCCCAATTGCGCGACCAAGAAAGGCAATTTTGGAACTAC
ACATCCGACGGCGGAAAAACGGTGTCTGCTCGGAATGATTTCGCGCAGCAACCAAGTCAAGAAAAAGGCAATGCTCGCGCTTAAAGCGCGCTCGGTTCGTTTACCTTCGAGGAAGA
CAGCGCAACCCGCTATCTGCGCGCAACGACACAGGCTACGCGCCCATCCGACGATCTGCTGCACTTTATCCGCAAAACAGCAGCGCGCTCGCCATTTCCTACTGGCGCGCGCT
CATCAAGATGATTGTTATGCGCTCGAAGAGCAAGAGGTTGGCATCGCGCTCGAAACACCTGCTTCACCCCGCTATTGTCGCGTCCGAGAGGGCTGGCAGGGAAGAAAGGCCACG
TACAAGACATCGCGCAAGAACACCCCGACCTGTCGGAATACGAAGTGTTCGCTGCGGCTCTCGGCTATGACCGAACAGCAAAAAATCTGTTTGTGCAACAGCATAAGCTGCGCGA
AAACTGTTTTCCTCCGACGCAATTCAGCGCTTCGCGCATCA

SEQ ID 4390

MNHTVTLDPQTFAAGDGTVLAAAARQNLNLPSCKNVCGQCKAELASGDIQMGHSEQALSEAKAQQKILMCRTTAQSDININIPGCKADALFVRLTPARIESMVPKHDVAFIKIAL
PKAPPPAFYAGQYIDLLPGNVSRYSIANSFPDQGBILHLHRRRENGVCSMTIFGSEPKVKEGIVRVKGLGSPFLQEDSGKPVILPATDTGYAPIRISILLDIRQMSRAAHFYWGAR
HQDDLYALEBAQGLACRLKNTCTFPVLSRPGEGWQGRKHVQDIAAQDHPDLSEYFVACGSPAMTQAKNLFVQHKLPENLFFSDAFTPSAS

SEQ ID 4391

ATGACTTGGGAACTGTAATCGCTTGGAAATCCAGTCCAATTGAACACCAAAATCCAAATCTTCAGCGGTGATCGACCGCATTCGCGCGCAGAAACCAACGCGCACGCGAGCGTAGTGG
AATGCGCGCTGCGCGCGGTACTGCGGTAATGAACCGCGAAGTCTGTTGAAAAGCCATCAAAATTAGGTTTGGCTTTGGATGCAAAAATCAACCGGAAAAAGCTGTCGACCGCAAAAATA
CTTCTATCCGACTTGGCGAAAGGCTATCAATCAGCCAGTTGGATTTCGCGATTGTCGAACACGCAAAATGGAAATCGTGGTGGCGCGGATGTAAGAACCATCAAGTAACCCGCGC
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GTTCAGCAGCGGACGATGCTGTCGACCCGGAAGGCGAAACCCGCGTGTGCGCTGAAAGAACGCGCGCAGCACTACGCGTACTTCGCCGATTCGCGATTTCGTCGCGCTCATCTTT
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CGTGCAGGCTGCTTATTTGAAGAAGCGCCAAAGAGAGCGGACAGGCAAGCCGACTGCCAAGTGAACGCGCAACTTCCGCTACGCTGAACAAAGAGGCTATGGAATTCGCGAC
AGCCGATTACCGCGCCACGCTTGCCTGCTGGCGCAAAATTCGCGATGGCAGATTAAGCGCGCAAACTGGCGAAAAAGGCTTTGAAGCATGTCGCGCGGAACCGGAAACAGCATTG
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AAAAGCCCTGAATCGATTGTCGCGCAAGTGTGAGAGCAGCAAGGCAAGCCAAATCCGCTCAGTTCAGGAGTTGATTAAAGCCAAACTTGCC

SEQ ID 4392

MTWETVIGLETHVQLNYSKIFSGASTAFGAEPNAHSAVVECALPGVLPMNREVVEKAIKLGLALDAKINRNVFDRKNYFYPDLPGYQISQLDLPIVEHGLEIIVVGGDVKTINVTRA
HMEEDAGKSVHEGLNGATGIDINRAGTLPLEVVSEPMRSAAEAVAYAKALHSLVTLWDICDGNMABGSPRIDANVSVRPGQAEFGTTRBIKNLNSFRPLDQALNYEAEQIEILEDGGT
VQQAHLFPDPEKGETVMRLKEDAHYGYFPDPLLPVILSDAQMQKAKAEMPELPEKMAARFVADYGVSEYDARLLTASRVQAAFYEEAAKESGQKPTAMNMNGELAATLNKEGMELAD
SPITAPRLAALVGLADGTLGKLAKEFAMWAEPTSIABEIEKHSLLQMTDGTGAVEAMVDEVLANNAKAVEQFKSGNEKALNAIVGVNKTSGKANPAQVQELIKALIA

SEQ ID 4393

ATGAACGAGAACCGCACCTTTACCTTCCCGGATTTTCGACCGGTTTACAGCTATGCGCTTTATATCGGCTGCAACATTTAAAAATACACATTGCGAAAAATTTTCGGAAGAAAAAGAAATTT
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TTTAGATCGATGACGCGCAGATTTCCTCATGGCGGAAAACTTTCGCGACAGAGCTTCTGTCCAAATGGAAGACTGCGCTTCCATCTGCTGTCGCGACCTTTTCAGACGGCATCAGC
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CAGCTTCGCTACAAGGGCGCTCAGGTGAAGAAGCAAGACACCGTCCGCGCATAACCAAACTTCACGCTTACGTCCTCAACAACTGATGTTAACCGCACTGCAATTTTCGCGC
CGCATTAATATAGACGCGCGCATAGGCAATGCAACAAATACAGTCAAAATTCGCTGGAACCTTAAAGAGCGCGTCAAAATGAATTAACGACGATTCGCGCAGGAATACGCGCGCAAGT
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CAAGATGAAGGACAGTCTGAAACAGAGACGCGCGCATTTTCAGACGGCATCAACCGGAAAAACCGCTCCGCGGACAGT

SEQ ID 4394

MKQMRITFFPDPFTVSYAPLYRLQHLKYTLRKFFGKKEIYAFEPVNASPIRQGLFLHCPQDAYPILLREFVDRFRNCKRRILDAMTADFLMAEKLFGTDVLCQMEDCRPHLVLAHLSGDIS
LWLNRRDNCVEBAGWSLSLRDEAGNRLYMATFAVGTGTHLLTASVQGPSGEAKDVTTRITKQLHGLRPQQLHVTALQYFAAALKLDGAIGIAQKHQVKLEWKLKRRVKNYDAPHQEYAS
LERDGYWHLPTPARKDLADIESKKRSMYRKRYEMLDVMVAKMDSLTARGISDGTQTEKPLRRTV

SEQ ID 4395

ATGACCCAAATACACATTGAACAGGACGAGCGCTGTTGCGATCCAAACAGATTTCGCGCTGCAACTGGCAAGCGCATACCTTCCGCGCATTCGCGAAAAATCCGCGCTCAACGCGT
ATATCACCATCGACCAAGATAAAACCTTGCAGAAAGCCGTCGCGCGGACGACGATCGCGAGGCAAGCTTCGCGCACTTACCGCGCTTCGCGTACCAAGACATTTTCGCGCA
AACCGCTGGCGCAGCGCTGCGCTTCCAAATGCTCGACAACTTCATCTTCCCTTACACCGCCACCGCTTCCAAACCTGCTCGACGAAGGATGTTAAGCTTCGCGCGCACCAACATG
GACGAGTTCGCTATGGGTTTCGACCAATGAAAACCTATCTTACGCGCGCGGCAAAAAACCGTGAATCCGGAACAGTACCGCGCGGTTCGTCAGCGGTTTCGCGCGCGCTGTCGCGCG
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CTACGCCCTCCAGCTTCGATCAAGCGCGCCGATGGCGCAAAACGCCGAAGATGCGCGATTCTGTGTAATGCAATGGCAGGTTTTCGACCCCAAGACTCCACCAGCTTCGAACGCCGAAAA
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TGCTGAAAGCACAAGCGCGGAAGTGGTCGAAGTTTCCTGCGCAAAACCAAGCTGTCATCCCGCTACTACGCTCCGCTCGCAGAACGCCGCAACACCTTCACGTTACGACGG
CGTACGTTACGACACCGCTGCGCCCAATTCGCGGATTGGGAAGAAATGTACGGCAAAACCGCGCGGAAGGTTTGGCAGCGAAGTCAAAACGCCGCATCATGATCGGCATTCATGCTACG
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CCGACCCCAAAATCGGAGCGGATCTCTCCGGTTGAAACCTACTTGAGCGGACATTTACACCATCGCGCTCAACCTCGCGGACTGCCCGCATTAACCTCAACAGCGATTGGCAGCGCAACGACCGGAA
CGGACTGCCCGTGGTGATCAGCTTGTGCGCACTACTTCGCGGAAGCCAAATCTCGGTGCGCGCATCAATCCAACCTCAACAGCGATTGGCAGCGCAACGACCGGAA

SEQ ID 4396

MTQYTLKQAGSLQSKQISAVELASAYLAALAEKNPALNGYTTIDQDKTLAEARAADERIAQGNASALTGPVAYKIDIFCTGWRSAKMLDNFIPPTATVQNLDEGMVTLGRNM
DEFAMGSTNENSYGAANKPNWPEHVPGGSSGGSAVVAARLAPALGSDTGGSIQRPASHCGITGKPTTGTYSRFGMVAYASSPDQAGPNAQTAECAIILNAMAGFDPKDSTSFEREK
EDYTRDLKPLKGVKIGLPEYFSEGNSTDVQTLQNTIDLLKAQGAELVEVSLPQTKLSIPAYYVLAASAEAGTNLSRYDGVRYGHRAAQFDLEMYGKTRABGFGSEVKRRIMIGTYVL
SHGYDAYYLKAKLRLRVADDPQAFARCDLILAPTAPSAAPKIGADTSPVETYSIDYITIAVNLALPALTLPAFGSGGGLPVGVQLVGNYPARAKILGAHQIQLNSDMHGRPE

SEQ ID 4397

TTGGGTCAATAATCTCCATCTTAAAGGGCTTCGGCGGATTGCTGATGCCGTCTGAAGCGTATTTCGGATTATCTTCGATAACTTCGCGGTACGATGTACAGCGGTTGCGTACTTCCG
GCGAACGGCTTGGTATTTCGGCGCGCGGTCGGTTTCGGTTACTTCTTCAGCAGCGCGAGGGCGACCTTCGTGCGGGTCCGCATCGGCTCGATCGCGCTGTGTGATGTCTGCTCAT
CTGTCGACCATAGTGAATAATGCTGTTAATCT

SEQ ID 4398

LGHKSSILKGLRAVLLMPSEAYSDYSSITCGTMYRRLTSGATANYSAARSVSVTSSRRRRRATSCGCAIGSMPVLMFCISTIVKMSFNS

SEQ ID 4399

ATGAGTCTTTACGCTTTGCTCTTGGTTGCGCTGGGAATGTGATGGATGCGTTTCCGCTGCGCTGGCAAAAGGGCGCGCGGTTCAGGATGCCCGCGCAAAATTCAGCAACGGCTTTGG
TGTTCGGTACGGTTGAAGCGTTTCATGCCGCTGGCGGGCTGGTAGCGGTTTATATGCCAAGCCGTTTATCAGCGAATGGGACCATTTGGGTGGCTTTTGTCTGTTGGCGGACTGGGTCT
GAAATGATGTCGCGCAAGGGTTGTCGCGGAGCGGAGATGTGCGCGAAGCAAAACAGGAAGCCATGATGATGACGGTTTGTACTGCTTTTGAACCAAGTATTGATTCCATGATGCTCGCG
GTGGGCTTGGCGTTTATGAGGTTAAACATCGCTTTGCCCGCCCGCTAATCGGTATGGCGGCTACGGTAATGGTTACCATCGGGCTGACGGCGGGAAGGCTTTTGGCGTATTGTTGCGCA
GGCGTCCGGAATTTGCCGAGGTTTGGTGTGATTGCCATCGGTACATGACGCTCTTATCGCATTTGGGTTTGTATCA

SEQ ID 4400

MSLYALLLVALLGHSNDAPAVLAKGAARMPPRKIAATALVFGTVEAFMPLAGWVGFPYKPISEMDHWAVFVLGLGLKMMREGLSGEAEVRESKQESLWMTVLTAFGTSDSMIVG
VGLAFNEVNIAFAAVIGMAATVMVTIGLTAGKAFGVLFGRRAEFAGGLVLIAGTWTLLSHLGLIQ

SEQ ID 4401

ATGCTTTTCATGGCACTGACACTTGCAGAGTAGACAAAATCGCCGACTCTCCCGACTGCACTGACTGCGGAAGAAAAAGAAAAATCGTTCAAGAATTAAACGACATTTTCACTATGG
TCGAACAGATGCGAGAACATCAACACAGCGCATCGAGCGGATGGCGCACCCGACAGAGTTCGCCCTCCGCTCGGTGAAGACGAAGTAACCGAAACCGACCGCGCGCAATACCAAGC
CGTTGCCCGGAAGTACGCAACCGCTGTACATCGTACCAGTAATTCAGGA

SEQ ID 4402

MLFMALTLADVDKIALRLSLQLTAREKEKSLQRLINDIPTMBQMNINTDGIEMAHPEVALRLREDEVETEDRAAEYQAVAPEVRNRLYIVPQVIE

SEQ ID 4403

TTGCTTGGATTTTAAATTATAACGGAATAATCCGTTGCGCGCGCAATTTGCGAGCATCGGATGCTGCCGACGGGTTTGAAGAGGGGAAATATGGGATTGGGTATGGAAATCGGCAAGC
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TTCCCGCAACTGCGAGT

SEQ ID 4404

LLGLIITEKSVAAACISICLPHGPERGEIMGLMEIKLIVAPLVLINPFSALSLYLDLWNGHSTKERRKVARTAAVAVFAVIAVFIIGGALLKVLIGISVGSFQVGGILVLLIISM
MNGNDNPAKQNLGAQPETGQARPARNAGALVVPVIAIPITIGPGISTVITIASAARTYSDIALIILAAGLVVSAICYALLIVAGKVSRLIGATGLFILNRMGMLAAVSVELIVSGLKTI
FFQLAG

SEQ ID 4405

ATGTTTCACAGTGCAATGATTATACGGGCGAAACGCTTACCGCGCCCGCGATCAAGATTATGCGGAGTTTGAACCGCGCTGCGGATTTGAAATGCAACGCGAGGCGGTTCGCGCAAT
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SEQ ID 4406

MFHSNVNFTGETLYRRPDQDYAEFERRLADLKMHGFAQLGVTERAARLQKFAGRLEAEKERFAEMVCEEVGRCLHECRAETVKSELIRYARLAPKLLAHKTIATQASLSQVRFEPLG
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SEQ ID 4407

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AATGCGAAACCAAGGATGATTGATCCGTAATACAAATACCGCGTAACAAATACCTGCCGT

SEQ ID 4408

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SEQ ID 4409

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SEQ ID 4410

VMTDKAFIRVSLMADCPGRIGIGSGVFSFGFSRQGRHSALITWCFIYWGKTDSSQKYHMMVHLPYILAKKKIAGRNV

SEQ ID 4411

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SEQ ID 4412

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SEQ ID 4413

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SEQ ID 4414

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SEQ ID 4415

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SEQ ID 4416

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SEQ ID 4417

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SEQ ID 4418

MNYALDALWKLTSQPVRLDLSLITAPPLWQSGCELSVRELLGERGFRYLLALDADAPLITDYLQRAFPDHLGITYAEELLAFWFTNAPHKILHAYNLVFSQGTLAGAADVFSWLVQOP
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SEQ ID 4419

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SEQ ID 4420

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PGRANTQTEDIDILRGFPNTVSHRIKKD

SEQ ID 4421

GTGCACTCTTCGGAGCGGCAAAATCGGAGTTTATCTGGTTGGGGCAAACCTTCCAAATCGGGTAAATACCGCTGACCGGTGCTGCTTCAGCGCAACGTTAAATTTCCGACCTGT
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SEQ ID 4422

VQSPGAARSEFIWLGQTLFNRVKYRLTRVCFRRNVKFPFLKNSSDGISPSERRRRRIIPYSIPTENRT

SEQ ID 4423

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SEQ ID 4424

LRQYFGIGSHNIAAFQPSVLTRHIGNDAACFLDNQCTGNGVPRFEVELEKAVKTSCTCYGAQIQRSRAFAAASGGFCQKVFQNRQIFVHIALIDNREAGTDQAAVQFQDAVQDQDAVVQRA
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SEQ ID 4425

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SEQ ID 4426

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NDVYMASRGKALLANDRIIRVSNRIELNRLIGTFPPVQDMSMDKYLAILKDFLAKTAGGRREGAASLDLCAVATGRFDGFFENLKPWDIAAGALIVQEGGIVITMSGEDANLRSGLI
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SEQ ID 4427

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CGAATA

SEQ ID 4428

VPIPTAFLLAAGQEGGNGQMPFIAGNGNPVLYKRRITLNLSLFPQLFKGGLLESKSAVAENRHRGINKKGLYQISRYVTLEI

SEQ ID 4429

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SEQ ID 4430

SHLGLIQ*CRKIKRLKLYRFQTAFC*T*FSIGIIV*SY*K*NIDFPQ

SEQ ID 4431

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SEQ ID 4432

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SEQ ID 4433

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SEQ ID 4434

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SEQ ID 4435

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SEQ ID 4436

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SEQ ID 4437

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SEQ ID 4438

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SEQ ID 4439

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SEQ ID 4440

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SEQ ID 4441

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AAA

SEQ ID 4442

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K

SEQ ID 4443

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SEQ ID 4444

MSGIRKGFQACRQSVACECVFTSEIKPAALEVLKQNYPDEVYGDITKIETGDIPTDFDILLAGPQCAFSPAGKRLGFEDTRGLTFDFDVARILKAKPKGFIENVEGLVTHDRKDSIQ
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TKBGLRLFGYPDDYSFDIPKDRCDLLGNTVAVPVKAVSERILLTL

SEQ ID 4445

ATGAAACAAATTTATCGCCCTCTGTTTACATTAGCCGCGCAATATATGTTATCAGGAATGCGCTCTGAACAGCCTTCAGACGCATAGGTTTAAACCGT

SEQ ID 4446

MKTIVRPSVILSRNMYLSGMPSEQPSDGIGFNR

SEQ ID 4447

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SEQ ID 4448

MKAPTITAIIVAPLDRSNVDTDALIPKQFLKSIKRSFGPNAPDEWRYLDHGEPMGDKRPLNPDFSLNQPRYQGAQILLTRKNPGCGSSREHAPWALDDYGFRAILAPSPADIFFNNCY
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SEQ ID 4449

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SEQ ID 4450

VRII/ITIMELSMYAVVKTGGQYKVSUGEKLVQEIQAQLDSQIELTEVLIADGESVKVGAPFIEGAKVTAKVVAHGRGEKVRIFKRRRRKHYKQKQGHQNFQIIEIVAIA

SEQ ID 4451

TTGTGTAAGCTATTGAAAAATAAATATTGATTTTCCGCAAGATGGCTAAAGGTGCGATAGGTACACTGAAGAAATAATCGGCAGAACAGGTTTGCCTGCCGCTTTGAACAAATGATTTTA
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SEQ ID 4452

LCKATENKILIFKRDG*RCDRYTERIIGRTGLPAGLANDFNLPG*GIHDVFO

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 RGLNRKRNKMAKVKEGLEVSEVIVQEGVYTYETLNGAVCEPVVYMMDRFVIGGFFRVHEGRGADENLWAGGMVFPVPLSNSIPTGNGDNSQEAPEACKRVFEQWDSLGMPRSEKDCQVDNE
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CATCCGTCCTTACACCGGTTCTGAAGAA

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SEQ ID 4480

[illegible]

SEQ ID 4481

SEQ ID 4481

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SEQ ID 4482

SEQ ID 4482

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SEQ ID 4483

SEQ ID 4483

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SEQ ID 4484

SEQ ID 4484
 LTVMSGRTGRNSATQAQPERVMLGVVMLDKDQTSNAARLNGFQTALAEAVELVKAAGDSVRVETAKRDRPTALFVGTGKAAELSEAAVDGIDLWVFNHELTPTQERNLEKILQCRVL
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 YAKDQLPATFLDTYARRLYTSPACSIILTDTVGVFSDLPKLIISAFSATLEETVQADVLLHVVDAAARNSSQOQIEDVENVLQRIHAHDIFCIKVINKTDLPLPSEEQNTGIWRDAAGKLAARV
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SEQ ID 4485

SEQ ID 4485

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SEQ ID 4486

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SEQ ID 4487

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SEQ ID 4488

LIYKKNCHNKSXYAENMKRMVPIENGCSATVIHRASIWKKLIHIDIIPFVA

SEQ ID 4489

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SEQ ID 4490

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DENGTVFFKAQPFMAGNVFQFCHDVVAHGLILHN

SEQ ID 4491

GTGTATCAAAATCGGTATGGGTATGTAAAAAGCCGATCGTGAAGATGCGGCTTCAGGTATCGGTTGAATATTTCTTCAGAACCGGTGTAAGGACGGATGCTGACAGTTTTACGGTTC
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AACCTGCGGAATCAGCTCGTTGCCGTAGGCTTTAACGCCAAGCGTTTGGCTTC

SEQ ID 4492

VYQIGYGVCKKPHREKMLQVSVLFFRTGVRTDADSPVQRAFGEFDTITVNFGEQSVVFAHTTVVACVFEFTALAYDGTGCGQLVAVGFMQAQFGF

SEQ ID 4493

GTGGATTTATCGGACAAATGGAATAATATGTCAATATGGATTATTTTTTCCAAATCTGGCTCTGTGTATGACGGTGGCAGAACCAACATTTTCAATGAAACCATCTTTTCATTTTA
TTTTCTGCATAACTTTCTTATTTGTGACAAATTTTCTTATATATCAATCACAATGATAAT

SEQ ID 4494

VDLCRWNNYVNDYFPNTGVSVDGGRTTIFNENHPHFIPICITFLIVTIFLIYQSHEN

SEQ ID 4495

TTGGAATAAAGAGAAACCAAGCATATGGATTCTTACCTACGCGGAATGACGACGGTGTGTTGCCGTAGCCAAAGCAGAAAAACATCCCTATTGTCTATTATCATGATAGGACAGCAA
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SEQ ID 4496

LETKKPSIWIPTYAGHTTVFCRSQSRKTSLLSFYHDTARHLKINHYVIDI

SEQ ID 4497

TTGAGCGCGCATTTGTGGATCAATAAGCGCTTGAATGCCGTCTGAACGGCATCAGCAATCAAAAACCCGAATCTTGCCAATCAGGATTCGGGTTTTTA

SEQ ID 4498

LSAHLWINKPLEMPSEHQQSKTPNLANDSSFL

SEQ ID 4499

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GAGCGGCAATTTGTGATCAA

SEQ ID 4500

LSVHHWTDAYTFTTCIRDESLRFENGQFVWGLMADGKPLMRAVSASANWEEHLEFSSIKVQDGLTSLRQLKVGDEVLSIKKPTGTLVAGDLNPKHLYLLSTGTGIAPFLSITKDP
IYEQFEKILLVHGVRYKDLAYYDRFTKELPEHEYLGLVKEKLIYPIVSREEPEHGRGLTDLVSGKLFEDIGLPEKINPDRAHLGSPAMLKDTCKVLDGFLTVSPKTVRGDYLI
ERAFVDQ

SEQ ID 4501

GTGGTGTACGCAATACTTTTTGGGTATGAATGCTGCCATTTGGGTTTCCCTGTGCTAGTAAAAGAAATGGATAGTCTGTTGTCGGGACGTGCGGACAGGTGAAATGCTGCCCGATTCCG
GA

SEQ ID 4502

VVYGQYFLGIBECGLGLSVKEMDSACSGRAAEWKCLPDSG

SEQ ID 4503

ATGACCTTACCTATGACAGGAAACCGGTTTTCTATAGTCTGGACGAATGGCGGCAAAACAGGAGGCAACCATCGCCCCCTAAGTCTGTCGGCAGGACCAAGGTATGGGTACGCAAA
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TGGGGACGGGACCGCTCAGGCTGGCAGCTCGATTCTCTTAATTTCCCTCGCGGATATGCGCGG

SEQ ID 4504

HTLPQETFRPSILLDELAQKQATIAPYLLADGTQVWVRKAGREHARWRYALLGMVARYLKLGLVLPVSLGGEPALATESKRLYELRSAGIAVPELLALAKNALMFGNLEGIPLDTQIRQ
BAEAGKADAWLAGLEAIARVHKRQFLSQAFARNMMWDGNLSFLDFEDDPSEVLTLAQQRDWLCYIHTALILKNGGLLEAAAEKGGVLSQPAETIQKLIAGTVKPIPIRLSEHP
WGRDALRLAASISLISLADMPF

SEQ ID 4505

TTGTCGTCTTCCCGCGCAGGCGGGAATCCAGACTTGTGCGGCACAGAACTTATCGGGTAAAACGGTTTCTCAATTTTATGTTCCGGATTCGCCGCTGCGCGGGGATAACGATTTCAGSTA
TTTCTACATCGAATCCGCTTTTTATATCAACC

SEQ ID 4506

1SSFPRRRESRLVGTETYRVKRFLQFYVPDSRLRGDNDSGISTSNPLFIST

SEQ ID 4507

SEQ ID 4507

TTGATACACATTAAAGCTGAAAGTAAAAATCCGCATACACCCCTCCCTCGCATATTTCTTCAACAACGGGTTTGATATAATCGCCTATCTGTTACAGATAGTTCAAAACGGCATTTCAACCCCT
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GATTACCAAAACATGACCGT

SEQ ID 4508

Seq ID 4508
LIHIKLVKIRIHPLHISSTGFDDIAYLLQIVTAFKPLQMPSEIIGIRLCRGYFMSLSHDILVVGAGPAGLSFAAELAGSLKVTLIERSPLTVLQNPFDGREIALTHFSREIMQRL
GMWDKIPENETYLPRDAKVLNGRSDYQLRFPQTEARGEADCLGYLSLNHNIIRAAEYVWSQLDNVSIITDITAVKEVKTSDNEAQVFLENGDDIITARLLLAADSFPSTQTRQLGISSDMH
DYSRTMFCVCRKHITLSNQHTAYECFYHRTIALLPLEKRLTIVTIVTDTKINSVQNLSPEELAA SVKEQLKGRIGDMELVSSITHYPLVGMIAKRFYKGRSALIGDAAVGMHPVTANGFN
IGLSSADILAKLILEABORGQDIGAASLLEKYSSKHMLHAHPLHYGTMMLKLFNTETAPAKLLRGLVLRAGNNFPPLKKLITQQLTG

SEQ ID 4509

SEQ ID 4509
GTGCAGATGCCGCTGAAAAATAACCCCTACCAATGGAGAATCAAAACCATGAGCAACAACATCCCAACAGAACTGAAATACGTTGCCAGCCATGAATGGCTGCGCCTGAAGAAGACGGTA
CCATTACCGTCGGTATTACCCATCACGCGCAAGAGCTGTGTGGGCGACATCGTGTGTGTCGAGCTGCCCGAAGTCGGTGCGAACCTCGCCGCCGAAGACAGTCCGGTGTGGTTGAGTCTGT
AAAAGCCGCATCCGAGCGTGTATGCGCGGATTGCGGGCGAAGTCGTGTGCGTCAACGATGACTTGCAGGCGCGCGGAAACCGCCACAGCGACCCCTTACGGCGCAGGCTGGTTCTTCAAA
ATCAAAACCTGCCAATCTGCCATTACGACGCGCTGCTGACTGCCGAACAATACGCGGGCGAAGTGGAT

SEQ ID 4510

SEQ ID 4510
VQMPSENNPLMEVQTMSSNIPTELKYNVASHENLRLEEDGTTITVGITHAQELLGDIVFVELPEVGANLAAEQSGVSVKKAASDVYAPIAGEVVAWDDLPGAPETANSDFYAGWFFK
IKPANPADYDGLLTAEQYAGEVD

SEQ ID 4511

SEQ ID 4511

ATGCGGCTCGTAATCCGTTTTCCTGCAATTTTCGACAAACGAGAAATAATCATGAGATACATCAGCACGCCGCCGGCGAAACCGCACAAACCGTTTCAGCGAAGTTTATTGATGGGCTTGACACCGACGCCGCCGACTGATGCTGCCGGAACATTATFCCGCAAACTGGCGCGAAACCTTTGGACAAATGCGCGCGTTTGGCTTATCCGAAATGGCGTTTGAATCATGTGCGCTGTTCTGTTACCGGATATTCCTCGGAGCAGCTTTGGCGCGCAATCTTCAAGCGATTTCAGACGGAAGCGCGTTTCGGTACTAAGGAATCACCCCGCTCCGCAAGCTTTTCAGAGCGCATCAAAATCCAAGCCTTGCTCAACGCCCGCAGCTGGCGCTTCAAGATATCGGCATGCAAGTATTTGGGCAATCGCTTTTGGGCAATCGCTTTGATATATGTTTAAACAAGAAGCGAAAAAAGCTCAATATCTTGGGCGCAACAGCAGCGCGATACGGGTTTCGGCTGCGGAATATGCCCTTGGCGCGCAAAAAAGCGTGAAACGTATTTATGTGTTCGCGCCGACGGTAAATGAGCGCGTTTCAAACGCCCGCAGATGTACAGCTTCGAAGCAGGGAATATGTTTCGGCTGCGGAATATGCCCTTGGCGCGCAAAAAAGCGTGAAACGTATTTATGTGTTCGCGCCGACGGTAAATGAGCGCGTTTCAAACGCCCGCAGATGTACAGCTTCGAAGCAGGGAATATGCGCAATPATCGCCGTAAGAGGGAATGTTTGACGATGCCAGGACATTTGTAAGCGAGTGCAGAACGATGCCCGCGTTTCAAGGAAAAATACCATATCGGTACGGTCAATTTCGATCAACTGGGGCACAAATPATCGCCGTAAGAGGGAATGTTTGACGATGCCAGGACATTTGTAAGCGAGTGCAGAACGATGCCCGCGTTTCAAGGAAAAATACCATATCGGTACGGTCAATTTCGATCAACTGGGGCGCATCGTCGCCAGCAGTGTTTATTACTTTGCGCAGCTTTTCAAGCCACTTCAAGCAATGACGAAACCGTCAGCTTTTTCGCTACCGAGCGGCAACTTCGGCAAGCTTTTTCGCGGGACACATACCCCAACAAATGGGCGCTGCTTGCCTGTCGCGCTGATTTGTCGCGACCAATGAAACGATGTGCTGGAGAGTTTTCGCAAAACCGCGCGCATATCCGCCCGCGCAACAGCGCGCATATTTATGTAACTTCAGCCCGCTCTATGAGCAATTTTCAAAGCTCCAACTTCGAGCGCTTTCGTGTTCGACCTGATGATCGGATCTCTCAGGAAATCAATACGTGTGGGCGGAAGTTCGCGCGGACGCAAAAGCTTTGACCTGCGGTTTTCGCTTGAACAAAGTCGCGCGCAAAATACGGCTTTTACCTCCGCGCAAACTTACCCACGCCGACCGCTTCGCAAGCTTTCAGACAGCTTTCAGAGCAAGACAAAGAACTCATCGACCCGCATCTGCCAACGGCGTAAAGTTCGCCCGCAAGTGCAGCGAAGCGGGGAAACGCTGGTTTGTTTTGAACCCGCTTGGCGGCGAAATTCGATGCGACCAATACGCGAAGCGTGCAGCGATGTCTGCCATTTCGCGCCCGCGCGCTTGAAGGTTTGGAAAAACCTGCGCGAGCGGTGCAACCGTGCAGCAAGTGCAGTTCGCGTAAAGGCATCATCGAACAAACCCCTTGGT

SEQ ID 4512

SEQ ID 4512

NPSESVLQFRQTRKIMRYISTRGETAHKPFSEVLMLGLAPDGGMLPEHYPIQIGRETLDKWRGLAYPELAFEMCLFVTDIPEDDLRLILNRTTYEAAFQTKRITFVRTLSGDIKIQALS
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RIVAQVYVYFAGYFNATSSNDETVPSCVPSGNFGNVCAGHIAKQMLGFLPVCLIVATNENDVLDEFFKTKATYRPRNSAHTYTVTSSPSMDISKANSFERFVFDMLDRDPQKQINTLWAEVAAGK
GFDLRFALDKVGKRYGPTSGKSTHADRLATIRQVYBQDKELIDPHTANGVKVAREVREAGETVVCLETALAAKFDTATREAVGDVALPRPAALBGLLENLPQRVQVTPNSADAVKGLIIBQTL

A

SEQ ID 4513

SEQ ID 4513
ATGTTGCCGGGCTCAACCGGATATTCAAACGGTTTGCTCCAACACTCGGAACGGGGCATATAAAGCGCGCCTTCGCGTTATCCGAACGGGGCGGCTAATCAGATCTTATCGCCATAAAAGCGGGGTTTCAACCGGAAAGGAATTGAGATGAATAAAACCTTGTCATTATTCGCGGGCAATTCCTCGGCGGGTGCGCCGCGCGGGCAACACATTTCGGACGCTTAGACGGCGCACGGGTATGGTGCGCAGCATCGTCAAAATGACGCTAGAAAAGCCAATGCGCTGCGGAATTGGACAGGCGCAGCAATGGCGTTTACCGCGCTGGCGATGAGTGCCGAAACACGGCGGAATGGGAAACACAGATTTCGGCTGCGCTACCGAAGAAGCACCTAACCGACTGACCGGCAACGATGTGATGCAGATGCTGAACAGTCCACGCGCAATCAGGCACCTTGCCGCGCTGACCGTCAAAACGGTTCCGCTGCTTCAAACCGCTGTACCGC

SEQ ID 4514

SEQ ID 4514
MLPGFNRIKRFAPTLGTAHKTPPFALSRTGRLIRSYRHKRGFNRKGIEMKTLILPAAILGGCAAGNITFGSLDGGTGMGGSTVKMTVESQCRARLDRRSEWRILTALAMSAEKQAEW
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SEQ ID 4515

SEQ ID 4515
GTGTGGCGATGGGTGCGGTGCGGATGCTGCCCGGTATCCCTCCGTTTTTGGAGCAGTTCAAAATCTTTGGGCTAGGCTGAAATCGAAATGCCGTCTGAACCGGTTTCAGACGGCATTTTTG
CAAACAGGCAAAATGACGGCGGCGGATTTTTTATTTTCCCGAT

SEQ ID 4516

SEQ ID 4516
VNRWVRSGCCPVSLRPFWSNNLWARKSQMPSEPVS DGI FANRQNDGGGIFYPFD

SEQ ID 4517

SEQ ID 4517
TTGACGATGCTGTTGGATAATTGGGCTTAATCGCGTGCAAAGAACCGACGCGCAATTAGGTTTTGTGCGACGAGTATTGATACCGGCAGTAGGTTTCTTAATCTTGTGTGGCGATGG
GTGCGGTCGGGATGCTGCCCGGTATCCCTCCGTTTTTGGAGCAGTTCAAATCTTTGGCC

SEQ ID 4518

SEQ ID 4518
LTHLLDNLGLIGCKERSAQLGFVGRVLIPIAVGFLILCVANGAVGNLPGIPPFLEQPKSLG

SEQ ID 4519

TTGCCGACGCGAGAAATTTTTGGTGTCTTCCATTTCCGGTATTTGGCTGTGCAATGTGGTCGCCGATTTTTAGGACATCAAGTGTTCAAAAATCAGCTATCCGGAACCCG
ATAAGGTATTTGATGAATATAGACGACACCATGACAGTGTCTGTCTCGTCAAGCAGTGGGTCTTATTTAGGGGGTCAAAATTTTACCTCTCTTGGGGAACCTTATATCGTCCGGCATC
GATTGCCAAACACCCCATTCGGGGCGGTGCGGTTTAAACGCGGTTTATGATTTATCGCGGGTGTGGGGCTATCCGATGGACTTGGCGATTTGGCAGCCGGTATGATCGTAGGCGTA
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SEQ ID 4520

LPTAESFLVFFAVLAVAMWSPDFLGHQVFKISYPEKTKVLMNIDDTHTSCSVQAVSILGGANFTSSHTYIVPASTAKEPIPGGAVLTAVLICIIAGLWGYPHDLAIWQPVILVGV
CLPILLRAGMEMTRKGTQSAALVFFSSVNSIRFSAGR

SEQ ID 4521

TTGAAACTGCCGAAATGCCGTCTGAAACGTTTCAGACGGCATTTTGTATATGAACCGTTTCCGCTTCCATATCTTGGCAGACGGTTTGCAGCAGATTCCGATACGGCAGATGTTT
CAAGCAGAAAGGAAACACA

SEQ ID 4522

LKTAEMPSFTFQTAFLYEPFCGPHLGRFPAADSHADVSSRKETQ

SEQ ID 4523

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CCCAACAAGAAATCGTTGATTTCCGTGCAAGCGCGTAATGGCAAGTAATAAGCGCAAGATAAACGAAGCATATTTGGATTATTTCTGATCTCTAACTGCCCTTCCGCCCAAAAGCAAG
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SEQ ID 4524

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SEQ ID 4525

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SEQ ID 4526

LGLPDSFVLENVRYELLIAASILLVSGFPLPGANLPQTHGLPIPMIPIVVSAGGHPLAFGISIAVLGLLMLFRGGSINAKLTSNGVCGLLLYLGFITGQVKKLFSWAGGFNMPYLA
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SEQ ID 4527

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CGAGTGGGAGGATTGATTTCTGCGATGCGGGAACGATTGGAAGTGGTGTGTTGGGGCGCGCGCGCTTTGCGGCACCTTTGGGGCTGCG

SEQ ID 4528

LGFWGYGFRTPVSKRKVMRPFYEARYIRRVMEKHNGTYRDLHRPASEFATREYLEHLQIMQPKRWRPNLPFRDYRFWEEDLIAMAGTIGKVVHVGSGGVCRTFGAA

SEQ ID 4529

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SEQ ID 4530

MYPSLCGFLYLGNRLGLLLKINFLIKHVFNCISFPDDDY

SEQ ID 4531

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SEQ ID 4532

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SEQ ID 4533

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SEQ ID 4534

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SEQ ID 4535

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CGTTGCTCTCGGACAC

SEQ ID 4536

LCDPQTLIDLWAGGIGVAMVQGNKABAAKEGAGVAITESCRRHSMPLNFTYAREYEDNPHVSLILLECEVKVGVQAVQPPVVSIN

SEQ ID 4537

ATGAACCGTTTTCGGTTCCATATCTTGGCAGACGGTTTGCAGCAGATTCCGATACGGCAGATGTTTCAAGCAGAAAGGAAACACAATAAAAAATAAAAAGCTCCGAACAGTCCGAGG
CTTTGCTTTCAAC

SEQ ID 4538

MNRFAVSISLADGLQIRIRQMFQAEKHNKNKKASEQSEALLSN

SEQ ID 4539

EQ ID 4539
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SRVVEAAVAQQCYARFASABGFEGPRRAAGAADKDFLPERAFACGGDVVAFVFGKGVGIGAEDPGCPVAVIACGLAAGELVAREAVGEAVVFRGLDDGDFFAHVA*NLLPVQTFAPVAPTVN
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DFGEVFGVGFPGAAGEVQEV*NLFGVRHVRFGCQRQFGVIFKABQGGFGCVFERAVDVGGGVVEFVAV*KPASTGNVGAVDLPAQFAYAGVLDNGKVVKNLQADFVTCFAPALRGGGKXGE
RVFGNAGKRKCGIVKVNARVGRV*DVLGEFGGLRAPGLGQFQFCLPFRQFRAAQVETIAQVVIELGFLCGKRCCKFGGIFDGFEAUVQFDVLSDFGEBEDGFRHQFVIDGAQFGRVDDGV
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SEQ ID 4541

SEQ ID 4541
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SEQ ID 4542

SEQ ID 4542
 LRAKVIMLKNEIRGGIGIPPDWATMRGQAKKTNVFADAEKRVPFREKRIVQHEPLIRFPSVWLNDIGAAPLFGRRPHFIATHECLPDSRFNSKPFQYFVQTWIAADGGVQAPQGGFFGYGTARI
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SEQ ID 4543

SEQ ID 4543

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SEQ ID 4544

SEQ ID 4544
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LHI GELAGALPFLHNLKIDG IHSNMLYVKKGTSTPQEVVVKNLSEVLDSMNYGERLPAFTVTSKNFVNGKYIDDTHLMEDALTVEYSARNGDKNNKDDYKSPNGSEMTAEKAGDDYV
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SEQ ID 4545

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SEQ ID 4546

LRVQVFLRGIFETAPKSNVLTGNNKI SITTEBDGLGLGVNGLQSNPSYSGHTTGTFINNQPSNTTQPSLDGTSTIELKAVKGNNEVDLNVKNHASVKGITTSKATLEAEEDNIVRVK
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SEQ ID 4547

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SEQ ID 4548

LELITTEGADGDLVNGSYGIRSFADLKLEYKPELSVRNHDIIFNNDPQSDVDPYSGNIHLVVGKIQFNLNVADKVTDPHTHJEKLVNDNALVRYVNNITPSDENDKGSISSFHKTG
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SEQ ID 4549

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SEQ ID 4550

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SEQ ID 4551

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SEQ ID 4552

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QKQFD

SEQ ID 4553

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SEQ ID 4554

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SEQ ID 4555

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SEQ ID 4556

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 PFDFTENAEFFCSQISQIEDKKQLLALKALQTAKELYNLRQGSHEFLAHLDFDKLNLRYRETAARLDTLNLAEKLQGDTHALLNEALEVDYFQVKIEAELEKLADLDKDRKVRRE
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SEQ ID 4557

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SEQ ID 4558

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SEQ ID 4559

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SEQ ID 4560

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 ECEGTSGRQRVNNALKFLLELPPEPQIQQSIAVLSALDKIALNKKQINARLEMAKTYLDYWFVQFDPDANGKPYKSGGDMVFDLTKREIPKMGWSIELQSLAKIPNTTKILNK
 DIKDFGKYPVVDQSDQDFTCGPTNDEKSIILNPQDAHLIFGDHTRIVKLWNFQYARGADGTQVLSNRMENFNLFYQLINQIDLSYGYARHFKFLKEFKIILPKSDISQKYNELANTFFVK
 VRNRLKQNHILQIRDLFLPLMNGQVSVRCGARDG

SEQ ID 4561

ATGGATAAATCTTTAAATATTTAAATATAAGTAGTACATCTTGTCTGTATCAATATATTTTATTAATTCGAATATATATATTAGACCTTACTTGGTTTATCGTGTAAATTTCAA
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 ATTTCTTACTAGTTTCACTGCTTAAAGTCAATTTTATTTAACCCTGTTTCTTATTTGCTATCGATTATTAAGCAAAAACTGAATCAGGTTATTATTAGTCTGATAGTAAAC
 AGGAATTTAGAAGCCCAAGAGTGAAGTTCGATGCTGATATCGAATTAATAATTTTACTTTCTTAGAAAAA

SEQ ID 4562

MDKLKPIILLNISSTSLISYFIKSQYIILDLTFWYFVVISNHNIEPISKLSLLFYFLIPFIATATVLMLSKYLKDEPKQGEVKELEYVNDNPLPSYLGYPFVALSIPDNLLFLFVMTGI
 IFLLVSCSKSFYFNPVFLFGYRFYQAKTESGLLVLSKQEFRTQSVSSIAVYRINPFLEK

SEQ ID 4563

ATGAATTTGTTTGTAGCTAAATTTACTTGAAGAAAGATTAGTAAAAATATTATCTGATGATCATATTTTCCCTGACTTTTCTTACGAGAAATTAATTTTATAACATATACTATGATT
 ACAATCTTGATGATGATGACTTGGTTTCAATTTGAAATTTAAAGAAATCAAGATTTTGTCTAAGTTTGGATACTCAAAATTTATTGATTCAAAATGTTTAGTGAAATAAAAAGGA
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 GGTGCAAACTATGCGAACCACAAGACTTATTGGTTATTAAGATATTCCTGATGCTGTTTATATAATAAGGATGATAAATTAATATTAGAACCTTTCTTCTATTTCAAAATATTTTA
 AAGGGATGAAGATTGTATCGAAGCTACAATFACTGAAGTACAGCAATTTCTAGAAAGCGATTTTATTGATTAAAGAAAGATTTTAAAGTGAAGAAAGTATCTTATCCCAATAGGAA
 AAGAATAGCTTTAGTTCAGATAGATTGAATAATATGACGCTAGATCAAGACAGAACTATTAATTAACCTTGTGATATAATAATAATATCTTGAATTTAAACGAGATGGCTCTCGT
 GTAGAAATTTCTACTGATGATGACGCTGAACCAATTTGTTATATGTTATTGATGAACGTTATTACCAACAGCATTAGGAAAGAGAAAGGTTGGCAATAGTGTTCACCTATT

SEQ ID 4564

MNFVLAKITCKKDLKILSDHIFPDPFSYENLNFITTYNDYLDLDTWQIENLKNQDPCPKFLDNLNFSKMFSEIKKEEINIEKLKYLVSCTNDALFFQKITSSILLKKHLITCGN
 GAKLCEPDILLVINDIPDAVYIHKDKLIFRTLSLSNIFKGIEDLYREATNTEVQQLFESDFIDLKEDFLSEKVSIPNKRIALVQDRINMMLDQRELLNYLAENYNNILKFNADGSR
 VEISTDVLKHLLYGIDERYTTALGKEKRLANSVQPI

SEQ ID 4566

SEQ ID 4567

SEQ ID 4568

SEQ ID 4569

SEQ ID 4570

SEQ ID 4571

SEQ ID 4572

SEQ ID 4573

SEQ ID 4574

SEQ ID 4575

SEQ ID 4576

SEQ ID 4576
 NLYICFTYCIISVQTKRTRSVGLDFAFFGPRVTSNSSPRRRESGSSGFCVISDEFNLHWFPGFSLSGKERHKYFPNQTKCRLGQFQTA

SEQ ID 4577

ATGACCGACACAGCCGGCTTGGCCGCGCAACCTGCGGCAATGGATAGCGGAACACTACGGCGGACTGCAAAACCGTTTGGCCGAAGCGTTGCCCTCAACACAGGCGAACTCTCCGCC
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CACCATGTGCCATATTTCCCCCATCCCGGAAATCTTAGCCGACATCAAGCCGGTAAATGGTCATCATCCGATGCCGAAGACCGGAAAAAGGCGGACCTGCTGATGGCGCGCAA
TTCGTTACCCCGGAAGCCGTCACCTTTATGATCAACACGCGCGCGCTTAGTCTGCTGCTTATGGAAGGTGCAATGGTCGAAAACTCGGCTCGCGGATGATGACCCAAAAAACGGCG
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CAACAGGCGGAAAGCGCGCTGTCATCTCTCGCAACACCGAAGACGCGCATCTCTGTCGACCGCACCTTACCCAAAGCGCAAAACCAAGCTTCAAAATGGGACAGCAAAAGCTACG
GCATCGCGCGCAAAATCTTCGCGGCTCCACGTCAAAAAACTGCGGCTCTCGGCCAACCGTCATCTTTCACCGGCTTCCCGGCTTCGCGCTCGAAGTCGTCGCTTTGAAGAAGCGGA
AAAA

SEQ ID 4578

MTDTAGLRRLNRQLARHYGGLQNRFAEVALMTGELSAALKNKSPGKKARKIQAAMKPAFWLDTERTGRPPGHTGKTMHSISPIPELLADIRAGKMTITDAEDRENBGLLMAAQ
FVTPEAVNFMILKHARGLVCLPMEGAMVEKLGLPMTQKNGAQYQNTFVSI EAAHGTITGISAADRALTIQTAVSPYAKPADIVQPHIPLRAQKGGVLVRAGHTBAGVDLAQMNGLIPA
AVICEIIDNDGTMRMPELMKFAEHLKI GTIADLIEYRSRTESLLEDMDAPVPTWGEFQHVVDKLSGETHLALVKGTPSADTBTLVRVHEPFSVMDFIQANPRHSWSLPAKLERV
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SEQ ID 4579

TTGTTTTTCGCAATCGGATATTTCGCTTTTGGTAAACAGATCCGCTTTGAAGCCGATTCGTGGCTTCAGACGGCATTGCCGCAACCCCGCGCGGGCGGCTGTTCTTCCCGCAC
GCTTC

SEQ ID 4580

LFPAKSDYLPFGKMPFEAGFVADGIAATPPAGRLFLPARF

SEQ ID 4581

GTGCGGGAAGAAACAGCCGCCCGCGCGGGGTTCGCGCAATGCCGCTGTAAGCCACGAATCCGGCTTCAACAGGCATCTGTTTACCAAAAGGCAATAATCCGATTTCGCGAAAAACAA
ATTTGCTTTTGTAGTAATACGCGCTTACAACTCCGTACATCCGATTCTTCAAAAGGATAAAACGA

SEQ ID 4582

VREETAAPPAGLRQCRKPRIRLQTASVYQKANNPIWRKTNLLPSKYALTIRYIRFLQRIK

SEQ ID 4583

TTGATTCCCGGGTACGCGATAGCGGTACGAGCAGGCGCAATACCGGCAATCTATGATGAATGCCGCTTCCCGATAAAAAACGAGCGGATCGCTTTTACTTTCTACAAGTAACAGGGC
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SEQ ID 4584

LIAGYIGGTSRRNTGNFMNNAAPPITRGRIAPYFLQVTGLFFARF

SEQ ID 4585

ATGTTTGATGGCAAGTAGAAGCAGATGAAAGTTATTTTGGCGGACAACGCAAGGTAAATGCGGTGCGCGTGTCCCGGAAAGTCGAGTATTCAGGCTTCTCAACGAAATGGCAAGG
TTTCTTTCGCGTCCGTTATGTACGTTTCGTAAACATTCGAAGACTTCTGAAACCTGCGCGCGGTTTCGTTTCGTACCCCCCTGTTAGATAAGGGGGGAAGATTGGAAGCGGTTGCGG
GCTTCTGCGGTCCGCGCGCGCTCCGTATCATCAGCGCGCAACCGCTTTTTCATCCCTGCTTATCTTCCATGGTGCAGAACTCTCAAAACGCGGCAAAAAAGCCCTGTTACTTGTAGA
AAG

SEQ ID 4586

MFDGEVEADESYFGQRKGKCGRGAAGKVAVPRLKRNKVSFAVRYVRFTTFEDFLNPARRFGRFTPLLDKGGKIRSGCRLPAVRRVRHHAGNRLFHPLLIIFGHANPQKRAKSPVTCR
K

SEQ ID 4587

GTGGCAAAAAACGCTTTTGCCACTTTGCCGCAATTCGCGCGGTACCGGCCGCAAAATGCGCGCACGCGCTTTCAGACGGCATCCGGATGCGGATAACGCTGAATCAGCGCGGAA
TCGGCTATATATACAAATATATATGCGCGCTCCGCCCGCTTTTCCACAAGGTGCGGACTGTTTGGCGGCATCGCAAAATCTTTTCAAAATCCGCAAAAAATATGACTGAACAAAAACA
CGAAGAAATACGGGCGCGACAGCATCCAGTGTCTGCAAGGCTTGAAGCGGTACGCAAAACCGCCCGCATGTACATCGCGGACACGCGAGGCGCGCTGCACCATATGGTGTGTGAA
GTATTTGACAAACCCATCGAAGCACTTCGCGGACATTCGCAAAATACGCTAACGATACACGCGGACCATTCGCTCAGCGTGCAGCAACGCGCGGTATGCCACCGGCAATCC
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SEQ ID 4588

VAKKRFCHFAKFRARTGRKCAARPFRHRPDADNAESGGEI GYNTQLYAPSRPLFPQADCFGGIAKSFQNPAKNMTBQKHEEYGADSIQVLEGLAVRKRPGMYIGDTQDGSGLHMFVE
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GTTVRFLAGTETFGNIEYSPDILAKRIRESPLNNGVDIELTDERDGHESFALSGGVAGFVQYNNRKTPLHEKIFYAFGEKDGMSVECANQWNSYQESVQCTFNINIPQDGGTHLAL

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LADQCEKDPALSELVYVEGDSAGSAMQGRDRKFOAILPLKGLILNVEKARPEKMLASQEVATLITALEAGIGKEEFNPEKLYRHRIIMTDADVDGAHIRTLLITFFYRQMPLELVERGYI
YIAOPPLYKAKYKQERYLKDELEKQWLLGLALEKAKIVSDGRPIEGAEADTAKQFLAKTVIEQESRPVDELVRAMLHASPIDLTSSENADKAVAEISGLIDREKAEALERIIEGHEGH
RFIKITRKLHGNVWVSYIEPKFLNSKAYQTLITQTAALKGLVGEKALYKGENEYDADSPETALDILMSVAQKMSIQRYKGLIGEMNPEQLHETTMDFAVRRLIAKVRIEDAIADSEVFTL
MGDEVEPRRAFIENNALIAQHIDA

SEQ ID 4589

TTGCGCGGTGTCTGAATGGTGGTTACAGACGGCTTCTCCCTTCGGTGGACGTTATCTAACCGCGCTCTCCAGATTGTTTGTTCATGTGCAGTCCCTGATACCTGAGCGATTAAAGG
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ACCACCTGCTGAAGAA

SEQ ID 4590

LRGCLNGSGDGLLPFGGRYSNAALQIVCFNVQSLIPERFKGVCAFPGYTVVGCNTLLHLSRLCLESANWASRLKRDANRPPLFSDHPFKTKFVPDDGITYMLIWSPSMRIAANTRTDNPH
SLKRNANMPQLTLDKTDIKLQVLQENGRITNVELSERVALSPSPCLRLRLKQLEDAGIVRQYAAIISPESVNLGLQAFIRVSIKAKDAREDFAAASVRKWPBVLSCFALTGETDYLLQAFP
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SEQ ID 4591

TTGAAACGGCATTGTTTTCGTGGTATAAATCGCGTTTACTATTTTAGAAGTTTGAGACTGATTATGGCAGAGTTTGCAAGTGACCGGTAAACGCCGATGTCGGCAACACCGTAT
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CGCAAAAGTAGGCATTGATGCTGATTGGCTGATTTCGCTGCTCGCGCGCAAGCT

SEQ ID 4592

LKRHCFSWYKSRFTILEVWRLIMARVCKVTGKPRMSGNNVSHANNKTKRRFLPNLQSRFFWVESENVRVRLVSNAAALRTIDKVGIDVVLADLRAGEA

SEQ ID 4593

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CGGTGCCACTTTGACGACAGGCCAACCCGAATATCAAGCAGGAGACTTTAGCGCTTTAAGATAAGGCAAGCAATGCTGTAATCGCGGACACGCTTTGATGCCCCGTGATACCGAATTC
ACACGTATCTTGTATGCCAACAAATCACTTGATCAGTACGCGCGCAACAGCAGGCATTGC

SEQ ID 4594

MNKTLYRVIENRRKAGVAVAEITKREKSCADSGSGSVYVKSVSFIPTHSKAPCFALGFSLCLALGTVNIAFADGIIIDKAAPKTQATILQTNGIPQVNIQTPTSAGVSVNQYAFD
VGNRGAILNNSRSNTQQLGGWIGQNPWLTRGEARVVVQINSSHPQLNGYIEVGRRAEVWLANPAGIAYNGGGFINASRATITGQPOYQAGDFSGPKIRQGNVIAHGHLARDTDF
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SEQ ID 4595

TTGTATCGTCCCATTCGTATTATCAATGACACCGTAGATTGCTGACCATCGTGAATAATCAGTTGTTGATTGGTCTGCTATTCGCCATTTTGTATGTTTCAGGCTGCC

SEQ ID 4596

LYRAIRIINDNGRLITIVMNQLLIGRYFALILVQAA

SEQ ID 4597

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SEQ ID 4598

VIPISHVFLYANKITLISTAEQAGIRNQQLPASSGNVAIDANGRLVNSGTMAAANVQDMNNTAEHKVNIRSQAFENSQAVSQGTQIHSQSIQNTGKLLSAGTEDLAVSGSLANQNGEI
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RGLIDGQQTQIQAGQMNIOTGRITYGDNIAATAATRLNDQENGTAIAARENNILGIEQLNRENSLIYSNDMAVGGALDNDQATGAQRIHAGAIIEAAGKRLIGVEKLHNTNEHL
KQLVETGRERIVDEAFGRHELIREGTQHELWGFVYNESDHLRTPDGAHENVHXYDEYKVTQETQVTGAPAKIAGSDLIIDSKAVFNSDSRIIAGGNCICLKQKVCITISPKLARR
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SEQ ID 4599

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SEQ ID 4600

LGLMIGFALALSIGCTNANMIACLNPAGIIGNNITAKDVIGVSLQYNLLAFKGAALSSFVMTLGTGND

SEQ ID 4601

TTGCACAACACTAGTGGCGTCCGCGTCGTAAGGACATGATGAAACAGGGCATCGTGAACAAAATATATCTTTGCGGAGGAAATCACACGCGACATTTCACTGGGTTTCATTTGCCTATGAAT
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CAACAGGCAAAAGCGCACAAACT

SEQ ID 4602

LHNWRRARRKHDETHRENYTLPEEITRDISLGSFAYESHKSKALSRHAPSQGTLPQSNRDNIRTAKSNGISLFPYTPNSPTPLPGSSLYIINPANKGYLVETDPRFANYRQWLGSDYML
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SEQ ID 4603

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SEQ ID 4604

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SEQ ID 4605

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SEQ ID 4606

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SEQ ID 4607

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SEQ ID 4608

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SEQ ID 4609

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SEQ ID 4610

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SEQ ID 4611

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SEQ ID 4612

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SEQ ID 4613

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SEQ ID 4614

HQKLKPSAIIAPHILFRCKRSADAALGRILTRAKHLFFFKLTALFFW

SEQ ID 4615

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SEQ ID 4616

VGLFSDGFRFRFLFFISYKHVIFKSPMEFFYLFVCFCALL

SEQ ID 4617

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SEQ ID 4618

LCIAIARLHYLDQSYETFLFLQKCISSLSLITVSPIDGCLPFLTSAAPTPEAVSQDDILQORQEKQLREQMQPEQDVRLDGTDGTGIEKMATQVGGANSDEASPCFPISEVELVGEAA
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SEQ ID 4619

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SEQ ID 4620

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SEQ ID 4621

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GGA

SEQ ID 4622

MYDKHKSCRFPAGSFCPMFPAVDPNRVKFPLAHYFKIEILYFISLLKRCSHFFIGFIIHHLIYGFWRQGLTAFAAVIDFWNRGNAPKESKATRPDAGGAIHLLFVAIGADSCDDYV
G

SEQ ID 4623

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SEQ ID 4624

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SEQ ID 4625

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SEQ ID 4626

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SEQ ID 4627

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SEQ ID 4628

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SEQ ID 4629

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SEQ ID 4630

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SEQ ID 4631

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SEQ ID 4632

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SEQ ID 4633

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SEQ ID 4634

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SEQ ID 4635

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TTAA

SEQ ID 4636

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SEQ ID 4637

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SEQ ID 4638

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SEQ ID 4639

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SEQ ID 4640

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SEQ ID 4641

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SEQ ID 4642

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SEQ ID 4643

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SEQ ID 4644

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SEQ ID 4645

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SEQ ID 4646

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SEQ ID 4647

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SEQ ID 4648

LPLGDSVGIHSTAPKMPHILQNNANDARYAETVDEKIIIIYLSISHKRPICKMP

SEQ ID 4649

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SEQ ID 4650

PLQRQRQHARRNQPAYPFLRVAFVQENHRI

SEQ ID 4651

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SEQ ID 4652

VFVMAIDDLSTAVDLSRALVEGGIPTLEITLRTFVGLAIRLIAKEMPNAIIGAGTVTNPEQLKAVEDAGAVFAISPLHESLARAGNRSGIPLIPGVATPGEVQLALEHGDITLKLFPAB
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SEQ ID 4653

TTGTCTGAAAACCTTAAACCCCCCATCCCGTTTGACCTCAACAAAAACGACACCCCCCACTTGAGAACCGAAATGTCCAAACTGACCCCCCGGAAATCTGACCGCCGCGCAGTTGTG
CCTGTGATGGCGAT

SEQ ID 4654

LSENLTPIPFDLNKNDTPHLENRVQTDPPRNPDRRSCACDGD

SEQ ID 4655

ATGAACACACATCCCTATCCACCCCAACTCGCGGAAATCACCGGGCGCATTTATCGAACCGAGCGCTCGACCGCTGAAAAATATCTGGCGAAAAATCCGAGTGCCAAACAGATGGGACGCT
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SEQ ID 4656

MNHTPIHPKLAETIGRIISRPTRKYLAIRSAKQMRRLERNQGCNLAHGYAAMPKSIKIEMLQETVPLNGIITAYNDMVAHQPFKDFDQIKDEAQKNGATAQVAGGTPAMCDGI
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MGVHLPAFAAFVPHYDRLREALTRYAAGHLARGIKNGTIKPLGEMLEKSFINALIGLMTGGSTNHTMHLVAMARAAGVILNWDDEISSIIPLLIRVYPNGKADVNHTAAGGLPFVIR
ELLDAGLHDDVDVTVVGHGMRHYTKEPFLIDGKLEWREAPETSGNDDILRKADNPFSPDGLRLMKNIGRGGVVKVSAVREGCRIIEAPAVFNDQREVLAAPFERGELERDFICVVRYP
RANGMPELHKLTPPLGILQDRGFVALLTGRMSGASGKVPASIHNTPEALMGNIKARTGDLIRFDSVTGELNVLINAEWNVREVERIDIGANQCGGRELPAFRSMTSSAETGAHS
PGGEFA

SEQ ID 4657

GTGGATAGGAGTGTGTTTCTGCTCTCTGCGGAAACGGGTGGTATTGGGATTTGTTTGTGCTTTCTGATTTTGTATCGGGTATGTTAGACGGTGAGTATAGTGGATTAAT
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CGGGTGTCTATTA

SEQ ID 4658

VDSVVHVRSPGCTGWYGFVCAFLIFVSGMLDGEYSGNLNARSGVASPCRTICAVCGSPPCPDNLHHTLKGTPSESGKRVLL

SEQ ID 4659

EQ ID 4659
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SEQ ID 4660

[illegible]

SEQ ID 4661

SEQ ID 4661
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CGGTCTGGTGCGCGAATACCTGTTAAGAAACAAGCCGCTCGCGCAGTGTGGATTTCCTATGGTGGGAAGACGGAAAACTGAACCGAATTACATCCCGATGCTGTTGTGCGATTATGCGCTG
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TGGTGATACACACGCCGCTTACCGCGCCGACGAGCGCATCAGCATGACTTTGGATGCGGATGCCATATCTGGGCATGTATTTTGGCGATACAGGGCGAAGAGAAAAAGCCGTGTTGCA
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SEQ ID 4662

[illegible]

SEQ ID 4663

SEQ ID 4663
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CCGACCCCTATTCCCGGATTTTCGACGTATTCAACGATATGCTCGACATTCGCGATCGCCGCCGTTTGTGAAAACCGGCTTGGAAGGCATCGTCCAAATCGCCCGCTTTCATCCCTTTATTTCCA
TTTGAAGCGACGGATTTAGACGGCATCTCGGCAAACTACACCAACCGGTTCTCCCTATTCGACGCTCGACCTCATCTCCGGAAGGCTGGAAGGCTGCGCAAGCGGCACAAGCTTTCCCGACGCTTCGG
CAATATTTCGAACGCAATATCGCCCTCGTGGCAAAATGGGACATGAAGGCTGGGCAAAACCTCGGTATCACATCTCGCCCTTATCGSCAATAAGAAAAATTTTCAAAA

SEQ ID 4664

SEQ ID 4664
 MNIDTSENKDAVAHTGQNLKAVIGLNLCPFAKAPHVKNLVRIASEAKHLDGFLDLDEELQRLGNTPATLETTLLVHPTLFPDFVDVNDMLDIADAAVWNGLEGIVQIAPFHPYFQ
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SEQ ID 4665

SEQ ID 4665
ATGTCCTTCTACGCCGAATAAACACGCCGATTACCCGAGGCTGGTTGCCGACATCGCGCGACAAACGCCCGTTTCGCAATTGAAAACCGCGCGTCGCTGATTGAGAAAGTCGCCGCTCTGC
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CCACCTGAAAACGTC

SEQ ID 4666

SEQ ID 4666
MSSTPNKHADYPRLVADIGGTNARFALETAPCVIEKVAVLPCKEYDFTVTDVAVRAYINQSGATGVRHAAFALANPILGDWVQTHNHNAFSEIETTRQALGLDTLILLNDFTAQALAVTQTSS
KDLMOVGQKRPVEFAPKAVTGPCTGLVSGLVHSPAGVVALAGEGGHTSFPFPDDMEVLINQYAKNKYRHVSAERFLSGAGLSLIYETLAVQKQAEPAKLPSEITEKALNCESPLCRQAL
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SEQ ID 4667

SEQ ID 4667
TTGCAGCAGGGCCGCAATTATCGAAGGGCATATCATTATGTAAAGCAAAATCAGCGAATCACTGGCCGACCTGTCCGGTGCAGAACGCAAAGTTGCCGAATGCGCCTTGGCAGAACCCAAAGT
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SEQ ID 4668

SEQ ID 4668
 LQQGRIIEGHTIMLSKISSESLADLSGAERKVAECALAEKPFVVAHAVAETIADRASVSQPTVIRFCRSLGYKGLPEFKLSLSASIGHEGMPYVHEBLNADDEMANVVEKVLGNAAAALLGER
 RFLKESELENGIATLMHARRVEFYGVNGSIVAQDAQHKKFPFGMSVYAVVDTHTQLMAASVLSQDVLVAISMTGSSIELLDVASTAKENGASVIALTRNDSPLAQADCVLSVATQENA
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SEQ ID 4669

SEQ ID 4669
ATGGCGGAAACCCGCCCTTTAAGCGGCAGGGTTGGGGTTTCCGCCAACCCCTTCCAATCGGGCGGTACGCAGGGTTGCCGCTTATGTGCGCATCGATGTGCGGAAACGCCGCCCGCT
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MAETPPFKAAGFGFAATPSKSGRYAGLRIMCASHCGNAPRHGKPOSgayr

SEQ ID 4671

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CGGCGGAAAAATCAATACCACCGAAACCGCCGCGCTGCTGCATGTCGCGCCTTTGCGAACCCGCAACATTTCGCGGATTTATGGTTGACGCTGAAAGATGTGATGCCCAAAGTCAACCCGCGTTTTG
CAACGTAATGGGCGAAATTGCAACGAAGCTCCGACGCGCTGCGTGGCTATACCAACCAAGTCACTATCCGACGTTGTCAACATCGGCATCGCGGATTCGGGATTTGGGCGCGCTGACG
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SEQ ID 4672

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QRMGEPAEHVRSSGWSGLYTNQVITDVVNIGIGGSDLGFLPHTCTALPFGPHRIANMHFVSNVDGSQLRDVLKSVHPETTLPIASKTPTTQETITNALPAREWFLNHAGDEEAVAKHPAAVS
TNRKAAVEFGIDIANETGEPFWDVWGGRYLSWSAIGLPIMLYLGEENFIEMLNAGHLMDOHFINTPIELRNLPVILALIGITWYINYYGGGSHVIAPYDQHILHRLPKFTIQQLDMESNGKQVTLDG
KAVGHTSPITLWETGNGCHQAPFLHQGHKATITLIDLASLEKRSNLPGHHEILIANVFAQAEAFMCGKTDPDEVRALKAQGDDEARI BELVPHKFTSGNRPTILILADKVNPNRNGHSLI
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SEQ ID 4673

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SEQ ID 4674

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SEQ ID 4675

ATGCCCCAGTACCGCAACTGGCAAAACGGTTTGGGTGCGAAATGCGCCGACGGCGACGAATACGGGTGGCACAATCTGACTGCCGTACCAAGAGAAATCAATGCGAAAACCAAAGAAATCC
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SEQ ID 4676

MPQYRNWQNLGAKCADGDEYGVAQSDCRTREINAKTKETQGYLID

SEQ ID 4677

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SEQ ID 4678

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SEQ ID 4679

ATGCCGCTGTGAAACGGGAGGACCAATGGATTATCCACGCGTTAAGGTTGCGGCATTTGGCGTGGGTTACGCTGTCTTTGGGGCTTCCGCTATTATTAGAGGTTTATGATACGACCATCGCCA
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SEQ ID 4680

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DMDIGNVWIPQFQWGVGVAMPFLPLTTITLSHMKGGQIAAAGSLNFLRLVLMGGVGVSVVSTLWERREALHRTFAEHITPYSATLHETAHLSDQGISDQGLGIINNTITQDGFIIISN
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SEQ ID 4681

TTGCGCGCGCTTTGGCATCGGCAAGCGCTCGGCAACCGTATCGCGGACAGGATGCGAGCCCGGAGATCGGGAATAATCAGCCCCAGTTGCTTTGATCGGGGTTTGGAAACAGCACGGG
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GTCAATCAGA

SEQ ID 4682

LRRLWHRQARRQFYRRQDAAQIGNNHAFVALIGVLEQHGIVNHCFLSRICGIGKVQTRRGFKNDKKAADIIPASKFQSR

SEQ ID 4683

ATGTTCCATCTCGAAGGCGCTTTTGCGAGAAAACCTGCGGATTCGCGAGGCGCAAGCATAGAGGTTAATCGGGAACAATCCCGATTATGCGGATGCGGTGTTGCGACGATGTTGAAGCGG
ACGATGCGGCATTAAACCGGACAGGTGCGGTTTAAACGTAGTTGGCGGCAACATATCTCAACCGTGTGATGCTGCACTGCGCGCGGTATGAAACCCGAGCGGTTTGTGCGAAGCC
GCT

SEQ ID 4684

MFHLEGLQENLPIPEAQSEIENRNDPDYADAVLWIMVEADDAALTGQVRFNVSNPQHILNRVDACTAARHETRAVFWRKPF

SEQ ID 4685

ATGCCCCGCCAATCTCGCACTCTTCGCCATTCGCGGAGGCGGGAATCCGGAACCCAAACGCGGAGGAACTCTATCGGAAAGAAATACCCGACCGCGGTATTCGCGGCGAGGCTGGAA
TCCAGACCCACAACCTTAAAGCGGTTTATCAGAAAAACCGAAACCGAACCGCTTAGATTTCGCGCTGCGGGGATGACGAAGAGTTGGGGAGTGACGAAGGCGGGAACAACCGCGCAA
AAAGCGCGGACTCTTCAGACGGCATCGGCAATAAAAAAGCCGAAATAATCGCGCTGAAAT

SEQ ID 4686

MPRQCHSSPPFRKRESGTQTRQESIGKNNPTAVIPAQAGIQTHNVKAVYQKKPKFNALDFRLRGNDRELGSDEERREQPRKKPTPSDGIGNKARKKNAES

SEQ ID 4687

TTGGCGGTGCGAAGCAGGAAGAGCAAAATCAACGGCACGCTCCACAAGTATTTTACACTGGGCAACCAACCCAGACCGCGCGCGCTCGGTACGAAGACCGCAATGAAAGCGAAA
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AAAATGTGCAATCAAGACCGCGGACCTTGGCGAAGCGGTGTTCCGGATAAAGTCCACGGCGAAGCCGCAACGCGCGGCGCTGGACGCTCAAGGCTGGCGCAAGGTTTGCAGGAA
AAAGCGGACCGGACCAACCCACACACCGCCCAATCCAAGGCGTGGACGAAAAATCAGCGCGCGCTTGGCGGCAATTCACACGCAACCATCGCGCGCTGGATATTGTCAGAT
TCCCGGACGGCAATGATACAGACCGGAGTTACAGGTTTGCAGAGCGCGGACGCGCATAGGAAACGAAAGTTGCTTCCCATCGCTTTGCGGACGGCAACGCTCAATGCTTCGTATC
CGAACGCCATTTCGGGACGCGTCAACGGCGAAGGCAACCAACCTGGCTGTTATCCGCGCAAAAAACCGCGCGCGCATATTATACCACTGGTACGAAGAGCAGTTGCGACTGGAGCC
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GCCGCCACGAGGCTCGACTTCCCGTGGGGTGC

SEQ ID 4688

LAVGKQJEDIKRHVHKVPSHWANHPDAAVGYEDRNERQRSALVSTWTDGLDNLNGFLTPRLDSKMTGGAENRPAKLVKLCTKAADTLGEAVFRIKSHGETANAGALDASRLAQLOE
KADRDHTHTAQIGLDEKISAAVAQFTRQTIIGVDIVRFDGTHIQTSYRPARGGSPFIGNEVVPLAFADGNVVKFVSERHSRGRVNGERQHNWLFIRAKNHAAAIITNWYESSCDWMA
IGKSASGNAASPTPIVPEIPEIDREPPRESGRSSTGLRNRPRHGLDFPVGS

SEQ ID 4689

TTGAACAGCCTCAAAACCGACGGGCTCTATTCCTGCGGACGGCGGTGCGGAGCTCGAACCCTGCCGTTGAAAAACACCGCTGCCATATCCAAGTCATCGCGGACGCAACCCGCGTGGT
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GATCGTGCTTTCCCAAAGCGCTCGAAACCCCGGAGGCTATCTCAAGCGCGACGCGACGATCTTTGCACAAAACACCTTCGAGCTTTACCGCGCGCTGGGCAACAAACAACTGC
CGGAC

SEQ ID 4690

LNSLKTGVSILPTAVGSSNLPEVTACHIQVIAGTQFGWCRQLGYPAYTSDVYERYQTSSANDWSAWKKLNSBGI PAGAIVSFPAVRNPAGYLKADGTIFAQNTFTSTFTAPWATQTN
PT

SEQ ID 4691

ATGGCAACGCAACCGAACAACCAATTCGACCAAGCCGCTCCGCTCATCGAACCGGGCAGACGCTCGTCTCGGCCAGGCGCGCGCTCAACCAACCATGCAAGCCCTCGGCAAC
GCACCCCTTTGCTCAAAAACCAACCGAAGCCCTTCAGACGGCATCCGACCAAAAGCCGCGCAAGCACCGCGTCAACGCGGCGACGCGACTGACGGCGCGGCGGACGCTTCGCCAAAG
CCGACCATTCGACTGGGCGCGCGCGGCAATCACCGCAACAAGCCAAACACCGTCCCAAAAACCGGACACACCCACGCGCATGACACCGCACGACCGGACCGCGCGGCGATCGTCCGA
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ACCAACCGTTACCGGCCAAAAACCTTACCGCGCAACCAATTCAAAGCGGATCCGGCTGTCCGCCAACCGGACGCA

SEQ ID 4692

MANATEQNQFDQAVRLIEPGDSVVVGPGAPVNPQLQALANRTLLLNQTEALQTSADTKAAAATAVNAGDGLTGGSLAQSRITLALGAPGQITATSDNTVPKNGHHAIDTARTDRAGIVR
LDNAISEAEDTAATPKAVKLTALDQARAAATADLKVSLSDNQTVTGKTPFAETQFPQSGIRLSANPTH

SEQ ID 4693

ATGATCGGTCTCTTTAATTCGCTCGGCGGCAATCTCCCTGCTGTTGGGGATAATCGGCATTTTTTTCGCGCTGTTCGCGACCAAGCGGCTTCGTAATCTCTCCGCGCGCTGCTGGGCAA
AGGCATCCCGCGCTTTACCGCTGCTGACCGGACCGCTATTTTCGCGCGGATGGTTCATACTGGGAACAAACGCGCGAGTCCCGCGCAAGCGCAAGATTTTCGCTATGAGTATGAT
GACCGCATCTGCTGATGATGTTTGGCAGTTTCCCAACGCTGTTGGTGGGCGGCTTCATCGGTTTTTTGTTTCCCTGTGCGCATATGATGTTGGCGGACGACCGGAATCT

SEQ ID 4694

MIRYLLIACGGISLILGIFLPLPTTFFVLLSAAKAKASPRFHWLHRHRYFGPMVHNBQNGAVPRKAKIFAIISMNTASCLMMFQFFQRMVWGAUVSSVFCSLVAIMMWRPES

SEQ ID 4695

GAGAATCGTCTCTTTGAGCTAAGGCGAGGCAACGCGTACCGGTTTTTGTAACTCACTATAAAGGCTTTTCTAAAATATGCAGATATCGAATGTCGAATTTGCTTATGATTACGG
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GAAAAATATATTGAAGTCCGATCCCTAATCAAGCCTCAATACCGGAACCA

SEQ ID 4696

ENRSL*AKARQRTGFC*STIKGLF*NMQIFBCRICIMTVFCLIRLKMVFRLNQIIFAETLKNLPYLPDRHQDFVVVTEKNILKVRIPNQSLKYRNE

SEQ ID 4698

SEQ ID 4699

SEQ ID 4700

SEQ ID 4701

SEQ ID 4702

SEQ ID 4703

SEQ ID 4704

SEQ ID 4705

SEQ ID 4706

SEQ ID 4707

SEQ ID 4708

SEQ ID 4709

SEQ ID 4710

SEQ ID 4711

SEQ ID 4712

SEQ ID 4713

TTGATCAAGTCCGCGCTAAACACATCGTACAGCGCAAAACCGGATGGGAATGGCAAATCCGGAACAAACATTTTTCAAAGCGTACAAACAAAAATACCAACCGGAGGTTGGTATTTC
TTAACTTTTGGCGGGCGGACGGGGCTCGAAACCGCGGACCAACCGGCG

SEQ ID 4714

LIKSALKHIVQRKTFGHEWQNPETNIFQSVQTKNINRRLVFLNFWRGGRGSNPRPPA

SEQ ID 4715

SEQ ID 4715
TTGGCCCTTATCCCTTTTCAGACGGCATCTCAAGATTCCGGGTCTGCGCCACATCCATATGGCGACAAGGGAACAAAAACCGATGAAAACCGCCCCGACCCACCAGCGTTGGGGAAACTGCCAA
ACATCATCAGGCAGGATCGCGTCTATCATGCTGATGGCGAAAAATCTTGGCTTTGCGGGCACTGCGCGCTTTTGTTCACGTTA

SEQ ID 4716

SEQ ID 4716
LPLSLSDGIQDSGLRHHMATREOKTDETPATHRWGNCONIIRQDAVIMLMAKIALRGTAFFCSQL

SEQ ID 4717

SEQ ID 4717
ATGACCGACCGCCAANTAGACAACCTCATCAAACCCGCCACCATCGCCGACACCGACCCCGCGTCCGGGCACAACACGGCGGCATTACCACCGACTGGCTGCCCTATATCGTCCCTTTGC
AGGCGGCGTGTCAGTAGCGGCATCCCAAGTGTGCGGGAAGCTGSCACCATCTTATCCCTCGCGGGAACCCGAGAACCGCG

SEQ ID 4718

SEQ ID 4718
MTDRQIDNLIKPATIADTDPA~~SA~~HN~~TA~~ALPPTGCP~~ISS~~PLQAACQY~~GA~~SQVSAKPAPSYPLANPRTA

SEQ ID 4719

SEQ ID 4719
TTGGTAGAAAAAACAACGCCGCTGTGAACCTTCAGACGGCATTTTTACCCACCCCCAAACCTAAAAACCAACCAAGCCCTACACGGCTTGCCCCACCTGCGCGCGCCCAAAA

SEQ ID 4720

LDRKNKRRLKPSDGIFYPPPNLKTTHKPYTACPHLAAAPK

SEQ ID 4721

SEQ ID 4721
ATGCGAAACAAAATAAACCGCAACGACATGGAACCTCGGCTACACGCCCTTACAACCTTCGCACCCTGGCGCAACCGCTGCAAACCTGACACAGGCCGAGTTGGCGCAAAATCGTCGGGGTGAAGC
ACTACATACAGGTAGCCCGCTGGGAAGCCGACCCGATACCGAAACCGCGCGGGCCGATATCCGCTGGAAAAATGGCGGCAGTTCTCGATTGGATAGAAAAACAAACGCCGCTC

SEQ ID 4722

SEQ ID 4722
MRNKNINRNDMELGYTFYNLRTLNRNCKLTQAEIAQIVGVKHYIQVGRWEAEPDTETTRADMPLEKWRQFLDWIEKTNV

SEQ ID 4723

SEQ ID 4723
TTGCCGTTTCGCGCAGGCTTCCAACAGAGTGAGGTTATTTTGGGGCGGCGGCGAGGTGGGGCAAGCGGTGTAAGGCTTGGTGTGGTTTATAGGTTTGGGGGTGGGTAAAAAATGCCGTC
TGAAGGTTTCAGACGCGGTTTGTGTTTTCTATCCAATCAGAGAACTGCGGCATTTTTCACAGCGCATATCGGCCGCCGCGTTTCGGTATCGGGTTCGGCTTCCACAGCGGCCTACCTGTA
TGTAAGTGCCTCACCCCGCAGATTGCGCCAACTCGGCCCTGTGTGTCAGTTTTCAGCGGTTGCGCAGGGTGCAGAGGTGTGAAGCGGTGAGCCGAGTTCATGTCGTGCGGTTTATTTGTGTT
TCGCATATTTTGTGGGCTGTACTAGATTATCCCTAAATTCACACCGATCCCGCAGGATTTT

SEQ ID 4724

SEQ ID 4724
LPPFAGFQQSEVILGRRRGGGKRCRAWLWFLGLGVGKKRCLKVSDGVCFFYPPEELPPFFQQRHIGPPRFGIGFGFPAAYLYVVLHPDDLRLGLCQFAAVAQGAQVVRKVAEFHVAVYFV
SHIFCGCTRLSLNSTPIQDF

SEQ ID 4725

SEQ ID 4725
ATGAAGATAACACACTGCAAAATTAAAGAAAGAAGTACAAAAGAACCGCTCCGTTCCTTTTGTAACGGGAAGTTACCGCCCGTTCGCCGCCGATATTTTGGGTATCCATCCGATTCCGGCG
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CACACCGTCCCGCAGCTAAAAATCTGCGGGATCGGTGGAATT

SEQ ID 4726

SEQ ID 4726
MKITHCKLKKEVQKEPLRSFVPEVTARSAADILGIHPDAAALFYRKIRTVTNHLALAADEVFECFAGPGGSGSYFGGRRKGGRRGGAAGKAVVFGIPKRNGRAYTVAADDAEPEITLLPAVKI
KIMPDGIYYADSPGSGKLDAGGFTRCRINRSKEPADRRNHINGIGNFWNQAKRALRKYNGIDRKPPPLRECEFRIFWGPSPQLKILADRCGI

SEQ ID 4727

SEQ ID 4727
GTGTGTTATCTTCATATTTTCGAGGGTAACATATCTGCTAATCTGGTACAGACCTATTTTTTGA CTGCCGGCGGCAGGTTTCGGTAAGGACGGCGCAAAATCGGGCTCTGCTCGCGGT
TTGCCCGCGAAAAAATAAAATCGTAAAGGGTGATCGCGTTTTTCGGAATGGCGGTAATGCCCGCGGGCATTGCGCGTCTGTCTCGCTGTGGATTTTGGCAATCAGGCGGGGATAGCGGC
AATGGGTAAATGAAACGGCTTGGCGCGTCTTCCCGATAATCCATTGCGGGTAGCGGTGAA

SEQ ID 4728

SEQ ID 4728
VCYLHISRVTYLLIWRPYFFDCFAAGFGKGGKSGFVCRFAAEKNRIVKGDVFGMAVMPARAFVCLPVDFGNQAGLAAMGNETACAVLPDNPFGVAVE

SEQ ID 4729

SEQ ID 4729
ATGAACACAGCCGCACTATTCAACCGCTACCCCGAATGGATTATCGGGCAAGACGGCGCAAGCCGTTTCATTACCCATTGCGCGTATCCCGCGCTGATTGCCAAATCCACAGGCAGACAG
ACGGCGAATGCCCGGGCGGGCACTACCGCCATTCCGAAAACGGCATCACCCCTTTACGATTTTATTTTTCGCGGGCAAAACGGCAGACAGAACCCGATTTCGCGCGCTCTTACCGAAAC
CTGCGCCGGGCGAGTCAAAAAATAGGGTCTGTACCAGAT

SEQ ID 4730

SEQ ID 4730
MNRAALFNRYPEWIIIGDGRSFITHCRYPRLLIAKIHRTDGBCPGGHYRHSNGITLYDFFGGKPADEARFAAVLTETCRRAVKKIGSVFD

SEQ ID 4731

SEQ ID 4731
ATGCGAGACATCCTGCCATCCGACAAGCGCGCGCAACCGCCAAAAACGAAAGGAATCCAATAACACATAATCGAACAGAAACAAAACGACCCGAGTTAAGAAAAATAGATGCCGAATCG
CCAAAATCATTGGCGACGCGCACAAAATCAACGCGGAATCGTAAAAATAGCCCAAGAGTCCCGCTGTGTATCCCATGATGCGCGCCACCGGTCTGTGTACCGCCATCGCCGCCGTGTGGC
ACTGATATTCAAATTTGCC

SEQ ID 4732

SEQ ID 4732
MADILPSDKRRPPKTKGNPINIIEQETKRTELRKIDAEIAKIIDAHAHINAESVKIAQESRWYPMHAATGLVTAIAVLALIFKFA

SEQ ID 4733

SEQ ID 4733

TTGAAATAGTGGCGGCTCTGTTTCATTTTGTGTAGGGATAAAGCCCCCTCGCGGGGCTTGTGGTCAGGCAAAATTTGAATATCAGTCCCAACACGGCGGCGATGGCGGTAACCAAGACCGGTGGCGG
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 TCTTGTTCGATTATGTTTATGGAATTCCTTTCGTTTTTGGCGGTGCGCGCGCTGTGCGGATGGCAGGATGCTGCCATGTATGTATGT

SEQ ID 4734

SEQ ID 4734
 LNSAALPILLRDKAPRGACQANLISANTAAAVTRPVAIAINGYQRDSWAIPTDSALILCASAMILAISASTFLNSVRPVSCSTMFIGFFPVFGCCRRISDGRMSANYVC

SEQ ID 4735

SEQ ID 4735
ATGCGTGGCGGGCGGGCGGTGTTTGCCATGTCATATATAAACGAAATATATTTTCAGTTTTCGCCACCTGAAGCGTGTGTTTTTTGAATATTGCATCTAAAAATCTGACT

SEQ ID 4736

SEQ ID 4736
MVRAAVFAMSYINEIYFQFCHLKRCFLNIASKILT

SEQ ID 4738

SEQ ID 4739

SEQ ID 4740

SEQ ID 4741

SEQ ID 4742

SEQ ID 4743

SEQ ID 4744

SEQ ID 4745

SEQ ID 4746

SEQ ID 4747

SEQ ID 4748

SEQ ID 4749

SEQ ID 4750

SEQ ID 4751

ATGGCAAACACCG

SEQ ID 4753

AAGAAGATAATTTCCTTTTTTTTGGCTGGACACCAACACGTCACCGGCTTCCAATGTAAACGAGGCAATCCGGGTTTTCATCCGCGCGGGTGGGGGGCGAGCAACAAAGAGTTTGAAG
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SEQ ID 4754

KEIISFPFACDHQHVTAFCQKRGIRVFNPAAGAADEQEFDAVSRRHRADCFADGVCPSQRKGVADGFAIFABSCLIITTKQSLQRGITAVADICHLIDVPRRAVTVQHLIACQHESG
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NQNHQRHGDVLIHQHARHLTVRLPQLRFRQNPANRRGRHRQARYGKRIPIERHARQHOYAHYRQHNRADLTAQTEHQPHRPPLQ*KLQDAEHQBNHPDQAIIRRMARFKNQJAE
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SEQ ID 4755

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CAGGATTTGTGGCG

SEQ ID 4756

LSDARSKISILLSSAEPMSLRKIITHIDAFYASVELREQPHLGRPVVVAEGARSVICAASEYARQFGLHSAMSVATVKRLCPQAVVYVPHFDLYRQVSAQIHAVFRYFDLIEPLSLDE
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QDLMA

SEQ ID 4757

GTGCGCACTCGACTGCCTGAAAGCGCGCGAGCTGATTTTCAGACGGCATCAAAACATGATGAAACTCAATGCCAACAGCTCGAAGCGCTCCGCTACCTCGCGCGCGCTGTTCTGTC
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CGGCCCGCGGAT

SEQ ID 4758

VRHSTASKAAQTDPRRHQNMKLNAQOLEAVRYLGGPLFVLGAGSGKTGVITQKIKHLIVNVGYLPHVVAITPTNKAABEQERVAKMLPKPQTRGLTICTPHSLGMKILREBANHIGY
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LMLKLTAEGMPTAVGDDQSIYAWGANMENLRKQENYPMKVILEQNYRSTARILKIANKVIENNPFLTKKLWSQLGEGEPVKVACQNEQHEADVVSQIVKQKLIIGDKTRYAD
FAVLYRGKHQARIPEERLARGARIYRLSGGQSFDFKAEIKDVLISVRLANPNDDPAFLRAVTPPKRGIDVTLGLKLNAYHEHECSLYEAAQNEEALATLNNWQHQAQFMDMFGNYRA
KAEIDEAGEFINSLBEIDYENHLMQNEEGKAGEIKWRNVGELVSWFARKGERDKNVIELAQTVALLTLEKDEESTDAVSLTSHAARKGLBYPTVFLVGCBEGLPHENDSIEEGNVBE
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SEQ ID 4759

ATGCACACCGCTGACCGTCAAAATACCGTTATCGGAAGCGCGCGCACCAAAATCGCGCTGCGCGCTTGTGCGCCGAGATCGCGCGGATTTATCTCCGCTGCTGCTCCAAATCAAAAC
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CGTGGCGCATCTGACTGCTCGAAGCGCGCGAGC

SEQ ID 4760

MHTSLTVKNTVIGSGRTKIAVLVARDAADLSSVLSQIKNLPDIVEFRADFLCAGSIGEVLRHTQAVRDALPDKPLLFTRRRHCEGGSFPCSDYYFELLDALIESRLPDIIDIELFSG
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RAALDCLESAD

SEQ ID 4761

ATGACCGCCACCGCCGCGGATTAGACCGACTCTCTCCCAAAACCAATGCGCGAATGCGGCTATGAAGGCTGCCCTGCGCTACGCCCGCGCGATGCTGCGGGCGAGCGCACAACTCT
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SEQ ID 4762

MTATAADLRLLPQTCRCBGEGCLPYARAMLGEAHNLCPAGGATVVRDLAALLGKPLVAPAKTQAKALARIDETACIGCTACIRACPADAMGAKLMHTFTVDECTCGCLVAPCPV
DCIHMQPVADTVLPRRRFSILSDSRFAAAEHARARYLKRNERKQREADERKAMLAEREAVRNARPTPTPEKPAFNPADILAKAMAKAQTOQDLAAADNRQGYQAKQIAEREREL
RRAQRIMKYGSDSEKAALEYLKQYKAKQEAQNTAS

SEQ ID 4763

ATGTCGCCCAACAAAGAGCTGCAAGGCATCTCTCTTTGGGTAAACAAAAACCAATATCGGACCGGCTACCGCGCTGAAATTCGCAAGCAATCGACAAACAAACATCCGACAAACG
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CCTGAAACTCTACCTCTTCAGCTTCCGCAACACCGCGGATTTTCATGAAGACTGCTCAACATCATCATGAAGACCTCATCGCCCTGATGGATCCGAAATACATCGAAGTGTTCGGCGAG
TTCACACCGCGCGCGGATCGCGCTTCATCGCTTTCGCAACTACGCGCAAGCAGGACAGAGTTGAAGCATTTGGCAGCAACACCGCTGTTGCGAGCAGCAGCAACAA

SEQ ID 4764

MSRNNELQGISLGNQKTYPTGYAPEILEAFDNKHPDNDYFVKVCPPEPTSLCPMTGQPDFATIVIRYIPIHKMVESKSLKLYLFSFRNHGDFHEDCVMIIMKDLIALMDPKYIEVFG
FTPRGLIAVHPFANYGKAGTEPEALARKRLFEDHAQ

SEQ ID 4765

ATGACGACCGGATTCATATTCGCGCGCGAGCGCGGTGTGCGCGCGAGCCACATACCGCATTTGTTCCGGAGTAACCCCATGTGACAGCAGCAAAAGCAAGCCCTTCCGCGCGACTGG
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CGGCTTCCCGCGCGCGGATCGTCGAAATCTTCGCGCCGGAATCTTCGCGCAAAACCACTCTGCTCGAAGCGCTCGCCCAATGCGCAAGAAACCGCGCGGTGTGCGCTTGTGCGAT
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ACGCGAGCAGAAACCGCGCGCAACCCGCAAGAA

SEQ ID 4766

MTDRFIFRAARVAPQPTYRI CSGVTPMSDDKSKALAAALAIKESFGKGAIMKMDGSOQENLEVI STGSLGLDLALGVGGLPRGRIVEIFGPRESSGKTLICLEAVAQCQKNGVCAFD
AEHAPDPVYARKLVKVEEYLSQPDTEQALEICITLVRSGGIDNVVDSVALVPKAEI EGDMDGSHVGLQARLMSQALRLKLTGHIKRNTLVVFINQIRMKIGVMPGSPETTTGGNAL
KPYSSVRLDIRRTGSIKKEEVLGNHETRVKVIKNAVPPRAEFDILYEGEISWEGELIDIGVKNDIINKSGAWSYNGAKIGQKDNVRVWLKENPEISDEIDAKIRALNGVEMHITG
TQDETDERPER

SEQ ID 4767

TTCCTCGCTCTGCGCTACTATTGTACTGTCTGCGGCTCTCCGCTTGTCTGATTTTGTGTAATCCGCTATACCAAACTCAAATCAAGCGCTCCGGAGGCGGCTCAAAAAACGGTA
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SEQ ID 4768

LPRLAVFLVLSAALRLVLI FVNPLYQNSNQAVRRRLKKNKTSQQKYRLSGFQVLFPGSFVAVGVFLRPGDVHIFYAVEGADFCVDFVGNFVGFVPQDADVFLATDFRAVVAVPRAGVDDV
VFHADVDQFAPPTDAFSVEDVKLCITFERGGDFVDFDAGFVAQYFFAFDGSAGADVADGRIEFQVAAAGRLGAAEHYADLHSDLVDEHNQRI GFDFVSGQFAQSLTHQARLQSDVAV
PHIAPDFGFGDECGYIDYHYTAARTDERVADFQSLPAGIGLQVKLPDFYAFAGVNGIEGVFGIDKGAHA VFLALDGFPEACGFAGGFGAEDFDAPARQAADSEGV

SEQ ID 4769

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SEQ ID 4770

LLIHYIFTRRGEKYSCYSPTIARFASILRLLYG

SEQ ID 4771

GTGCAAGTATTGCACATAAAGGGCGCAGGCTTATCCGTAAGTCGCGCGAGGATAGAGGCAAGCGGCGTAGGTCGGGCTGTAGCAACTGTATTTTCAACCGCTCGGGTAAAAATA
TAGTGGAT

SEQ ID 4772

VQSLAKKRAQSSVESAQDRGKAGVGRAVATVFTPSGKNIVD

SEQ ID 4773

GTGCAATACTTTTCACCTGTCTGAACAAAAATCAACAGACCCCTTATATCAAAATGCAAAAAATATGCCGTCATTCGCGGAGAGGCGGGAATCCAGACCTGTGCGCACGGAATTTATCGAG

SEQ ID 4774

VQYFALAEQNSNDPLYQMKICRHSREGGNFDLSAREKPIE

SEQ ID 4775

SEQ ID 4775
TTGCACCTGTGCTGAACAAAATTCAAACGACCCCTTTATATCAAAATGCAAAAAATATGCCGCTCATTCGCCGGAAGGCGGGAATCCAGACCTGTCCGGCACGGAATTTATCGAGTAAACGGTTT
TTCAGATTCTACGTTCTAGATTCCCGCCTGCGCGGGAA

SEQ ID 4776

1HLINKIOTTLYIKCKKYAVIPAKAGIOTCRHGNLSKTVFQILSRFPPARE

SEQ ID 4777

SEQ ID 4777
ATGCGAGCGCGAATCACTGGAATTTGGCGGCAAAACCGGCCATAAACAGATATAATGCCGCCGAACCCCTCGGACGGCATTCGCCCTTCCTCTATTTCATTAACACAAAACAGGAGTATTCA
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SEQ ID 4778

SEQ ID 4778
MAARITGGIGGKPAINRYNAARTLTALPLPSFIQTQGVFSMFGKAGLGGLMKQAOQMENMKKAQAKLAETRIEGEAGNGLVKITMTCAHEVRRIDISPDLIQEAAADDKEMLEDLILAL
KSARGKAETANKTNGAFTQDLPPCGVGDFFR

SEQ ID 4779

SEQ ID 4779

ATGCTAGAAATACGCCGCGCCGAAGCCGCCGTTTCAGACGGCATTTCGACGACACCGGACAGAAACATCAGCAACCGAAACCAAGAGAAAACATCGGCCATCAAGTTCTCGCCCGAAAATGGCGCG
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SEQ ID 4780

SEQ ID 4780
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IDAASNTGIDNIREVLENAQYPTAGKYKVVIIDEVHMLSKSAFNAMLKTELEPPHVKFILATTDPHKVPVTVLSRCLQFVLNNMTAQQVADHRAVLDSKYLAYDPPALQILGRAAAGS
MRDALSLLDQIALDSGKVAENDVRQMGIVADKQYLYELLFGVINQDGEALLAKAQEMAAACAVGPDNALGELAILLQQLALIQAVPSALAHADDPDSDILHRLAQITISGEQIQLYQYIAVHG
KRDGLGLAPDEYAGFMNTLLRMLAPALAAASCDANAVIENTELQSPSAQTAEKTAARKKPPQPREADAQPTFVQTASAAAMPSEBGTQAPFVSHQENNVPFWEDAPDKTETAAGTARTSAK
SIQTASEAETFPENQVSKNKAAADNETEASLSEVPSENPIQATPNDEAVEVETTFHEAPAPRFYGFDPNDCCPFEDGVETIPPMANVLPAIDTAGGTDEBARAGGIGGNNTPSAPPKFSPE
NWAATVRHFARKGLAAQMPAQHSAWTEYRSDTGLMVLAMTAEARATADKKRLDKIROTLAQAYGLQITLQTEDMRDEAGRETPAMQDKRVQAEDRQKQALLBADPAAQKILQAFGAQWQF
ESI.KLAANRP

SEQ ID 4781

SEQ ID 4781

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SEQ ID 4782

SEQ ID 4782
MPRIAALPHLVNQVIAAGEVVERPANALKEIVENSIDAGATAVDVLEGGGIRLIRVGDNGGGIHPDDTELALHRRHATSKIKTLNDLHEVASMGRFGEGLASIASVSRILTLSRQEDSSHA
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KGGTKDQKCYFVNHRFVRDKVMLHAVKQAYRDLVNLNATPAFVLFLLELPEAVDVNVHPTKTEIRFDRSRQVHQLVFHTLNLKALADTRANLTSVSNAGVELHDITGVTPAPMPSSENDGEML
FDSASNHTPGNPKPDRNAPGSSGKTAHPMPYQAAARPQQHSLSLRESRAAMDITYAELKYKTTDDIDLELSQFEQARGNMNPSETPAHKTDPTLSLSDGIPQSQSELFFLGAIAQLIGIYILAQAE
DSLILLIDHMAAAERVNYEKKMRQROREQENLQSQHLLIPVTPAASHEECAALADHAETLAGFGLGLSDMGNTLAVRAAPVMLGKSDVVSRLARDVLGELAQVGSSQYTIASHENRILATNSCH
GSIRAGRRLTLPENNALRDMENTPRSNQCNHGRPTWVKLTFLKELDTFLRQ

SEQ ID 4784

SEQ ID 4785

SEQ ID 4786

SEQ ID 4787

SEQ ID 4788

SEQ ID 4789

SEQ ID 4790

SEQ ID 4791

SEQ ID 4792

SEQ ID 4793

SEQ ID 4794

SEQ ID 4795

SEQ ID 4796

MIQIGIIMGSSNDWPMVRQAQFLLEFGVEYEAERVVSARHTPDLMPFEYAEARARGIKAITLAGAGGAHLPGHVAAKTTVPVLGVPPVPSKYLRGEDSLLSIVQMPKGVPVATTATGEAGAA
NAALFAISMLANENPELAKLADFRAKQBOTVLNLELBOI

SEQ ID 4797

TTGACTATATTTTGTACTGTCTCGGCTTCGTGCGCTTGTCTGATTAAATTTAATCCATATATTTTCAAAATTTGAAACCCGCACAGATTGTTAAACCCCAAAACAGGGCGGGCGAA
ATTCTCCGGCAATGGGTTTCATGCAAAACAAATGCCATCTGAACCCCGAAACAGGGCTTCAGACGGCATTGTGTATTTCGCGACGGCGGGTTT

SEQ ID 4798

LTIPLVSAASSPCPDNLHLYIPQKLPQIVKPNRGRNSSNGNFMQTKCHLPENRASDGICVFDGGF

SEQ ID 4799

TTGTACGGCAGCCCGCTTTGCCATGCGCCCAACAGATGCGGATGGCGCGCAAAAAAGACCGCGCTTACAAAGGACAAGACCCGGCCAAAGTAACGCATTATTTGACACGGCGGGCGG
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TTGGCTCAAAATCGGTGATTATTTAGATAATGCGCGATTTCGCGGTATGGTGTCTTACGGGGAACCGCGGAAAAATGGGACATAAGGTATTGCTTCCCGCACCTTGTTCGCCCGAGC
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SEQ ID 4800

LYGSRRLPCAQTDADGAQKTKAAYKGQDPKVTHTLTPAGPSCQVRVCDETGFDRRLFRPYARSLKGMARISGKRYRRLSLVSAQVGNRPAPMVQNTVAGVFFEARFQQLLPA
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SEQ ID 4801

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SEQ ID 4802

MKITHCKLKKEVQKEPLRSFVPEVTARSAADILGIHPDSALFYRKIRTVTNHRLALADEVFERPAGPGSGCFGRRKGRRGGAAGKAVVFGIPKRNRTTYVAADNAEPETLPPAVKK
KIMPDGIVYADSPSGRKSADAGGFTRCRINRSKEFADRRNHINGIGNFWNQAKRALRKYNGIDRKPFPPLRECEFRNFGTSPRLKILRDRCGI

SEQ ID 4803

TTGAACAACAATACAAACACATCCGAAAAACCGGAACCCCCCGTCAGATTGTCAACATTTTAAACCAAAATACCCAAGCAATACAGCCCCCGTTGCCGATA

SEQ ID 4804

LNKQYKHKIRKTGTPRQIVNLNQMTQAIQPLRI

SEQ ID 4805

GTCCCGGTATGGAATACTCGTCAGGGGTAGCCGCGCGGATGCCGAGCGCGTGAATCATGCCGCTGAAAAATAAATCTTTAGCAGCGATTGACCGTTTCTGACGGTTTCAGACGGCTT
AAACCTTCAAAACCGCGCTGACGACCAAAACCGCAATAATGTCCGCGCGGTTATGCCCGGTGTCTTTGTGCAGATGGCTCTCATCGCCGATTTCACACACGAGGATTCAGCGCT
GCAGCGGTTCCGGATGCAATCAATCGACACCGCAT

SEQ ID 4806

VRRNEILVRGSRPDAERVNHAA*K*IPQRFRDLTVQTA*TFKTAADDQNGIMSAGIARVSFQMALIADPQHQRIRLQAPADQIDSRH

SEQ ID 4807

TTGTATCTATTTGCTAGCATGATTTTATGTTTGTAAATCAATATTTGATATTTTCCCGTGTTCGGCGGCATGGAATCGGGCGGAGGGCAGGTATTTCCATCTCTGCACAAAG
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GGCGCAGCAGGAATGTCGACTACACCGTACGGGTTTTTCCGTGATGGAAATGAGCCACCGTTTCGGAATGTTTAAAGCATCTTGCATCATGCGGAACAGGATTTGAGGACGCTTTG
AAAGTGCCTGACACATATAAGATATTTTCTTCAGGCGGAGCAACAACCAATTTAATATGGCAGCATGAATCTGGCACACGGTTTCCGCACTGCCGACCGGTGTAACGGGCACT
GGAGCGGTATCGCTATGAACAGATGAGCGCTTTGACCGATACGGAATCCGTTTGGCGCGCACGGGGCGAGCAGTTGCACTATCTCGACCTGCCGCTGTGGAACCGTGGGATGTTGC
ACCGGATTCGGCGTTTGTCCATTTTGGCGTCAATGAACTGTCAACGGGCTGCAATACCGTGAAGTGCCCGCTTTTCAGACGGCATGCCCGCTGTGTGCGATATGTCAGCGAGATT
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ACGATATTCGGATGTTTCACTACCGTTCTCAITTTGAACCGGACGCTATGTACAAACCGCGCTCAACTTACGCGATTATATGTCGGGGCTGTTTCCGCTGGCTGCAGGCGAGGG
CGGTGTGAAAAAATGAAGCGGTCAATCGGCTGAAGCGCAACCTTGTATGAGACGATAGATGGCAGCGCGGTTTTTACATCAACGATATTCATCTGATGCGCGCTCCAAAATGAAC
GTGGCTTCAAAACCGCAAGCAGGACTTGAACCGCGTTTGTGCTGGAAGCGGAATTCAGGGCTTGTGCTGTTGAAGGGCTATAAGTCTGTCGCGGGGATGCGCGCAGCATTATA
ATCGATGCGCGCTTGAAGCGTTCGGGCTTTGCGAGATTATGCGCGATTTCACACGGCGTTACGGT

SEQ ID 4808

LYLTVASMI FPFVNQYDIISRVRAAWNRAEGRYFSLKACCKPKIGQVIVQNGCINSLYPIYNSAGPAVLPEAVLTAQQEMSDYNGTGFSVMEMSHRSEMFSLILHAEQDLRQLL
KVPDNYKILFLOGGATTQFNMAAMNLAHGFRTADAVVTGNWSRIAYEQMSRLTDEIRLAAHGGEQFDYLDLPVETWDVAPDSAFVHFAVNETVNGLYQREVPRLSGMPPLVVICMSSRI
LSREPIDVADYGLIYAGAKNIGPAGVTVVIVREDLLERCNDIPDVFNYSRLNRDGMNTPTSTYAIYMSGLVFRWLQAQGGVKIEAVNRLKAQTYETIDSGGFTYINDIHPDARSKN
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SEQ ID 4809

ATGGCATACTCTCGGACTTAAGAAACAAAGCTTTAAACCATAGCGGATTAACAAAAATCAGGACAAGGCGCGGGCGGCGAGACGGTACAAATGGTACGGAACCGATCCGCCCGCGCTCC
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TCAAGAAACACGCTTACCTCGCGATTCCGCTTAAAAACAAACAGGCGAGC

SEQ ID 4810

MAYSADLRNKLNLHSGTLKIRTRRAADGTNGTEPIRALHHLRESFPLSRGGATPYRFLIRYITDNAKTPAKPQQLRITQETRFCTGFAKLNKQAA

SEQ ID 4811

TTGTTTTTAAACAAAAACAGATGCCGCTCTGAACCTGGTTAAGGTTTCAGCGGCATTTTCATATGGCTGCGCTTTTTACAGTATATTCAAT

SEQ ID 4812

LFFNKKQMPSELVKVQAASFGAFYSIFIN

SEQ ID 4813

TTGTTGAATGTTATAGTTTATGTTTTTAAACAAAAACAGATGCCGCTCTGAACCTGGTTAAGGTTTCAGCGGCATTTTCATATGGCTGCGCTTTTTACAGTATATTCAATAAAAACA
AAATAGTACACACTCGACGCTTGAAGGTT

SEQ ID 4814

LPEIIVYVCLTKNRCRLNWLFRRHFMALFTVYSIKNKIVQHSILKV

SEQ ID 4815

TTGCTCCCTGCCGTCAAAAAGAAATCATGCCGACGGTATTGTTATGCCGATAGCCCGGCGAGCGCGGCAAGTTGGACCGGGCGGTTTTACCGGTTGCCGATCAACCGTTCCAAGG
AATTTCGACAGCCGTGGAACACATTAACGGCATTTGGGAACCTTTTGAATCAGCAAAAACCGCGCTTCGCAAAAATACAAACGGAATCGATCGTAACCTTTCCCGCGCTTTGAGGGAATG
CGAATTTCCGACTTAACCTCGGCACACCGCCCGGCGAGCTAAAAATCCTCGCGGATCGGTGTGAAT

SEQ ID 4816

LLPAVKKIMFDGIVADSPGSRGKLDAGGPTRCRINRSKEFADRRNHINGIGNFWNAKRALRKYNGIDRKPPPLRLRECFRLNFGTTPRQLKILDRCGI

SEQ ID 4817

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CGGCGGCATCATTAACGCTTGCATCAATCCTATGCGAGACAACTCACCATTGAAGGAATTAATGTCTGGTAAAGACGGTGTGTTAAAGTCAATACAGAATGGAACCTCGCCGGGTGATGAT
CAAGGAGGAATTTCTCAATCTGATTACTTGGAAATCAGGCGATGCTTCAGGAAAAACACCGTCAATTTCTAGTGGTAAAGATGGCAAGAAAAATATTATCGACGGTTCGATCGCGGAAC
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GCAATTTATCGGCAAGGATCGGGAAGCAACAGACATAAAGGCTACCAAGGCAACCGTGGGT

SEQ ID 4818

MRFPPIITNAVLIKITNAMEPKSEDIGITIKLTKATPHLKDTSITPEGTTLLSGT/LSNLTSLSGTTSVFERGTTNGGIIITLANQSYADK/IEGNYVKGKLVKNTWNSPGD
QGGNSQSDLEITGDASGRTTVISVGDKGKNIIDSGISGLSDRYKRAAVVKVLGDKGAETGKLNIEDAKHTYTMRTDTSCTAKTTGAGELQVSHKDEAGATEYFWTLTTPNQDKTII
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SEQ ID 4819

TTGGGGAGCGTTGTGCCGATGGCGTAAACGGCGGCTGCACCGGCTGCTGAGGTTGAGTTTCGGAGCAGGTTTGAACGTGGACTTTGACGGTGGATTTCGGCAAGATCAGGTTGGCGG
CGGATGATTTGTGCTGTCTCTCGCGGAGATAGCCCAAGATTTCAGTTCAAGAGGGGTAAG

SEQ ID 4820

LGDUVVDGVNGLHPAAEVEFAEQVLNVDFDGGFGKIEVAGDDFVAVSCGELAQDFQFTRGK

SEQ ID 4821

ATGACCATCAAAATCATCTGATAGACGACCACACCTCTTCCGCGCGCATCAAGCCCTTTTTCGCGCCAACACGGTTTGAAGTCATCGGCGAAGCGCGAGCGGACTCTCGGGCA
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GGCGATAATGATTCTCGCCGAGATGACCGCAAACTCTGCAAAAGCCTGATTTCCTCCCAACCTGCCAAAGGACGAGGCACTCTCTCACTTACCCCTCGTGAATGGAATCTTGG
GCTATCTCGCCGAGGACACAGCAACAAATCATCGCCCGCCACTCGATCTTCCGAATCCACCGTCAAAGTCCACGTTCAAACCTGCTCGCAACTCAACCTCAGCAGCGGGTGCA
GGCGCGCTTACGCCATCGCGCAACAGCTCCCCCACTGTGCGCGAA

SEQ ID 4822

MTIKIILIDHTLFRSGIKALLSRQHGFEVIGEAADGLSGIKMISRLQPDVVLIDLDMPGMNGREALSQIISINPQAVIMLTVSEDSDDLFECRMIGARGYLKKNINADFLIESIRKAAE
GDNVFSPEMTAKLWLSLSPQAGRTQALSSLTPRELEILGLTAAHNSNRIARHLDLAESTVFKVHVQNLRLKLNLSRVQAAVYAIRHNVPQPVPE

SEQ ID 4823

ATGGGCATCAAAAGTCGCATCAACGGCTACGGACGATCGGCGCGCAGGTTTTCGCGGCCATCTACGACTATCAGATTCAAGACCAACTCCAATCTGCGCGCTCAACGCGCAGCGCGAGCC
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CAACCTCGCGCACTGCGGTGGAAGAAGTCTGGTTCGATTGTCATGGAATGACCGCGCGCTTACCAGCAAGAAAAAGCCAAATCCACTCGAAGCGCGCGCAAAAAAGTCTCTC
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CGGTTCGCAAAAGTCTTGAACGAAAGCGTGGCATCTGTCAAAGGCGCAATGACCACTCCACGCACTGACCAACGCAAAACCGTTTACCGAGCTGCGCCACAAAGACTGCGCGCGCGCG
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CATTTGCTTTTCATGGATTCAACACACACCAAGGAGCGCACTTTCGAGCAACGCTGACCAAGTCTGCGAGCGCAACATGGTCAAAGTGTTCGCGTGTATGACAACGAATGGGCTT
CAGCTGCCAAATGCTGAACACCGCACGCGGTATGTTTCGCACTTGAAGTGGCGCGCTCAA

SEQ ID 4824

MGIKVAINGYGRIGRQVLRAIYDQIQDLQIVAVNAGSLETAHLTKPDTVHGRFADVSHDGNLIVNGDKIPFFSTRNPAELPWKELGVDLVBECTGAPTSEKAKIHLESAGAKVL
ISAPGGDDVDATVYVGVNDSVLTADMTVVSNACTTINCLSPVAKVLSVSVGIVKAMTTHAL/TNDQTVTDVVRHKLRRARSGVENMIPKTKGAARKVGLVPELKGRLDGLAIRVPTVNV
SLVDLSFQAAARDTTFVEINALMKAVSEAGALKGVLYNTLPLVSMDFNHTTEASHFDATLTKVVDGNMVKVFAWYDNEHGFSCQMLNATARRMFLEVRPLK

SEQ ID 4825

ATGATACTGCCAACCCGATTTTCAGACGGCATCCCTCTTCCCTGCGCTGAAACTCTGACCGGCTTGTGGGTGGTTCGGCGGCACTGCTGTGTTTTAACGCTGCTGCTTTCTTTCC
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ATTTGAAAAAAGTTTAAAAACGATTTCCCAAAGCGATGCCATCCATCGCTGATTCCCTTCGCAATCCCTTGCCTACGATTGATACAGTCCATGCTGATTATCGACTGGCAGGCCAAC
ATCTCTCCCTCCGTTGCAAGGATACCGCGCGCCACACAAATCGAGCTTTACCGCTTTCGCGCAATATCGAAGTGTTTTTCAGGCGTTGGAATAATCGCGCGAAAAAACACTTGGTGGC
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CGGTACGCGGATTTGACATCTCTGTTCCCGAAGACGCTACCGCCGAATTCAAACAGGTTCGGCGGTTTTCACCAAAATGGCGCTCAGGCTGAAGACTTTATACGATGATTGGAAGGA
CAGGTTGCGGAACAAACCAACCTTTGAAAGCAAAACCGCAACCTGACCTGCTGATCCGGAACACGCGGACCTGCATCAATCTATACGCGCGACAGGCGCGGAAGAAATTTTGA
ACCAATCTTCGCGCGCGCGCGCAATTCGCGCAATCTGCGTGGAAAAAGCTTCGACACAGACATTTCCGTTCCATACGCGCGGAACACGCGAAAAAGCCCTTTTGGAAAAATACCA
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SEQ ID 4826

MLPFRFSDGIPLSRLKLLTGLWVGLAALSVVLTLLSFRLENAASVIEAGNLKMQAYRLAYMAGEGSPRAQIDNQIARFEKSLKRIQSDAIHPLIPSDNPLAYDLIQSMLIIDWQAN
ILPLQAYRRPTQIELRYAGNIELFLQALENAGEKNITWLRFPQWVIMLATTIVSSVIMLPWQIVVIRLQALREGAERIGQRHFDIPVPEDGTFEFKQVGRCPNQALRLATLYDLEB
QVABQTHNLEKQNRNLTLLYRTTRDLHQSTTPROAAEEFLNHLPAVGAQSGNICLENGSDTILSVHTAEHGKPPLEKYHDETFPIEYQNEKLGMSLGFSDGTSITGDDRTLLQTLIRQ

LGVS LAGAKQEEBKRL L AVLQERNLIAQGLHDSIAQLTFLNLQVQMLETAFANKEKREAAENIGFIKTGVQECYEDVRELLLNFRFKI SNKEFPPEAVDLFARPTQGTITVETVWENG
FLPTQDEQLQMIPLQESLSNIRKHARATHVKFTLSEYGGRTMTIQDNGQGFDFEIKI GEPTGSHVGLHIMQERAKRIRAVLEIRSQAQQGTTVSLTGAPKESLP

SEQ ID 4827

TTGGCAGTATCATATTTCGGAGGAAAGTCGTTTTAAACGGTGCAAAACATATCATTTCTTGAATTAGAAAACACTGCTCAGAAAGGACAGGTTAAGGAAAACCTTAAGCCTCAATGCTTTCA
GTGTTAAATCACGTTATGATAAAATTCAAATAACA

SEQ ID 4828

LAVSYSESRFKRCKQYHSLLESTTAQKQGVKENLSLNAFVSKRYDKIQIT

SEQ ID 4829

ATGAAACCTCAAACTTTCCAAAAGCCGCCGCATTA AAAACGTTTCGATTGATTTTGGCAGGAGCCCTGGCCGACCGTATGGCCGGGGAAGACAAGGGCTGGCACTGTTGGAAGCA
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GTCGCCGCTTTGAAAGCGTCTCCAAACGCACACCGTTGTCAANTCGCTTTATGTGGAACGCCGTAACGATGCACACAACTATGTATATCCGTCGCAAAATTCGCAAGCGCGA
TTCCTTATCTGTTTTCCGGTATGAAAACATTAAGAAGCTGGTTGCAGCAGCAAGGGCGCGCGCGTCAGATTCGAGTTTGACGGGCATTTTCCCGACTTGAAACAGCAAAACCGGATTTCGA
GGAGGA

SEQ ID 4830

MKTSNFPKSPFALKTFALILAGGLADRMGGEDKGLALLEGRPLIDRVIGKIRPQVSHIVISANRNLEAYARRSPHVFPDARQWQHFGLSALCTAANDLQLAADWLLIVPCDMPYLPDDL
VARFESVSKRTPLCNAFVYETPVTHYNYMYRPIQLQSAIPYLFSGMKTLSMLQQQRARVPRFEPDGFADLATQTDLQEG

SEQ ID 4831

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TGCCCATTTGTCGAAATCGAACGGGACGGGTTCACCGCAGCGTTTGGTTTTCGCTCCCGCAGCAACTCAAAACCTATATCTGACCAAGGGTTTCGTCGGCTTGGACGGTTGCAGCGCTGAC
CATAGGCAAGTCGAAGACAGCGCTTCAATGTCATCTGATTCCCGAAACTTTGGAACGGACGCTGTTTCGGCAGCAGAAAGCGGAGACAGGATCAACATCGAAATCGATCCGAATACG
CAGGCAATCTGTCACACCGTTCGAACGGCTGATGGCGCAAGATATGCAAG

SEQ ID 4832

VQDRRPARKGKVAYRAVFARTGGTTPSEGVSDGIFRGEMLQFAPFLPTQGNRIMFTGIVQGLKLTAIHRPSEAFQTYVVELPQEAENLQHGASVANNCCCLTITEIEGNRVSPDLMAE
TLAKTNLGLLKEBDCVNIERARFGEIGHVMSGHMTATVPIVIERDGFNRVWFALPHELPYILATKGFVGLDGCSTLIGKVEDSEFNVHLIPETLERTLFGSRKAGDRINIEIDPNT
QAIVDTVERLMAQRYAK

SEQ ID 4833

ATGCAAGTAGAGTAGAGATGGAATTGAACGAATTCCTCGATAAAGCCTATGCGCGTTTTCGGCGGTTTGGATGCCCTGCTTCCGCCGCAACCCGGGCATACGGATTGGAACCGCGCTTGCCT
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SEQ ID 4834

HQSEVENELNEFLDKAYAVLRRLDAVLPPPEGHDTWNAALFRWQSAKKGFLEHLPDPHVPLSLRAGVGRQTELLVRNTEQFIAGRPNANNVLMSCARGTGKSSLVKALHIEYADKGLRLI
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SEQ ID 4835

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GAAGGAAGGC

SEQ ID 4836

MIKIKGLNLPIAGRPEQVIYDGPATTEVALLGERYVGMPSMKIKEGEAVKKQGVLFEDKNKPGVVFPTAPASGKIAIHRGKRVLSQSVVIAVEGNDEIEFERYVPEALAKLSSEKVRNR
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SEQ ID 4837

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GCTTTCATACGTCPTTTCCGTTTGTTCACAAACGGCAGTTGGACGGGCTTGGCGCGCTGTCCCAATTCACACCTTTGTCGGACGCAATCGCGCTGGCAAGTTTTCGCGCGCTACCGCGCTC
GGACAAATCCTTGATATTTTCGATTTCGACAAATACCGCGCTGAAAGCGTGGTGGATTGCCCGGCGCATCAACCGTATCGGCAATGCACTGGACACGTTAGTATTTTTCGCGTTG
CCTTTTACGCAAGCAGCGATGAATTTATGGCGGCAAACTGGCAGGGCATCGCTTTTGTGCAATTACCTGTTTCAAACTTACCGTCTGCACCTCTTCTCTCGCCCGCTACGGCGGTACT
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SEQ ID 4838

MYALTAQQKALFRLVLFILILIAASNYLVQFPFRIPGIDTWTGAFSPFPIFLATDLTVRIFGSHLARRIIFWVMPALLSYVSVLFHNGSWTGLGALSQPNITVVRILALASFAAYAL
GQILDIFVFDKLRRLKAWNLAPAASTVIGNALDITLVFAVAFYASSDEFMAANWQGIAPVDYLFKLTVCTLFPLPAYGVILNLLTKRLTALQTKQMDRPFVPSLQNP

SEQ ID 4839

ACAAAGGAACAAACCATGGGCATCAAAGTCGCCATCAACGGCTACGGACGCATCGGCCGCCAGGTTTTGCGCGCCATCTACGACTATCAGATTCAAGACCAATCCAAATCGTCGCCGTCA
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CTTCTCTCGACCGCAACCTTCGCAACTGCGGTGGAAGAACTCGGTGTCGATTGTTGTCATGGAATGCACCGCGCGTTTACCAGCAAAAGCAAAATCCACCTCGAAAGCGGC
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CCTGCGCGCGCGCGCGCGCGTGGAAACATGATTCCGACCAAAACCGCGCGCGCAAAAGCGCTCGGTTTGGTCTTCCCGAATTGAAAGGACAGCTCGAGCGGCTTGCATCCGCGTG
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SEQ ID 4840

TKETMGIKVAINGYGRIGRQVLRATYDIQDQLQIVAVNASGSLETHAHLTKFDTVHGRFEADVSHDGNLIVNGDKIPFFSTRNPAELPWKELGVDLWMECTGAFSTKEKAKIHLESG
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SEQ ID 4841

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SEQ ID 4842

VLDPQFVHRKIHAGVVAADFIIARLVPIKNIRNDFDRAAAAVFGMHNLTQRPVARIHFEGGADFTQLIVLTLCPPEPAYVAVRLKIVRGDISRGGVGLKAGQSHF

SEQ ID 4843

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SEQ ID 4844

VAANESWQESKAILKKEAAGLAKRQAGSGTAFPLIRIFRTITLIAV

SEQ ID 4845

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SEQ ID 4846

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SEQ ID 4847

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SEQ ID 4848

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SEQ ID 4849

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SEQ ID 4850

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SEQ ID 4851

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SEQ ID 4852

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SEQ ID 4853

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SEQ ID 4854

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SEQ ID 4855

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SEQ ID 4856

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SEQ ID 4857

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SEQ ID 4858

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SEQ ID 4859

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SEQ ID 4860

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SEQ ID 4861

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SEQ ID 4862

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SEQ ID 4863

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SEQ ID 4864

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SEQ ID 4865

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SEQ ID 4877

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SEQ ID 4878

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SEQ ID 4879

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SEQ ID 4880

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SEQ ID 4881

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SEQ ID 4882

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SEQ ID 4883

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SEQ ID 4884

MFSLEWIGLRYLRKKNRGMPSFTIMVSIAGIALGVTAIIVLVSMNGFQKEIRGQLNVPAHEIGYIDNITDWRNLLRFAENRKLIAAPVYSNQALLANAGEIRGVQIRGILPSE
ERKVVEYGDMPAGKFDLIPGEFDIILIGLAEALGAEGDKVTITVTPGNNVTAGIVPRLKQFTVVGVLVKTGVYEDNSLAMTHIQDARVLYRLDKVAGLRKLADPQNAIPALITATLI
PEAQRTDVTWDRWTSYNSRYFEAVELEKRMPIILTLIAVAAPNLVSSLVMAVTEKQADIALRLTGLSPAGVMKIFMVQGAFFSGFTLAGVVCGLWGNVGRVVAFFENLLGVHLLN
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SEQ ID 4885

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SEQ ID.4886

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SEQ ID 4887

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SEQ ID 4888

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SEQ ID 4889

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-375-

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AA

SEQ ID 4890

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SEQ ID 4891

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SEQ ID 4892

RRPARRTGPKHRQDRERHNCQGAAYAWQFSKNTDGIQNH

SEQ ID 4893

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SEQ ID 4894

VPFEGIRGGVLPFTVIGTPAPPARHSGGLFL

SEQ ID 4895

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SEQ ID 4896

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SEQ ID 4897

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SEQ ID 4898

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SEQ ID 4899

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SEQ ID 4900

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SEQ ID 4901

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SEQ ID 4902

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SEQ ID 4903

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SEQ ID 4904

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SEQ ID 4905

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SEQ ID 4906

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SEQ ID 4907

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SEQ ID 4908

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SEQ ID 4909

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SEQ ID 4910

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SEQ ID 4911

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SEQ ID 4912

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SEQ ID 4913

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SEQ ID 4914

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SEQ ID 4915

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SEQ ID 4916

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SEQ ID 4917

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-377-

ATATTACGGCGCGGCGCGGCGCGCATTCGCCGACCGCTTCGCCGCGGTTGCCGATATCATCGACATCGCCCGCTGGTTGAAGCGGACACCGCCACCGCGTACCGCATCTGGCGTTCCAA
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SEQ ID 4918

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SEQ ID 4919

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CAACCG

SEQ ID 4920

MLFEENPIDGQFAEYECGAGGIRLAGQSFHKPVLVHKDSVCLPQCRITSLDLPENLLSDIKPVDYPEILLIIGTGAQEFIHFKIMADFSRIGISVECMNTDSAFRTLVFLHSEGRRAHAHL
QP

SEQ ID 4921

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CGGACGGGCACTCGGACACAGACAGGTAATAACCGCTTAAGCGTA

SEQ ID 4922

VIDDAVAVFLGDFVLQGFDFGIVEFRYLAALHADDMMVVVALVQLINRLARFKNALQNALLELRQHAVNRRHTDFHALFQQNAVHIFRPTQMLFRVLLLEQIQNLQTRAGNLQTAVFQLRW
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SEQ ID 4923

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SEQ ID 4924

MADMKRLKHLMFSPFIDNPIALQVLGICSA LAVTTKLQTAIVMGISVALVTGFSFFLSLVNRYIPNSIRIIVQMAIIASLVTLVDQLLQAFAYELSKQLSVFVGLIITNCIVMGRAEAF
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SEQ ID 4925

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SEQ ID 4926

MAVFPPLSAKHKYALRALAVSIILVSAAYIASTEGTERVRPQVEQKLPLSWGSGVQYAYVWQEAQVPGDSLADVLARS GMARDEIARITEKYGEADLRHLRADQSVHVLVGGDGSAR
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GSTGRSTGPHLYEARINGQPVNPFVSVALPPELTQADKAFAAQKQKADALLARLGIPTVTVSQSD

SEQ ID 4927

ATGCATGAATACCGATTCCGCAATTCAGGACATTTGGTTTCTGCACTCGGAAGGCGCAGGGCTTGGGCTTGGCTTCAACCGTAAATTTCCCGTTTCAGACGCGATCGGCACTGACTTTCA
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SEQ ID 4928

MHEYRFGIDIGFPALGRAQGLGLASTVNFPPQTASALFTFR

SEQ ID 4929

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SEQ ID 4930

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SEQ ID 4931

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GTGTGCGGTGCTGATTTACCTAAATCAGCAGCATCAGGAGGGCGGATACCGCCTGAAATTTAAAAAACTTAGTCAAGAAAGCCAAAATACACACAGGAACAAAAAGAAAAACAAAAA
CATGCCGGGAAAAAGAACAGACAGGCTGCCAAAGCCCCGAGGAAAAATCAAAAA

SEQ ID 4932

LKLRNRSLSPSDKEARAGCLSLPANNGIIRTLPPPFYTTGNIIRLFAALGLLSLGGAAAQASIYHCNSNGKSVYTSDFSGSCADADLPKISSHQGGYRLKIKKLSQEAKIHTGNKKKKKK
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SEQ ID 4933

[illegible]

SEQ ID 4934

MKSKLPLILINLSLSSPLGANAAKIYTCYINGETVYTTKPSKSCHSDLPPIGNYSSERYILPQTEPAPSPSPNGGQAVKYKAPVKTVSKPAKSNTPPQAPVNNRRSLBAELSNRK
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SEQ ID 4935

TTGACAGAAGAAATGATGAA¹AAAGCAGGAGAA²TTTTGGGATAAGT³GGGCGATT⁴TACTGTT⁵TGCGCCCGTTGATATAAGT⁶TTTGGAT⁷TAAAAAAGTATGGGCGGCATATCCTGTGTGTC
GGCTGCCTGTAATCGTATTGAAGGTCAACGTA⁸TTC⁹CCCAATACCGGCTACACGTACAAC¹⁰TGTTCCGA

SEQ ID 4936

LTEEMMKKQENFWDKLGDLLFAPVDIMFWIKKVAAYPVCRLPVIVLKVNVPNTGYTYNCFR

SEQ ID 4937

ATGCTCGCTGTTCCGCGCAGGCATTGCCGTCAAATCGGCAATGGCGGAGGAATTCACGGCAGCTGGCATTTTTCATCTGCTGTTTTTGTGCGCTGGGACATAFTGGAATGGTGGCCTACCA
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SEQ ID 4938

MLAVPPOALPVKSAMAEFTARWHFHCCFCRWDILEWLP'TTTSKANPFCPCSCLSRLLONMSLKDGYFCLLFYLF

SEQ ID 4939

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SEQ ID 4940

LGVCPDARCSAAGIAROIGNGGGTHGTLAFSLFLSLGHIGMVAYHHIKGESVLPFLLI

SEQ ID 4941

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ATCAGCAGCAGGATCTGACTGCACGGATATGTTGGTA

SEQ ID 4942

MPAAEORASGHTFPNAOFGDGGVGGAVFTLADSLPYAPNROYOOOSDCTDMLV

SEQ ID 4943

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SEQ ID 4944

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SEQ ID 4945

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SEQ ID 4946

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SEQ ID 4947

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SEQ ID 4948

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SEQ ID 4949

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SEQ ID 4950

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SEQ ID 4951

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SEQ ID 4952

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SEQ ID 4953

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SEQ ID 4954

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SEQ ID 4955

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SEQ ID 4956

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SEQ ID 4957

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SEQ ID 4958

VHRAKCPYLPFPKFGYTDIALFCQTRFVGKCMFVFAAVAVLITELLTGTVYLLVVSALAGSGIAYGLTGSTPAAVLTAALLSALGIWFWHARTAVGKVEDSYQDLDTGKYARIL
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SEQ ID 4959

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SEQ ID 4960

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MELDKTFEERDEINSTVVSALDEAGAWGVKLYEIKDLVPPQELRAMQAQITAREKRARIASEGRKIEQINLASQREARIEQSEGEAQAANASNAEKIARINRAKGEAESLALV
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SEQ ID 4961

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GCAGACAAACAA

SEQ ID 4962

VNKTLLIALSALFSLFACSVVERVSLPPSYKILKIQGNELEPRVAALRPGMTKDQVILLILGSPILRDAPHTDRWDYTFNTSRNGI IKERSNLT VYFENGVLV RTEGDALQNAAFALRAKQ
ADKO

SEQ ID 4963

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CGGT

SEQ ID 4964

MEIILIGVMFTVIVLALALMILPAKSKLVSGEDITIKVNDKELTMPAGGKLLGALASQGI FVPVPSACGGGGSCGQCRVVVKSGGGDILPTFLSHISKREAREGCRSLCQVNVKTMIDIEVP
EEVFGVKWECTVISNDNKATFIKELKLAIPGEEGVFFRAGGYIQIEAPHTVAYKDFDIPKEYHEDKYNLQYVYSKVNPEILRAYSMASYPEEKGIIMLVRIATPPRPVNPAPPGQM
SSYIWSLKPDKVTISGPFGEFFAKDTDAEMVIGGGAGMAPMRSHIFDQLKRLHSKRKITFWYGARSKREMFVVEDFDQLAAREFPNFTWEVALSDPLPEDNDGTYTGFTHNVVYENHLKN
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SEQ ID 4965

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SEQ ID 4966

MYRRKGRGKIPKWMGAGAAPALVWL VYALGDTLTPFFAFAVLAVYLDPLVEWLQKKGLNRASASMSVMVFSLLILLALLLITVPLVGPNNLASRLPQLIGFMDNTLLPWLKNTIGGYR
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VAGILVEVPYLGATGLLLATVAALLQFGSWNGILAVWAVFAVGQZLESPFTTKIVGDRIGLSPFVWFLSLMAFGELMGFVGMAGLPLAAVTLVILREGAOKYTAGSYRGR

SEQ ID 4967

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SEQ ID 4968

MPRPFLRYIKSTLPKTIILRASIAEPFRROKSLRLPDSLISWFLKYCTSDAV

SEQ ID 4969

MTGAGGGATGTTTTFGTGTTCTGTGTTGCGTCATGATGTCTGCCTTATCGTGTAACGGTATGCCGCTGAAAGCGGGTTTGCCTTTCAGACGGCATCGGATGTGCAGTATTTTAGCCTAACCC
ACGATAACAGGCTATCGGGAAGCGGGAGGCTTTT

SEQ ID 4970

MRDVLFSCSVMMCCCLIVYGMPSSSGFAFOTASDVOYFSLNHDNRLSGRRRLP

SEQ ID 4971

ATGGGGGCGGTTTCATCCCGAGTTCGAGCAAGCGGTTTTAGAAAAACCGTCCGCTTCACGCCCCGACGACGAGGCTTACCACATCACCAACGGTCCGAGCAGCAAAAGGCAACTATACCGGTG
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SEQ ID 4972

MGAVHPEFEOAVLETVRLHAPD~~TOAH~~HITTRPSSKGN~~Y~~TGATVOVKVENOBOLDNTYRALTSHELVKVVL

SEQ ID 4973

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SEQ ID 4974

MKIIHKGLVEYLPTEAMKTPNAGRNADFEDELWVVEHPVPTQGLAGKPEHLIIRDIDPVVQIDRGQITYHGPCQLVWYTHIDFKRRKTSVRNIVSALENSIIATLAEYGI EAADPKR
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SEQ ID 4975

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SEQ ID 4976

LKHNSHRKQYTTMSIKTDDPKRIGLRGADKTARIPIKVVPLOEKLLKPEWIRAKLPSRKFFIKDILRBQKMTVCBEASCPNIGECFSKGTATPAIMGDICTRRCPDVDGHRPNMLD
PDEPKNLAESVKAMNLRVYVITSVDRLDRDGAQHFDCKIATRETSPTNKILELVDPRGLDIALKILAETPPDVNMHNLETHPSLYRKARPGANYQHSLLDLKRYKEMPHIPTKSG
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SEQ ID 4977

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CGGTTTTTTTGTCTGTCTAAACTAAGAAATCCATCTCATCA

SEQ ID 4978

NRALYAKAVGMNPLFKIQTIILINRAYSPMPKSVCCFLSVFFAARTKPNPSHQ

SEQ ID 4979

CACTAGACATCCGATTTGCACAGAAAGTTCTCCCGTGAACAAACCTCATCTCGCCCTTTCCGCCCTGTTACGCTGACCGGTGCGAGCTGCAAGCGCTCTCGCTGTTCCCTCTCT
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CCATACCGACCGCTGGGACTATACCTTCAACACCTCCCGCAACGCGCATCATCAAGAACGACGACCACTGACCGCTTATTTGAAACCGGCGTACTGCTCCGACCGAAGCGGACGCGCTT
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SEQ ID 4980

H*TSRPAQKGSFVNKTLILALSALFSLTACSVKVSFLPSYKLKI IQGNELEPRAAALRPGMTKDQVLLLLGSPILRDAFHTDRWDYFTNTSRNGLIKERSNLTVVFNGLVRLTBGDAL
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SEQ ID 4981

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GCGGCGCGCATAGTCACTTCTTTTCATCATTTGACTTTGATGGTATGTCGCTTCGCTGACCACTTGGATTGGCAACAGAAATCATAGTCCCAAGC

SEQ ID 4982

VFEAEYLTAELVQEDVVFHAQVFEHFDGLVHNRAAHKIPAVPRCFVVFQVFNHVVDARVAVPVVRQWVGQDVPSEVREFCRELVEVFDIEHFAFGACAVPEGDPFFGVQTFQL
VENVGTHRGHTRTAADKYHFYIGVFEKFAERAGNRNFVAGFERPDVGRHLSSRRICYGARRGRDTHVQHNDAPFRIIRSHRVGAQNLVHFGNVLQIVFVFPVFIPLNGNEVVFVNGVR
RGFDLNVAGAERNFPAFGNGKLEFFNERCFVVGNDGAFPPFHAHEFFGYPDVHVGFDIDLAGQTAAPACFAPADVQGLGRQNVAAAAPHNDALSARTAAATAGGDKDALAGKRAQEPF
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SEQ ID 4983

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SEQ ID 4984

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SEQ ID 4985

TTGGAAGGCATCGGGAATACGCCCTATTTATTTTGATAATTGTTGTATTTTAAATAGAAAAATTTGTCTATCGCGACAGCTTTTGATACAAATGACGATCCCGAACAGCGTTACAGAAC
GCCGTTTAAACCGCACGAAACCAAT

SEQ ID 4986

LEGIGYALFILLIVCILNRKFMPTAFAYNARIPNSVTERRILARNFN

SEQ ID 4987

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CGTGGTTTCTGCTCAAGCCGACCTGCAACCGAATACGAAGTGGCGGACGCTTTGAAAAAGGCACTAAACTGTCGGAAGAGGCTCAAGACTATGTTACGCGGACCTGATGTTGCGC
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SEQ ID 4988

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SEQ ID 4989

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SEQ ID 4990

LALVVVAFANQLDQALLFPQVVFVFFVFLGNHQVARNIVLSLFAQFDAPFQSVAHFVFLQVGFAGNHNVRADIQFGACHFRRTAQHQDASDEVFVCGFFPHLVLETFKFGVAFPG
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SEQ ID 4991

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SEQ ID 4992

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SEQ ID 4993

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SEQ ID 4994

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SEQ ID 4995

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SEQ ID 4996

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SEQ ID 4997

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SEQ ID 4998

MVRRSNTAFRRHLSGIGGHQVQPFLLRQQLIRRHQSRHRFFDIRQNVPAFALDCRHISPVQATLPROFLRLPTLVHAEKPHIVCQYRQILFVRQFGRQSFVAHHLFPDKWLKX
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SEQ ID 4999

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SEQ ID 5000

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SEQ ID 5001

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GTCAGTTTAAACAAACGCTC

SEQ ID 5002

LIMVIFYFYFCGKTFMARNRMLLPLLASAAYAEETPCFPLRSRPEFRLHEAEVKPIDREKVPQVREKGVQVQDGETLLKNPELLSRAMYSAVVSNINAGIRVILPYLQARQDKM
LALYAQGLLAQABGRVKEAVSHYRELIAAQPDAPAVRMRLAALPEDRONEAADQFDRKLTEDLPQLMEQVELYRKALRERDANKVNGFSVTRERNINQAPKQQQYGNWTFPKQVDTG
AVNYRFAEKKWSLKNWMTTAGGDSGRVYPGNKFNMTAGVSGGIGFADRDRDVLAVPHERRTYTGNDAYSANGARLYPHWQTFPMQTLSSAENGLKNTERRARSNDHQLQSNLS
VFYRNARFYWGLDPIYRNPADRGDNFRYGLRPAWQEWGSGLSLFLGVAKRHYEKPGFFSSFKGERRRDKESDTLSLWHRALHFKGITPRILTSRETSNDVFNEYKMRAP
VEFNKT

SEQ ID 5003

ATGCTTGAACCTGTCTTACGACTGGAAACCTTCAACAGCAGCGCAATGCCCGGAAGCGCATTTATTTGAAGCCAACCGCGTGTGCGTATTTTTCAGAGAATACAGCGCGGCACTG
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CTCCCTGCCCCGCTTTCAGACGGCATTCAGGAACAGATTGCCGATTTATCCAAACTCTGTGGGATGCAAACTAATGCCGCTCTGTAAAAAGCGGCGAGCGGTGCAAGAACTGTGCGAAAGC
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CGGCTGCAITTTAAACGCCAAGCGCGCCGAAGACCGCTGCTTTTCGATTTGACAGCGCAAGTTGCCGAAGATGCGGTTATCAAGATGAAAACCGCGCGCTCAAGCGAAGAACTGATGC
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SEQ ID 5004

MPENLSSALETFKQORNAEAHYLKANRVSVFPRYTTAAVETLLAALWAHFNQNSALCLMAVGFGFGRGEPYPCSDVDLAVVSPAPLSDGIQEBQIARFIQTLWDCKLMPVSKSGSVDELCE
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RRRQEAADLLTRAAPVPEKQKLLNALGSAFYARHQSREILWHAANLVHDFEPPIVRSRLPQSDSQVQVVFMPNGRPLFARLCRIFSRHGFIDLAARAFITHEHYILDTPITQIPSOHAP
EDYFDIQSALAEALNSFIHGHTVAETQSCNRRISRRSYMPIAPSITITPEEDYDPRYSVEITAVNRPLADNAEVEFFAHNVSLRYAKISTLDERVEDSFTVFSFLKNPKIQSSILQAL
LEQLA

SEQ ID 5005

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SEQ ID 5006

VHLAQTERPSIMRIVEKAYTFDDVLLVPAHSTVLPDVKLQTKLTREITLNLPLLSAAMDVTVEARLAISMAQEGGIGIHKNNPPEMQARAVSKVRHESGVVLDPTVAPTLLIREVLE
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SEQ ID 5007

TTGAAAGATTGCGTTTATTTCCACCGCGCTTTTAAAGCGGACGCTTTCGCGAGCGGGGTGCAACCGCGCTTCAGACGCGCATTTTCATTCTTTCGCGGTGCGGTGAGAAATGGCTTTGC
CGGTCCGCGCAATCAGCGCGTGGCGCTTGCCT

SEQ ID 5008

LKDCVYFHRRFKGRYSADGVQTAFRHRFHSFGVSVRMALPVRALSPGGLP

SEQ ID 5009

ATGAAATGCGGTGCAAGCGCGTTTCACCCGCTGCGCGAATACCGTGGCGCTTTAAACCGCGGTGGAATAAAGCAATCTTTCAATACGGCGCTTCGATGCTGGAATGATGC
GCCGCGCGCATATCAAAATATCGCGCGCGCTTCGGGAAAGTATGCCCGCGCTTCCCAAGCGCGCGCTCAGCAATTA

SEQ ID 5010

MMPSERRLHPVCRIPSAFTAVKINALIYQYGRFDWSEMRPPYQKIGRRLRESMPRPQAAPSA

SEQ ID 5011

TTGCGCTTTCGTTTTTTCAGCTTAATCGGAACCGGTTTCTTTCGCTTTTTCGCGATTTCGCGAAGCGGACGCGCGCTTCCCTTACTTTTCGCGCATGCGGCTGTTTTTTCGCGCG
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SEQ ID 5012

LPFRPLTLIGTGFAFFPDSATAGTLP/LPLPHRAVFPFAVVPDFPFAAPAGLADANLTFRRLLPSPAIRTKSIFPSSKSARATRTATLSPILKRMPLRSPSIAMISGRKLK

SEQ ID 5013

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SEQ ID 5014

SEQ ID 5014

MNKNIKSLNLREKDPFLSREQKYEHPLPSREWIIELLERKGVPSKIESLARELSITDEVEVFFERRIKAMARDGQVLINRRGAVCAADKLDLVKCRVEAHKDGFGFAVPLMPHDEGDFVL
YEHQMGVVMHGDTVTYVRPAGIDRRRREGTVDITVERAQSKVVGFRPYMDRGVAILEPEDKRLNQSTVLEPDGVARFKPESQOIVVGKIEVYPEQNRPAVAKILIEVLGDYADSGMEIEIAVR
KHHLPHRFSEACAKSAKKIPDHVRKSDLKGRVDICDLPIVITDGETARDFDDAVFAEKVGRNYRLVVAJADVSHYVRPDAIDADAQERSTSVYVFRPMIPMLPENLSNGICSLNPDVERL
CHVCDNVVITYAGNIKIEYRFYPAVVERSHARLITYNQVWKMLSGIGENPHKQAIDTLYKLFILQKKRLARGAVEFESVETQMIFDNGKIEKIVPVRRND AHLKIEZCMLANVCAADFFPKNSQ
KHTALFRNLHGPTPEKLAFLREQLGLGLQLGGGDNPSPKDYAALAEQFKGRPDAELLQVMMRLSMQQAIVYEPHCEGHFGLAYEAYAHFTSPIRYRDLTVHRAIVLRNKTATYTPKNSWQ
ALGVHTSPCERRADDAGRDVENWLKTTYMRDKVGEIPEGKISGVANFGIFVTLDDIHLGDVSYLSDLGEDYVFNFRPEIMAEIGERSGVRGRGVPVAESCKAKKPPVIVKVKRKGES
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SEQ ID 5015

SEQ ID 5015
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ACGGCATCGCGTATCATTTAAACAT

SEQ ID 5016

SEQ ID 5016
MFCGMFYPLPKPVRTQKAYPFKQYCSTCCRETEPDTETRRGDMLEKWRQFLDWIGKTPSETASRSRKARPNNKYRLKFFRRHRVSPKH

SEQ ID 5017

SEQ ID 5017

ATGAAACAAATCCGCAACATCGCCATCATCGCACACGTCGACCACGGCAAAACCAATCTGTGTGACCAACTGCTGCGCCAAATCCGGGCACATTCGCGGCCAACAGCAGGTGTGACGAGCGCGTGGTGTGACAGCAGCAAGCACTTGA AAAAAGAACGCGGCATCACCAATCTCTGCCAAAAACACCGCCATCGATTACGAAGGCTGCCACATCAATATCGTCGACACGCCGGGACACGCGCACTTCGGTCGCGAAAGTGGAGCGCGCTTTTGGGGATGGTGGATTGCGTCGCTTGTGTGGTGGACGCACAGGAAGTCCGATGCCGCAAAACCCGTTTCGTGACCAAAAAAGCCTTGGCTTTGGGGCTGAAA CCGATTGTCGTCATCAACAAAATCGACAAACCGTCGCGCCGTCGAGCTGGGTTATCGACACAGACTTTCGAGTTGTPCGACAACATTTGGGTGCGACCGGACGAGCAGTTGGATTTCGCCGAGGAT TTTACGCTTCAGGTTTGAGCGGCTTTGCGAAGCTGGAAGAAACCGCAGAGAGCAGCGATATGCGCCGCTGTTTCGACACCAATCTCTTGAAGCAGGACGATCAAAACCCGCAACGAGTTCGCGTGTATGAAC CACGAG GCGCGTCGCACTGCAAAATTTCCCAACTCGACTACGACAACCTACACCGCCGCGCTCGGTATCGGCTGTATCTTGAAGCAGGACGATCAAAACCCGCAACGAGTTCGCGTGTATGAAC CACGAG CAGCAAAATCGCCAAAGCGGCATCAACCACTTTTGGGTTTCAAAAGCTTGAAGACGCGTCGCTGTTGTTGGAAGAACCGCAAGCCGCGGACATTGTGATTATTTCCGGTATCGAAGACATCGGCA TCGCGGTAAACATCACCGACCAAGACACGACCCAAAGGCGCTCGCGATGTTGAGCGTGGACGAACCGACGCTGACGATGGACTTTATGTTAAACACCAGCCCGCTCGCAGGTACAGAAGGCAA ATTCTGTGACCAGCGGCCAAATCCGCGACCGCCCTGCAAAAAGAAATTGCTGACCAACGTTGCCCTGCGCGTGAAGACACCGCGATGCGCAGCGTGTTCGCGGTATCCGGGCGCGGCCGAATCT CACCTGACGATTATTGCTGGAAAAATATGCGCGCGGGAAGGCTACGAACTCGCCGCTCGGCAAGCGCGCGCTCGTGTACCGAGACATCGACGGTCAAAAGTACCGAACCTTATGAAAACCTTGACTG TGGACGTACCCGACGACAACCAAGGCGCGTAATGGAAGAACTCGCGCGCGCGCTGGCGGAACCTGACCAATATGGAAGCGACCGGCAACGCGGACCGCCCTCGAAATCACTATCTTCAGG GCGCGGCTTGATCGGTTTCCAAGGCGAATTCATGACCTTCAGCGCGCGCGCTCGGCTGATGAGCGCATGCGCGGCTGTGACAGCATGCGCGGCTGCAACCCGATATGCCGGCCGCCCAACCGG CTACTGGTGTCCCAAGACAGCAGGCGCGCTGCTTACCGCTTGTGGAATCTTGAAGACGCGCGCTATGTTCGTATCGCCCAACGACAAAACTACGAAGGTATGATTATCGGCACTC AGACCGCGCAGCAACGATTTGGGTGGTCAACCGCTCAAAAGGCAAAAACTACCAATATCCGTGCCAGCGGTACCGACGAAGCGGTGCCCTGACCAACCGCATCAACTGACGCTGGAAG GCGCGTTCGAGTTTATCGACGATGACGAGCTGGTGGAAATCACGCGCAATCCATTCGCTGCGCAAGCGTTACTGAGCGAATTGGAACCGCCGCTCATTTTAAAAAGCTGGAT

SEQ ID 5018

SEQ ID NO 5018
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PIVVINKIDKPSARPSWVIDQTFELFDNLGATDEBQLDFPIVYASGLISGFALEETDESSDMPLFLDPTILKYTPPASGSADEPLQJLQISQLDYDNTTGRGLIRGLINGKIPGQTVAVNHH
QQTAQGRINQLLEGKFLGRLEBESAGADIVISIEDIGIETVTDIDKDNKGLPMLSDVEPTLTFDPMFVNVTSLPAGTEPVTTSRQIRDLQKELLTNVALREVDADADYFVRSVGGH
HL/ITLLENMRRREGYLEGVKPRVAVRIDQKCEPYENITGVDPDQNGAVMELEGRGRELTNMESDNGNRTLETHYLIPARGLIGQGEFTMTLFRGVGLNLSHVFDYDPAVKKPDMPGRHNG
VLSYQGEQBAVAYALWNLEDRGRMFRVSPNDKITYEGMIIGIHSRDNLDVNNPLKGKKLTNIRASGTEAVALR/TPIKLTLGAEVFIIDDELVEITPQSTRLRKRYLSLELERRRHFKKLD

SEQ ID 5019

SEQ ID 5019
ATGGTTGATTCCATAACTAAAAAGTATCGATCAACCCATTTTACGAGGTACGGATAATGTCGTACAGCTTTGAAAAACGCCCGCAATACGATGATTGGATTGAATCGGCGGTCTGTGATG
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SEQ ID 5020

SEQ ID 3020
MVDSTKKVSNIPFYEVRLMSDSPENSPEYDDWIESGGRDEDEY EYYYNKNWQRRT

SEQ ID 5021

SEQ ID 5021

GTGCAGGTGTGCCGCTGTGTGTCAAAACATTTCGCCGGCGCATCAAAACAACCAATTGACCGCAATGCGGGCTCTTTGTGCGCGTCCGTCTCTTTGCGCGTATCCGATCGTGTGCGGACATA
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SEQ ID 5022

VOVCRICVKTFPGASKQPFDRQCGFFVAVRPFVSDACGHMAFPTGFNAKPPFERRPACQRLFFAVHFHAERF

SEQ ID 5023

SEQ ID 5023

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SEQ ID 5024

NFPVPHLSGESRRRLQTLALRPHFVFKARAEDSHKGTFGTLAVVGSAGHSGAPVLAASAMYLGCCKVRAGFNQDTPPFAVIAGFPETMLDTADGLTKRQGTINAWTAGCGLGTDAAAVET
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SEQ ID 5025

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SEQ ID 5026

MENGKHFP SNRLKLRLNKPILPPETDYEKQNSLGLPHPPFLAACRI PALYVV

SEQ ID 5027

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TCTCAACTTTTCAAGTCTGCTCGCGTTTTCGCGAGTCCATATCGCCGCGTCCGCGCATATCGCATATCAAAAAGAAAAGAACTCGCCGCCGCGATGAACACGGCTTCAAATACATCG
AAGCGAAACCTCAATCCGCTTTTCGCGGCAAAAGCGCGCTTTCGCGCGCATTATCGGTTTCGCGCGCTTGGCGCAGCGCGCATCTGCTCTCTGTC

SEQ ID 5028

MMYSAKAGGDMLOMHTTVGLLVLLFLLVRLCWTGWSGSDARFSSPVRWAGIRGYLKNIGPEHTQPGHNPLGALMVVALLAAVSPQVGTGLFAANENTPSTNGYLAHLVSEHTGSLIRKIH
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SEQ ID 5029

GTGAATTATTTTCCCAATTTTCGCCAACCTCGCCGGCCGCCCGTATTGGTCGTAGGCGCGCGCGCGTCCCGCACGCAAAATCAGCCTGCTGCTGAAGCGGGCGCAGAGGTCGGGGTTG
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SEQ ID 5030

WNYFFIPFANLAGRFVLVGGGVAARKISLTLKAGAEVGAAKHLNAELSAALAAENKILWLAKAEFRAEHIRTVFLITIAASSDQALNRVFLAESCQKPVNVLGDRDHCSEFFPFSVIDRDP
VQIAVSSSGSPVPLARLLRERLEALLPSPGLDMABISGRWRDAGFYFPVQLVVRQADKADGFRGYQGRIERGSSVTVGQTVRIENGLTAEBVSEKIAPKGEVAQAFAGEAATIRLRDIDV
SRGDLFVDKNFPLAPOKHPEATLWFDERPLNTARKYLLKHGTOTVSAKVGELISVLVDRLEOBAGAESLMDNDIAKVRINLOKPVATTPYAENTAAGSFILIDEATYGTVAAGMIL

SEQ ID 5031

TTGTATCAGTTTTTTATGCGCGCTGTTCACAAACCTGCCGCCGATGCCCGGACAAATCGCGTCTGAAGCCAGAAATCGGGTTTCAGACGGCGGGCAAAAAACGGCGGTTTTCCGCGCGTTTCA
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GACCGCAATGCGGCTCTTTTGTGCGCGTCCGTCCTTTTGGCGTATCCGATGCGTGCGGACATATGGGCTTTTCCAACCGGCTTCAATGCCAAACCGGCTTCGAGCGCGCTCTGCGCTGCC
AGCGTCTGTTTTTTCGGCGTCAATTTCCATGCCGAAGATTTTGACCTGTGCAAAACATTAAAGAGCGGCAAAAGGC

SEQ ID 5032

LYQFFMFLQFTLPDAATMPSEARIGFYTAANKRRFSAGFIIMPRPSGROGSDRFAGRRTGPCRCAACVSKHFFAHQNHLLTDNAASLSPSVLLFPYMRADIWFPQASMPNRPSSAVLPA
SVCFPSISMPKDFDLCKTLKAAG

SEQ ID 5033

GTGTGCGGGCTGTGTCGGCTACGCTTTGGGCAAAAAGCAGGAAACGGGCAATCCGCAAGGGCTGCCCCGCTTCAGACGGCATTGCCGGCGGCAGAACCTTTTCCGTAAACGTCCTTTCCGCCCTCGCAAAACCGCAATGCGAAATCCGTTCGCCAGAAAGCGGCGGACAGCTGAAAGACCGCGGCATTCAGTCAAGCGCGCGCAACTGAAAGGCTACAGGGCGAAAAACATCGCCGGCGAAACGTGCGCTCGCTGCTGTACGTCACCCAGGGCGAAGCGCAACCGCGGAGAGAGCGCTCGTGTCTGCAAAACTGCTGAAACGGCAAAAAGACCCCGAAATTGGACAAACTCCAAATTTGCCGCTACTGGGTTTGGGCGACAGCTCTCTATCCGAATTTCTCGCGGCGGGCAAAAGATTTGCACAAACGCTTTTGAAGAATTTGGGCGCAAAACGCCCTGCTCGAAACGCTTGATGCGGAATTTGGACTTTGCGCGCGCTCAGACAGCATGACAGCCGCGCATTTGTCGCCGCTTAAAGAAAGAAGCGCAAAAAACCGCGCGCAACCGCGCGCAGGCAACGTCCCCCGCGGCTTCAGACGGCATCGGACGGCGGCTTGCAGAGCAGACCTTTTCCCGCGCCCTGCTGCGCAATCAGAAAAATCACCGCCGCCAATCCGA

SEQ ID 5034

VSLGSGYAAKAGNAGSAGLPALQTPALPAEPFVSVTLSASQTGNKASVADKAADSLKAAGIVQRRAEIKGYKAKNTAGERLLIVTSTQGEQEPPEAVVLHKLHAGKAPKLDKIQFAV
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SEQ ID 5035

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SEQ ID 5036

VRHIEIDLSGSDIHYLPDGLGVWVFNDPALVGEILDLLGINPATEIQAGKTLFVASALLSHFELQNTPTAFVKGATYADNDELDRIAADNAVLQGFVQSTPLAGVLRHFPKLTABQF
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SEQ ID 5037

TTGATTAAATATAATCGGAGGAACACAAATGACCGTACAGGCCAAGCAAAAGGTTTGGCGTGGCAAGAAAGCCGTATCCGACAACGAACGTCTGAAAACCGAAAGCAATTTTTCAC
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SEQ ID 5038

LIIKYNREHKMTVQARTKGLAWQEKPLSDNERLKTESNPLRGITLDDLKPLTGGFKGDNFQIRFHSMBQDGRDIRTEAKLEPLKPHLLRCRLPAGSSNRPSG

SEQ ID 5039

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SEQ ID 5040

VPKTLQTMPLRLHSLGLDSIATAADMNRNVLCTSNPIESLHRQAYEYAKKISEHLLPRTRGYLDMMVDGKKVQSSDDFLQEGEPILKTYLPRKFTAVVPIPLNDVDCYGNLDFVAV
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SEQ ID 5041

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SEQ ID 5042

MFFFAARVSTPQNSDTWYKIPPPPTLKNRTRCLKQPCLSDGIOTRKHMTPEYRSKSTSHGRNMAGARALMRATGVMETDFGKPIIAVANSPTQFVPGHVLHNMQLVAREIEKAGAIK
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TCGSCSGMFTANSMNCLTEALGLSLPGNSYLATHAGRKELFLEAGRMIVETIRYEBQDDETVLPRSIATKAFENAMTMDIANGGSTMTLHLLAVANEAGVDFKMDIDRLSKVVPPI
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GCVVKTAGVDESILKPTGRARVFESQEAABGILGNQIVAGNIVIIRYEGPKGPGMQEMLYPTSYLKSGLGKACALLTGRFSGGTSGLSIGHASFEABGGAIGLVHEGDTIIDIPIK
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SEQ ID 5043

GTGCAAAACATPAAAAGCGGCAAAAGGCTGAAGATTGACACCGTTACGCAAGCAAAACGGGTTTTCGCCGAATGCCGCGCGGATTGCCACTGACCGCTCGCGAGCAGCCGACCGCC
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SEQ ID 5044

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SEQ ID 5045

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CCCACTCTGTGTAATTTGGTGTAGGCACAA

SEQ ID 5046

IEYLLI*KFQLYFPANYIYDKTGKIIIPY*CCQTSIIQDFIILL*FSKLGIIIDIFILVLSVSIKDFQIAELLEFNFPVVCVINCRAQ

SEQ ID 5047

ATGCCGATGCCGTTTGAAGGCGGTCGCGCGGATCGCCCGTCTGTTGGGTGGCGGTAATAAAAAACAAACCGGTTTTCACAAACCGGTTTGTACGGGTTAATGGTCAGCGCGTCTGCTG
GTTGCCATTGTTG

SEQ ID 5048

MPMPFEGRSGLIARRLGGNNKQTVGLVTGLSGFNQGRVLRCHLL

SEQ ID 5049

SEQ ID 5049
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SEQ ID 5050

SEQ ID 5050
 MIINKFTWAMAVFSAILALVIGSGFTALEYVKEPPAAPYAVSAPKTAGVKPRILPERNPCCRLTVQTPRPFQTPAMRTDRILRTERQIIPFSSGSA

SEQ ID 5051

SEQ ID 5051
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TCCGTGTCGGTCCGCATCGCCGGTGT

SEQ ID 5052

SEQ ID 5052
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SEQ ID 5053

SEQ ID 5053

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SEQ ID 5054

SEQ ID 5054
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SEQ ID 5055

SEQ ID 5055

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SEQ ID 5056

SEQ ID 5056
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 VKPDGASNVRPLPEYDIRAGIDGEPKRLDDVAPVVEPIEDFGIERQVSLFPFRAAVEHNDVGFLGFPNQPFEPGVIVQFDGGKVGEGDEAVSHAVFLQDGGFKPVFDARIFDVQPVK
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SEQ ID 5057

SEQ ID 5057
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SEQ ID 5058

SEQ ID 5058
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SEQ ID 5059

SEQ ID 5059

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SEQ ID 5060

SEQ ID 5060
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IQLSTLLSIKTGGCPEDCAYCPSAHHWNLGKEQMDVDDEIVEKAKTAKSRGASFCMGAAWRGPKPKDVEVTSALIKAVKGLGMETCGTFGLMEGMAEDLKEAGLDYNNHNLDDPDR
YNDIITHRRHEDMDTLGKVRNAGLKVCQGGVIGMNETRAERAGLTASLANLDQPESVPIINRLVKVBGTPLADAEDLDWTFEVRVTSVARITMPOSYVRLSAGRSMPPEAMQAMCFHAGA
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SEQ ID 5061

SEQ ID 5061
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CGACATCTTCGCGGATCTGGCGCGGATACAGACCCAGTTCCACCACCTCGTGGCAGCCGTACCATCCGAAGGCTCATCGTCTGCAACGGACAGCAGCAAAAGCCTGCAAGATACTTTGGAC
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GGGATTGTATGGCGGCACAAACCGCATGAACGCGCTCGCGCTCATCGTCCCGCACGCCATTCGCGGAGTCGATGTTTCAGACGGCTCGCGAAGCCTGGGTGCGTTTAAAAACGTCAACGC

CCGCATGGAATCAAGGCACGGCAACGGCATCACCGTTTACGACGATTTCGCCACACCCGACGCCATCGAAACCGATTCAAGTTTTCGCCAACGTGTCCGGCGCGCGGCATC
CTCGCCGTCTCGAGCCGGCTTCAACACCATGAACTCGGCACGATGAAGTCCGCCCTCGCCGCAAGCCTCAAGAGAGCCGACCAAGTGTTCGTACGCCGGCGCGCGGACTGGGAGC
TTGCCGAAGCCCTCGCGCTTTGGGCTGCAGGCTGCAGCTCGGTAAAGATTTCGATACCTTCGTTGCGGAATTGTGAAAAACGCCGGAACCGCGGACCATATTTTGGTGATGAGCAACGG
CGGTTTCGGCGGAATACACCAACTGCTGACGCTTTGAGA

SEQ ID 5062

MKHIIHIGIGGTFMGGIAAIAKEAGFKVSGCDARNYPMSTQLEALGIGVHEGFDAALQEEFQADIYVIGNVARRGMDVVEAILNRGLPYISGPQWLAEVNLHHHVLVAGTHGKTTAS
MLAWLEYAGLAPGLIGVPEFVVSARLPQTTPQDENSKSPFFVIEADEYDTAFPIKRSKFVHYRPTAVLNLEFDHADIADLGAIQTPHHLVRTVPSEGLIVCHGQQSLQDTLD
KGCWTFPEVKFTGHWQIGEVNADGSPDVLDDGKAGHVANDLMGGHNRMLALAVIAARHAGVDVQTACEALGAFKNVRRMEIKGTANGITVYIDFAHHTAIETITQGLRQRVGSGRI
LAVLEPRSNWMLKGTMSALPASLKEADQVFCYAGADMDVAEALAPLCRLRVGKDFPTTFVARIKNTATGDHILVMSNGFGGIIHKLIDALR

SEQ ID 5063

ATCAGTTAAGCAACCATTTATTTTAACTTAATCCCATTCGGGCCAGTCTCTTTCATTGGAATTCCTCTTAAATACCTTATTTGTTGATGTGCGCATTAATCACAATTTCTCCCCCTTTT
TTTGTAAATACGTCTCTTCGGGAAAAATAATCCAT

SEQ ID 5064

IS*RTIIF*P*SHSGQPCFIWNS*ILIV*CAINHNFPSPFFCWTCCFGKLIH

SEQ ID 5065

GTGTTTGAACGTTTGGCAATGGCTTGAATTATATCGCAAAACGGCCGATGTTTCTATGCGCATGCCCTTTGAAGGGCGTTCCGGCGGCATCGCCGCTGTTTGGGTGGCGTAATAA
AAAACAAACCGGTGTTTACAAACCGGTTTGTGAGGTTTATGTCAGCGCTCTCGCTGCGCATTTGTTGTAGTAGTATTCGTAATCTTCATCAGACCCCGCGATTCAATCCAATCA
TCGTATTCGGGCTGTTTCAAAGCTGTGAGACATATACCGTACCTCGTAAATGGGT

SEQ ID 5066

VFDGFGKWLLEYKRTAGMFLCRLKGVRAASPVVWAVIKNPFVYKPVQGLMVSASCAVACSSIRNLHHDRIQSNHRIKRCFQSCQTLVPRKMG

SEQ ID 5067

TTGCACAGGTCAAAATCTTTCGGCATGGAAATGGACGGCGAAGAACAGACGCTGGCAGGAGGAGCGGCTCGAAGGCGGTTTGGCATTGAAGCCGGTTGGAAGGCCATATGTCGCAC
GCATCGGATACGGCAAAAGGACGGACGGCGACAAAGAGCCGCAATGTCGCTCAATGGTTGTT

SEQ ID 5068

LHRSKSFQMENDGEKQTLAQTALRFGIEAGWKHMSARIQYKRTDGDKEAALSVMKLF

SEQ ID 5069

ATGCGCGTATCAAAATGATTGGAAGTATATGCTTGTTCAGCGGTTTCAGACCGTATTTTCGGCAATGTTTACGAGTCCCGCATTAATGGTAAACCACTTACAGTCAAACTCCGGAA
AAGATTGTACCAACGCGGGTTTGGGGCGGATCGGTTACAGTTCGGTCAGGCTCGCGTGAAGACAGGCGGAAGACGCGAGTGGCGATTATTCGGACACGGTGAGGACGAAGC
CGTCCAAATCCGAAAGGAATGCACAGAAAGACGTTTCGGATGCCGCGCATCAGACCGCAT

SEQ ID 5070

MRVSKMIGSILLVAQTVFSANVYECRHNGTSYSQTPGKDCNTAGLRDRVYSSVRPAVKDRAEDAGVDYSDTVRDEAVQNPKNAGKQKDSAGIRPH

SEQ ID 5071

TTGATTGCGTTTCAATCAATCGGCTCTGATGCCGGCATCGAAGCGCTCTTCTGTGCAATTCCTTTTCGGAATTTGGACGGCTTCGTCCCTCACCGTGTCCGAATAATCGCAACTCCTCGG
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ACTCGTAACATTTGCCGAAAAATACGCTCTGAACCGCTGCAACAGCAATATATCTTCAATCAATTTAGATACGCGCATATTAACCTCTTTATGTTCTCTTCAAAAAAGGAATGTAT
TTCAATAGAATTTATCTAATCTTTTCATCTCTGCTCA

SEQ ID 5072

LIRFQSMRSDAGIRTVFLICPFRILDGFPVHRVRIIANSCVFRPVFHRPDRTPVHPIPPQTRVGTIPSRLTVTGFTMAALVNICRYGLNRCNKQYTSNHPFYAHIKLLYCSSSKKGM
FNRTSSNSFIPCS

SEQ ID 5073

TTGCTGAATTTACCTTGTATTATGACGAGGTTTGGAAAAGCGGAAAAATACCGTTTCGGCAACAGGAAATGATGACGATATGGACAAAGTGTCCGCCCTTAAGCGGAAGTTTAAAGACA
TTTCTGAATCAAGTAGGGGATGTTGGGAATACCGTTCAATTATGAGCAAGGAATGAAGAATTAGATGAAGTTCTATTGAAATACATTCCTTTTGAAGAGGAACAA

SEQ ID 5074

LNLPCYYDEVLEKRIKPFQKQEIDDMDKVSALKRKFKDISIKVGDGWEYFPNTEQGMKELDEVLLKYIPFFEEQ

SEQ ID 5075

TTGCAAGCTGCCATAAAACCGATTGCTGCCAAGCCGACACTTGTGTTAAAGATGCCGATAATGCCCAACTCTTCCTGATTACCGCAAAACGCCCTATTGCT

SEQ ID 5076

LQAHNKRLPAKPTLLVKDADNAATLPYLPTNALFA

SEQ ID 5077

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SEQ ID 5078

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SEQ ID 5079

TTGAGCAATATCTGTCAAAACCATTTCCACCATATCCAAAAACAAACCGCCGCCACGGCATTTGACATAAGATGAGTTTCCACTGCCGCTCTTCGCAATGCCGCTTCTTGGGCT
TCAAAGCACCGCA

SEQ ID 5080

LSNICQNHFIQNKTAATAALDNKMSFHCPSFRNAFLGFKAPA

SEQ ID 5081

TTGGATATGTTGGAATGTTTTCAGAGATATGCTCAAAATCGTGCTAATGGAATCCGAACAAATAAGAAATTTGGTAAAAATTTGTTAAATCAACGGAT

SEQ ID 5082

LDVEMVLTDLAQNRANGIRTNKEFGKPKVSTD

SEQ ID 5083

ATGCCGTCTGAAAAATCTATTACGGCGTATTGATTTTCTTATGATCGCTTCTATGCTGCTGTCACCGTTTATGCGGGTCTTTGAAGCCCAAGAGCGGCATTCGGAAGGAGC
GGCAGTGGAACTCATCTTATTGTCCAATCGCGTGGCGCGCGGTTTGTGTTGGATATGTTGGAATGTTT

SEQ ID 5084

MPSEKIYGVILFLICIASMLSPFFYAGALKPKAALRKDGQWKLILLSNAVAALVFWIWKWF

SEQ ID 5085

GTGAAACACATCACTGACCAATATGAACATATCAGACACCTGCACCCGCTGTGTGCGCAAGGAAAGTTTCAGACGCGAGTATGCCCAAAACCGTTTGGAGGGCGGTGCACTGCTTCAGG
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CGGCATATTGAAAAAATCAGCAGCTTGAGTTGTGCAGACGATATACCTTACACTGATGATATCCATTGGGCGGAACCTTGCCGGAACAAAGGCGAGTGTGGGTTTGGACGCGGTGCAA
GATCCGGCAATGTCGCGACCGCTTACGAGTTCGGCGCGGCGAGGGTAGGTACGGTGGTTTGGGCGAGGGTTGTGCGGACGCGGTGCGCCAAAGGTATTACGCGCGGTATGGCG
CGCATTTCTTGTGGACATTTATTCGAGCGCGATTGGGAAATATGGTTGGCGCACTATGAAGACCGTGTGTGCCACCGCGTTGCGCGAGGAAAGCAGCGCGTTTGTACGCGGAAGA
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GTCGCGATGGCGGACAAATCGCTGTGTTGAACAGATGCGCGCAACGGCGCGGTAT

SEQ ID 5086

VKHISSTNNEHRLHRLHLLSQKFRQYATVLEGVHLLQVFLQSGRRKPVVYIPEAKMPESEVLKLTAVLPEDGIFSVSDGILKKISSLSCADDILFLIDIPLGGLTPDKGDCAVLDGVQ
DFGNVGTVLRSAAGVGTVVLGRGCAWSPKVLRAHGAHFLDIYSQADLEKIWLAHYEDRVFATALREKQAVLYGEDICEPTAHVFGNEBAGVGKAVLDRADKCVRI PMHDATESLN
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SEQ ID 5087

ATGCCGTCTGAACACGCGCTGCCGAACCTTATCCGCGCTTGATATTTGCCCTGGGTTTCATCTTCTGAACGCGCTGTTCGGAACAAACCGCGCAACCGTTACCGTGAAGGCGAAACGA
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GACCCATACGCGCAACCTCGCTCCATCAGCGTGTCTCAGACAGTGCATGACGCGGACGCTTATCCACAGGATTATTTGTTTGGCGAAACCGAAGCTTAAAGCTTGCAGAGCA
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SEQ ID 5088

MPSEFRLPNLIRALIFALGFIPLNACSEQTATVTLQGETMGTITTYKVLNNRDKLSPAKIQKRIDDALKEVNRQMSYQTDSEISRPNQHTAGKPLRISDPFHVTAEAVALNRLTHG
ALDVTVPGLVNLWFGPKSVTRPSEPIKQAASTYTGIDKILQOGKDYASLSKTHPKAYLIDLSIAKFGVVDKVGLEKYGIQNYLVEIGGELHKGKNAHGEFWRIGTEQPNIIQGG
NTQIIVPLNNRSLINSGDYRIFHVDKNGKRLSHIINPNKRPI SHNLASISVVSAMTADGLSTGLFVLGETEALRLAEQKLAFLVLRDKDGYRTAMSEFAKLLR

SEQ ID 5089

ATGCAGTTTACTTGCACCGCGAGCGCAGTTTACTTACTTGGCGGTAAACGCGCGCTTACCGCAGCGAGGGCGCGCGTCCGCGTCTGCTCGCAGCGGTGAGTGGCAATCCGCGCGCG
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CTGCGAGGCGAGCGCGCTCGAAGGGCGGTTCGCGATTGAAGCGGTTCGAAAGCGCATATGTCGCGACGATCGGATACGCGCAAAAGGAGCGAGCGCGCAAAAGAGCGCGCATTTGTCG
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SEQ ID 5090

MQFYLPQAFQTYLGVNGGTFDSEGRSGCSAAVSGKSAPAFGQKPVLLCVTSIFSLLPLMPCGTQNLNLSANKWTAKNRRWQAGRRSKGGLALKFVGKALCPHASDTAKGTATKPKHCR
SNGCFDAPGNVLTTHRHCTAPCAAPQTDNPAAPKGA

SEQ ID 5091

TTGCTTTTCTTATCGGGATGAAGCCGCTGCTGACTTTAGATCGCTTTGAGCAATGCTTGAAGGATTTGTTTCTCAAGGTCTGAATGGAACAAACAGCAGTGGCATTAAGCGCGCGCT
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CGGAATTTATGCGATATGCTAGGGGTGGGCTGGAACCGTTAAGGTCTGCGTGTGGAACAAACCGTTTGGCATCGAGGCGCGGCAAGGCAAAAGCTTATGCGGATTTTCCGCAAA
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CAATTTGGCGCTGTTGCGGACAGCGGAAACCGTCCATTTGCGCTTGCAGAACTGTTGTCGCGATTTCAAATCTCGGTTTCAGACGCGATTTTTCGCGTACATCTGACTTTCCCTTTT
ATTT

SEQ ID 5092

LLFLYRDEAVLFLDAFQCLKDCFPQGLNGKRTAVALSGGLDSVLLHLLVCAGKRAGFVPEALHIIHGLSPRADWDWPCRNVCMLGVGLFVVKVCEKNGLIEAARQKRYAEFAEK
GFDVLALAHHRDDQIEFFMLAVARGGGLRALAAMPVRLPENGIIWRPLLPFSQDIWDYARKHGLPNIEDESNFTDYLRLNFRHRLPELSAQIPHFGRHVLNNVRLQEDLALLEV
VVQDCRWVCGAGYPTARWLTFSRRKTHILRNFLKENGIPVFNQNALADIARVLTEAKTRWNLLGPELHYAGRLFFVASEQLAKPAFLKDTISGNLKKIITEHRFVLRHPPFLPEA
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SEQ ID 5093

TTGGATTTTGAACACCCATAGCCGAACCTGACCAACAAATCGATGAGCTGCGTTTCTGTCGAAGCAGGCTGCGCTCGATATTTGCGACGAAATACACCGTTTTCGAGAAAAAGCAACG
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GCACGCGCAGCCGACATTTTCGCGAGCATCATCGGATTGTCGCGGATTTGCGCGGTTTCAACGCAACGAGCGTGTGGTCTGCGGCGCATCAGAAAGCGGACGCAAGGAAATATCCG
CGCAACTTCGTTATGCCCGCTCTGAAAGCTACCGCAAGCCCTGCGCTGATGAAACGCGGGAAGAAATTCGGCTTTCGCGCTCATGACCTTTATGATACGCGCGGCGGTATCCGCGCA
TCGCGCGGGAAGAACCGCGGCGAGTCGGAAGCCATCGGCAAAACCTGTACGAACTGACCCGAGCTGCGGCTTTCGCTTTTGTGTACCGTCATCGCGAAGCGGTTTCGCGCGGTGCGTTCG
GGTTCGCGGAGGAGTACGCTCAATATGCTGCAATATTCGACCTATTCGCTTATTTCCCGCAAGGCTGTGCTTCGATTTCGGAAGAACCGCGGAAAGCGGCTGATCGCGCACAGGCT
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SEQ ID 5094

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RNFMPPEBGRKALRLMKTAERFGLPVMTFIDTPGAYPGIGAEERGQSEAIGKNLYELTLRVPLVCTVIGEGSGGALAVAVGDVNNMLQYSTYSVISPBGASILWTAERKAADAAQ
LGITADRLQKLDVDTVIKEPLGAHRDFGQTNKVNKAVLEQLHEAQSTPLDLSRRFDRIMAYGKFSQ

SEQ ID 5095

TTGTTCAAAATCAAAAAACAGGTTTCATAAAATGAAGCTCTCATCAACAGATTCTCGCGCTATCATACGCTATTTGTCATATTCCGCGT

SEQ ID 5114

SEQ ID 5115

SEQ ID 5116

SEQ ID 5117

SEQ ID 5118

SEQ ID 5119

SEQ ID 5120

SEQ ID 5121

SEQ ID 5122

SEQ ID 5123

SEQ ID 5124

SEQ ID 5125

ATGATGGGAGGGAAGGCGGATTTTATCGGTATTTGGCGGTAGAGGGCAATTTGCGCGGCACGGGCCAATCTCTAGCGGTTTGCTCAACTATCGCGCAAAATCTGTGTTAAATGCCGCCTT
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SEQ ID 5126

MMGGKGGFYRYLAVBENFGGTAQSLAVCSTIGANSVKMPFSLYTPHROAEFMALQISEPGMSAAPHRRHLAAGIDLTSTNSLVATFVRSASACLEFDADGRVTLPSVVRYLENGGIEVGK
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IAYGLDNASEGTFVYDLGGGTFDVSVLQTLKGLFEVKATGGNSALGGDDFHLRLFCYLLQNLRLSLEQDSQLLSLVRAAKEQLTQTETARIQATISDGMADTISI SRAEFHNLQRL
VMKTLRFVKQALKDAGVGKNEVKGVMVGGSTRMPHVQAVATFFGQTFPLNLPDEVVAGAAIQANVLGNKADGEWLLDVTPLSLGLETTGGLAEKIIIPNSTIPTARAQDFTTFD
GQTAMTLHVVGGERELVSDCRSLAKPTLRGIPPMAGAAARIRVTFQIDADGLLSVSAQEQSTGVQAIQEVKPSYGLDDTTITQMLKDSMGNAAEDMAARARAEAVVEASLTDVNALEL
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SEQ ID 5127

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SEQ ID 5128

VKGLDYCRQKAESRSSFLSGFRFLTQEKQDAVTVLVAFPRELDDVDECSNPVDAQATIANWRGDLNAPGGAMPPEHFNQALRVKETFKLPKYLEALIDGMQMDLVQARTGSFEELK
LYCRVAGVVGCLLARIILGFSDGKLTLEYADKMLGLALQTLNIIRDVGEDARRGRIYLPMEEMQRFDVPAVSVILQCSPTGNFAELWAFQIKRARETYREAVSLLPDADKKAQKVLVMAAVYY
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SEQ ID 5129

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SEQ ID 5130

MPPEARFAGSDGIAALLRSVYTONALQEQIILPQTPSGFLPCHRNHSRAQHTVGGQITLLHHTNHGIGFLITGHRHLRLMDIRIELIARFRIDFLDLRGLIKRLQLIQSHLHTHFQRIET
TALIKRHHQIILDRQHFGKLLSGELVRIGNFLVAAQVLLVCQAQLFVFLQRLQNLRLQILISRLGSLFLYTVRISYCLDGFHRLHIFNRFFTVLLLCPLAHIVSLKTNWKS
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SEQ ID 5131

TTGTTTTTAATCTCGGCTTCTTTGACCGGATCGTACGCATCCGAACCCCAAGCATATGGCGTGCAAAACAGCGATAAAACAGATAATGTTAATAGATTAAACCGGACCGCTTGTCTTCTTC
AGTGTCATGAGAAATTTCTTGTTCAGTGT

SEQ ID 5132

LFLISASLTGSYASEPQAYGVQNSDKTDNVRNLRPLACFQCHEKFSFVKC

SEQ ID 5133

ATGATGAACACCGCGCATCGCGCCCGAAAAATCGCGCTCATCGGCGAGGCTGGCGCGGCTTGTCCGCCGCCCTACCTTGGCGCGGCACGCCGAGTTACCTGTGTTGAAGCCGCGCGG
AGGCGGGCGGAAGGCGCGCACACTGGCGCGGAAATACCGACGGTTTCGGTTTGTGGCAACGGGCGAGCATTGTTGCTCGCGCATACCGGGCGGTGTGCGCTGATGAAACCATCGG
TTACAGACCCCGCTGCGCGCTTTTTCGCGTACCGCTGCATCGGATATGACGCGCGTTTGCAGTTTCGCGCGCTTCCCTTCCCGCGCGCGCTGCATATTTTGGGCGCGGTGCTGCTTGC
CGCGCGGTACCGTCCGATTCAGAGCCAACTGCTTGCAGATATGTCGATTTGCAAGAGTCCGCAACGCTCGGACAGCCGACACAGCAGTTGCAATGCTGAAACAGCGGAACGTC
CGCGTCCGCGCTAATGCGAGTTTGGCAGCCCTTGTGCTGGGCGCGCTCAACAGCCTTTGGAACCCGCAAGCTTGGCGGTGTTGTGCAACGTTTGTCCGACGGCGTGTGACGAAAA
ATCCGCGAGCGACTATCTCTACCCAAACAGGATTTGGGCGCAATGCTGCGCAACCCGCTTGGCGGAGCTTCAACGGCTCGCGCGGACATCCGCTGAAACCGCGGTATGCCGTCTG
AACACCTTCCCGGACGGAAGTCTCTGCAACGGCGAAGCTTTCGATGCCGCCATACTTGCACCGCGCTTACCAAGCCGCGCTTGCCTGCGCGCGCGCTGCGCGGCAATGCGGACGGCAGC
CGGATATCAAAACCTTGCCTACCAAGCCATCACACCTGTATCTGCGCTACCGCAACCCGCTGCGCTGCGCGCGCGCTGCGCGGCAATGCGGACGGCAGCAGCAGTATGCTGCTT
CCGGGCGAGGCTCGGACTGCGCGAAACGAGTCTCCGCGCTTATAGCGTTTCCGACCGCTGCGCGCGTTTGAACCCGGGCTGGGCGGAAAGCCACCGGACCTCAACGCGATC
CTTCCGCAATTTGGGCGAAGCCGAGCGGTGCGCGTATCAGCGAAACGCGCCCAACCGCAACCGATGCCCTTCCGCGGATTTGCTGTGGCTGCAACCGGACCGGTATCTTCCCAAG
GCGACTACCTCCACCGCACTACCCGCGCACGCTCGAAGCTGCGCTACAATCAGGTTTTCGCGTGGCGGAGGCTGCTGCAAGCGCTGAACGATGCGCTGCAAAACCGCGCGGCGAT
CGGACGCTTTACAGGTCGCGCAAAACGCTAAATACAT

SEQ ID 5134

MMNTPHPRPKTAVIGAGWAGLSAAVTLARHADVTLEAGRQAGGRARTLAGNTDGFGLNDGQHILLGAYRGVLRIMKTTIGSDPRAAFRLVPLWHRMHGGLQFRALPLPAPLHILGGVLLA
RRVPSAFKAKLLADMSDLQKSARLQPDITVAQWLKQNVPRAAVWQFWOPLVWGAINTPLETASLRVLCNVLDGVLTKKSGSDYLLFKQDLGATVAEPALAEQLRLGADIRLETRVCR
NTLPDGLVNVNGEAFDAALATAPYHAAALLPEGTPEHVQTAQYQNLRYHAIITVYLYRAEPVRLPAPLTGIADTAQWLLCRGLGLPENEVSAVSVSDRVGAFANRAWKAHADLKRI
LPHLGEPRVVRVITEKRATATDAPPDLSSWLHRRHIFPTGDYLLHPHYATLEACRTIRFRVGGSLPAKPERCRLKTPAGITGLYKVRQNAKTH

SEQ ID 5135

ATGCCGACACTGACGCAAAAACCATCTTAGTTACCGGCGCATCGCAAGGCTTGGGCGAAGAGTCCGCCAAAGCTTACCGCGCGGAGGGGCGACCGTAATTTGGTGGCAGCGCATCAGA
AAAACTGGAAAGGCTATGACGCGATTTGTCGAAGCGGACACCCGAACTTTCGCGATTCGCTTTCGACCTGATGAGTGGGAGGAAAGAAATTCGAACGGTTTGGCGCCACCATTCG
CGAAGCCACGCAAGGCAAACTGGACGGCATGCTCCACTGCGCGGCTATTTTACGCGCTTTCGCGCTGGATTTCGCAACCGTCCGCGAATGGGTCAACCAATACCGCATCAACACCGT
GCCCCGATGGGCTGACCCGCGCTGTTCGCGTGTGAAGCAGTCCGCCGAGCGGCTGCTCATCTTCTGCGCGGAAAGCCACGCGCAACCTGCTGCTCCCGCGCCCATCAATTCGCGCACGCAATCAAA
CGTCCAAAGCCGCTGAACCTACCTGTGCAAGTCCGCCGAGCAATGGGAACGCTTTCGCGCAACCTGCGCGCAACCTGCTGCTCCCGCGCCCATCAATTCGCGCACGCAATCAAA
CCATCCGCGCGAAGCCGAGCGAAGCGCAAAAGCTACGGGACGCTACTGCCCGCATTTTGTCTGGTGGGCAAGTCCGCAAGCAAGGCGGAGCGCGGAAATCGTTTACTCT

SEQ ID 5136

MPTLTDRTILVTGASQGLGEQVAKAYAAEGATVILVARHQKLEKAYDAIVEAGHEPFAIRFDLMSAREKEFERPAATIAEATQGLDGIHVCAGIFYALSPLDPTVAEAVNQRINTV
APMGLTRALPFLKQSPDASVIFVGESHGEPKAYWGGFGASKAALNVLKVAADWERFNGNLRANVLVPGPINSQRIKSHPGBAGSERKSYGDNVLPFVWASAESKGRSGEIVYL

SEQ ID 5137

ATGCGCGCGGAAGGTACGGATATTTTCAAACGGAAGCGCGCGCGGGGATGCTGCTTTTCCGGATTTAGAGGTAAACGATTTCGCGCGTCCGCCCTTTGCTTTTGGCACTTGCC
CACCAGACAAATGCGGGCAGTACGTCCTCCCGTAGCTTTTGGCTTCGCTTCGCGCTTCGCGCGGATGCGATTGATGCGTTGCGGGGAATGATGCGGGCGGGGACGAGGACGTTGGCGCGCA
GGTTCGCGAAGCGTTCCCATTCGTCGCGCGGACTTTGCACAGTAGTTTCAACGCGGCTTTGGAGCGCGCGAAGCGCGCCCAAGTAGGCTTTGGGTGTTTCGCGCTGGCTTTCCGCGCA
GATGACGGACGCGTCGCGGACTGCTTCAGCAGCGGAACAGGGCGGGGTACGCCCATCGGGCGACGGTGTGATGCGGTATTGGTTGACCAATTCGCGCGACGGTTTGGAAATTCAGC
GGCGAGAGGGCGTAAATAATAGCGCGCGAGTGGACGATGCGCTCCAGTTTGGCTTCGCTGGCTTCGCGCAATGCTGGCGGCAACCGTTTGAATTTCTTTCTTCGCGACTATCAGGTCGA
AACGGATGCGCAAGGGTTTCGGGTGTCGCGCTTCGACAATCGCGTCATAGGCTTTTTCAGTTTCTGATGCGGTGCCACCAAGATTACGCTGCCCTTCGCGCGGTAGGCTTTGGC
GACCTGTTCCGCCAAGCGTTCCGATGCGCGGTAAAC

SEQ ID 5138

MRAEGTDIFQNGSAARAGCLPFPDLEVDFAAPFFAFGTCPDKCGQYVVPFAFASGFARMGFDALRGIDGAGDEDVGAQVAEAPFFVGGDFAQVVRGFGRAEAPFVGFCFAVAFADE
DDGRVGRLLQREBQAGQPHRGDGVDAVLVDPFGDLEIQRRREGVKIAGAVDDAVQFALRGFGNGGKPFEPFFFRTHQVETDGEFGVSGFDNRNVIQPFQFLMACHQNYGRPGVGF
DLFAQALRCAGN

SEQ ID 5139

ATGAAAACCGTTTCCGCGCGCATCGCTTTTCCGCGCGCTGCGGTTTCACTGACCGGCTGTGCGACCGAGTCTCAGCGAGCTCGAGGTTCGAAAAGTCCGCTCTCGCAATACGCAATATC
ACGGTGTTCGCAACCGGATTTCCGTCGGAACATTCGACAACCGCTCCAGCTTCCAAAAAGGCAATTTTTCGCGACAGTGAAGACCGCTGCGGCGACCGAGGCAAAACCATCTCGGTAAACACA
CCTGCAACAAACCAACCGCTTCAACGTACTGAACCGCACCAACCTTTAGCGCATTTGAAACAGGAATCCCGCATTTCCGGCAAGCGCAGAACCTGAAAGGCGCAGATTATGCTGTTACCGCG
GATGTAACCGAATTCGAGCGCAGAGATGTCGGCGATCATCAGCTTTCGCGCATTTTGGGTGCGCGCAATCGCAATCGCTATGCAAAAGTGGCTCTGAAATATCGTCAACGTCACATCTT
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AATCCGCGAAGCGCTGACAACTTGGTTCAAGCTGTGACAACCGCGCATGGAATCCAAACCGT

SEQ ID 5140

MKTVSAALAFAAAAVSLTGCATESSRSLEVAKVASCNTQYHGVETPI SVGTDFNRSFQKGI PDSSEDRLSQAKTILVTHLQQTNRNFVNLNRTNLSALKQESGISGKAQNLKGADYVVTG
DVTPEGRDVGDLQFLGILGRGKSQIAYAKVALNVLNVTSEIVYSTQGAAGEYALSNREIIGFGGTSYDATLNGKVLDLALREAVDNLVQAVDNGAQNSNR

SEQ ID 5141

TTGCGGAAGCGCCCAACAAAAAATGAATCGCGCGCGGGTGGCAGCGCCCATTTGGGACTGCTGCTTTCCCGTTTCGGGAGACAAAGAGGGCGGCTTCGCGCAATTTGAAGAAGAGAAAA
GGCTGTTTCCCGAATCGGGCGTATTATGGACTTCTGATGAAAACCGGTAAGGAGGCAAGGCA

SEQ ID 5142

LRKPPTTKMNAAPGAHAHLGLLLSRSGDKGAPROFEEKRLFPESGVFMDFLMTGKGGKR

SEQ ID 5143

ATGAGAAATTTTCTTTTGTCAAGTGTTAAAGTTATAATGATTATATATACACTACATCGCAATGAAAAATCGGGAAAAACAAAAACCCCTCCGCGCTCATTCGCGGAAAGCGG
GAATC

SEQ ID 5144

MKNFPLSSVKVIHIIYITLHNEKSGTKNPSAVIPAKAGI

SEQ ID 5145

CATTTTCGTCGCTTTTCCAAACATCACCGCAAACTGCGGCAAAATCCGCGCGCGGCTCCGCCCTTCAACACAGCGGCTCACCGGTAGCGGATGGTTAGGTCGACGCTCGGACGCGTGCAAA
AACATGCGCTTCAAACCAATTTTCGCAACGCGGTTGCGCTGATATCGCGTAGGCTTCGTCGCGCGCAATCGGACAGCTTGAGATTTCAGATGCACGCGGATTTGGTTCGTACGCG
CGGTTTTCAGCGTTGCCCGCACCAAGTACAGTTCGCGCAGCGCGACACCGTGCAAAATCGCGCTCTGAGAAACGCGTTAACAACAGCAACACGATATGCGCGGACTGCCCGCTCTCGCTGAC
GCGTACCATCTTTTCGCTTGTGCGCGCGGTATTTTGAACAGGGGAGTTTGACATGGAATTTGCTGCTCCGCGAGTTTGCCACCCCGCAGCGCAAGGTAGATTTTTGGGGTGTGCTGTTA
CGGATAGCTTTCGAGTTTTCGAGGAGCGCGCTGCTGCTTCTTCGCCACCATCAACAAGCGGCTCGTATCTTGTCCAAACGCTGGACCACTCAAATACTTCGCGCTCGGACGCGGCGCGG
GCAACTGTTTCGATTAAGCCCGGAACTCACGCGCTGCCACGCTGTACCGGCAACCGGAGGCTTATTTGACCAACAGTACGCGCTGCTCCTCATACACACTCAAACGCGACGCGCGGCTAC
GGCGGCAAGCTTTTCAGACGGCATTTCTTCTCGCCACGCGCACAGGCGGAATCGCACCGGTATCTCCCTCCGCAATACGGCTGTGCGGTTTCGAGCGTTTCTGTTTAAACCGCACCTCG
CGCGCGCGATTAATCGGTGGATATAGCCCTTGGGACGCGCTTGGAGATTTTTATCAGATAGTTATCAAGGCTTGACCGCGCTCATGTCGCAACCCCTATCAGGCTGACCGAACCTT
TGCTTATTTCTGCGGTTTTCAT

SEQ ID 5146

HFRPVQPHRLQIRRRRLRLQRLTRERMVQVLGRVQKHALQTQPLQTPVRLIIAFAVARNRTRALRLQMHADLVRTARFORCPHQSQVRQPDVQNAV*ETA*HTEHRHRLPVLAD
AYHLFALCAGIFEQGFIMEIVVRQFAHPQRKVDFFGVVTDSPVQPDERAFLRHQQAARILVQTVQDLQILRLRTGAALQFLPNAETHAAATVYRRTGRILIDQ*RVVLIHLHRLKTRRY
GGTPPRRHLRLHARRNPHRISLNTAVGFAFLVQPHLAGADNAVDIALGHALEDYQIVIKALTRLMFNGPNYQADRTTAYFVRFH

SEQ ID 5147

TTGGAGATGTTCAAATGAGTCGTGAAATGTTACAGCTGGCAGAACCTGGCAAGCGAAAAAGCGTTGATGCGGAAGTCGTCCTTCAAGCACTGGAATTCGCACTCTCTACCGCGGCCA
AGAAAAAGGCGAGACCGCGAACACATGGACGTGCGCGTCCAAATCAACCGCGATACCGCGGAATACCAAACTTCCGCGCTGGCTGATTGTTGGCGGATGAAGACTATACCTATCCGATGT
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CAATCATCTCGAACGATCCGCGATCGCGAGCGGAGCAGAACTGAACGAGTTCTCGCGCTCAAAGAGACATCGTGTCCGCGCAGGTCAAACCGCTCGAAGCGCGCGGATCATCG
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CACCGCGCGCAAAACATCATCTGAGCGCTACTTCGCGGATTTCTCGTCAAACTGTACGCGCAATGAAGTACCTGAAATTCGAGCGCATGCTTGAATTCGCGCTGTGCGCGCGGAC
CGGGGCCAAGTGCAGGTCGCGCTCAAAGGCAACGACGCGCATCGATCCGCAAGGCACTGTATCGCGCTTCGCGGTTTCGCGGTTCGCGGTGCTCAATGCGCTGAGCAATGAATTTGCGCGGAGC
GCATGAGCTGTCTTTCGTTGTCGCGGAGCTGCGCAATTCGTCATGAGCGCGCTTCACCGCGGAAGTACGCGCATGCTATCGACGAAGACAAACGCGCTGATGTCATGTCGTTG
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AACTGCTTGCATTTGAAGGATTTGACGAAGAAATCGTCGATATGCTTCGCAACCGTGCAGCGGATGCCATCTGACCATGGCGATTGCTGCCGAAGAAACTGGGCGAAGTGTCCGCGA
TATGCTTAACCTCGAAGCGGTAGATGCGGATATGCTCTCAGCTTTCGCGAAGCAGGATTAACACCGCGCAGCACTTGGCAGAGCTTGGCTGGACGAACTGATTGAATACCGGTGTA
AACGAAGAACTGCAAAAGCGGTATCTGACCGCACCGCAACACTGCTTACCGAAGACAA

SEQ ID 5148

LEMPKMSREMLQALAEALASEKNVDAEVVQALFALSTAAKKKADREHMDVRVQINRDTGEYQTFRRWLIVADEYTYPDVEKTIIEIIEIPEIDPTTIQIGEYEBQLNEPFGROAAQPAK
QIILQRIRDAERQNLNEFLAVKEDIIVSGTVKRVERHGIIVVAGKLDALIPROQMI PRENFRSGDRIRALFLRVEEIGNTGRKQIILSRTSGDFLVKLYANEVPEIADGMLRRAVAR
PGQRAKAVKANDQRIDPQGTICVGRGSRVNAVSNELSGERIDVVLWSPEPAQFVMSALSPAESVRIVIDEDKHAVDVIVAEDRLALAIGRGQNVRLASDLTGWQLNIMTSAEDERNA

EDAAIRRLFMNHLNVDEETADVLVQEGFATLEEVAYVPAEELLAIEGFDEEIVDMLNRNARDAIL/TMAIAAEKLGESDDMRNLEGVADMLLSIAEAGITTRDDLAELAVDELIEITGV
NEETAKAVIL/AREHWFTEK

SEQ ID 5149

ATGCCCTTCTGCTGCCGAACCCCTTGACCTCGCTGACGGTACGCCGTAATGCCGATTTCCGTCACCGCTCGCGCAGCTGTCGAGCTTGAACGGTTTGACAAATCGCCTCGATTTTT
TTCATAAAATTTCTTTGAACAAACAAATACAAACACATCCGAAAAACGGGAACCCCGCTCAGATTGTCAACATTTTAAACCAAAATACCAAGCAATACAGCCCCGTTGCGCATATAAT
GACAGCTTTTCAACCGCATTTGAGAGCGGAATCCATGTCTGTGTGTTTTCGCCCTTGGCGGGCTTACCGCCCTTTCGATTTCCGTGTCGAAAACTCTTGCAAAAAGCCGCCCATCGG
CCTGCCGAAGTCAAAATTAAGCAGCGAATTTGGTATTTCCGCCGCGAGAGAAAGCACT

SEQ ID 5150

MPLPAEPFDLADGHARNADFRQLAHVVELERFDNLDFFHKISFEQTIQTHPKNGNPSPDCQHFKPKYPSHTAPVAHIMTAFPTAFESRIHVCCFALARRYRPFPPCRKTLAKSRRT
PARSQIKQILVFRQREST

SEQ ID 5151

TTTGAACACCGCTTTAAACGGCTTGATCAGCACTTCGCTGTACAGCGCGCATGAACATAGGGATCGTCTTCAGCCCAAGCTTGGCGCGCATCCAAGACTCGAACTGTGCCACAATCAAG
CTGCCGAAACACGCTTCGGGATTGTCCGCGCAGCAGGTTGGGCCCTGCCGTGACGAGACGGCTTCCGATTTACAGCTTTCAGCGCTTTAAAGTGTTCGGGACGTGCCGCCATACGCGCTT
CATGCACATCTCCCGCTGTGTGCCAGCAACATAAATATCCACAGTCAA

SEQ ID 5152

FEHRFKRLDQHPVAHAGMNIGIVFSPSLRRIQRLELCHNQAARNTFGIVRQVWACRQQTAFRQRFQPFKVFGTCTRHTRFMHILFVCCQHQHIFHSQ

SEQ ID 5153

TTGGCGGAACGCGCCCTCTTTGTCTCCGAACGGGAAAGCAGCAGTCCAAATGGCGCTGCGCACCCGGGGCGGCATTCATTTTTTTTGTGGCGCTTCCGCAAGTATTTTTCCATCTT
TTCGCTCTGCTTGGCCACAGAGTGTCTGCTGTTTTTCAACCTTCATAGACGATATCGGATAACCGCCGTAATAATACAGGTTTTATGCCCGCGCGCGCAGCGGTGAGAGCCAGAG
CGCGCACACAGCGCAACACGGCCCAAGGTTTTTCGGATTCATCTCTCT

SEQ ID 5154

LAERALFVSRTGKQSQMGVTRGGIHFPCWRLPQSIFFPSFSACPTKCRFPNLRHRYDRNRNNTGFYARRRQAVRAKTAHSDKRPKVFPGFIISP

SEQ ID 5155

ATGAACCTTTGATTTTAGGGCTTGCCGCGCTGTGGCTCTGTCTGCCAGTTCGAAAAGCTCCGACCTCGACTACAGTCAATCAAGAAAGCAACCGGCTTCAATTTTTGGTG
TTCGCGCGCTGAACAGTTCGCTGATGTCAACGGCACTTGGGGGATGCTGGCTTCGACCGCGCGCGGATTTCCGAAGCGGCTATTACGCTTTCCCGCGCGAGTCTGGAGGAACCTT
CAAGAAACCGGCTTGACCAATGCCCGCATATTCACGCCGTCCGGCCGGAAGAACTGCATCAAAATTTCCGCAATGATGCGGTTTTGTACATTACGTTACCGAATACGGCACTTCATAT
CAAAATTTAGACAGCGTGACGACCGTATCCGCCAAAGCAGCGCTGGTTCGATTCCCGCAACGGGAAGAGTTGTGCTGGGTTCCGCCAGCATCCGGAAGGAGCAACACAGCAACAGCG
GCCGTGTGGGGCTTTGTTCGGCGCAGTGGTCAATCAGATTGCCAACAGCCTGACGACCGCGGTTATCAGGTTTCCAAAACCGCGCATACAACCTACTGTGCCCTATTCCCGCAACGG
TATCTTGAAGGTCCGAGATTCTGCGAAGAGCAGCCAAA

SEQ ID 5156

MKPLILGLAAVLALSACQVRKAPDLDTYSFKESKPASILVPPPLNESPDVNGTWGMLASTAAPISEAGYVFPAAVVEETFKENGLTNAADIHAVRPEKLEHIFGNDVLYITVTEYGT
QILDVTTVSARLWDRSNGKELWSGSASIREGSNNNSNGLLGAIVGAVNVQIANSLTDRGYQVSKTAAYNLLSPYSRNGILKGPFRFVEQPK

SEQ ID 5157

ATCGAATCTTGATCTTGCAAGCCGACCGCCCAAAATCAGCGCAGCGGTTTCAATATCCGAACAAGGTTCCGGTTCTGTATTTTGCAAGACCCGAACCTTTTATTCAAATTTAAACTTA
ATTCCGGCGTGTGTATGG

SEQ ID 5158

MRILILASRTAQNGATGNIRTRFGFCILQNFNLLFKPLNSGVVVW

SEQ ID 5159

TTGCAAGCCGACCGCCCAAAATCAGCGCAGCGGTTTCAATATCCGAACAAGGTTCCGGTTCTGTATTTTGCAAGACCCGAACCTTTTATTCAAATTTAAACTTAATTCGGCGTGTGT
ATGGTAAATTA

SEQ ID 5160

LQAAPPKIRRPVSISEQSGSVFCRTTFFYSNLNLIIPAWLYGKL

SEQ ID 5161

TTGTTAATCCACTATAACAAGCAATATGCCCTGACCGGCAAAACTTCCCAAACTTCATCAAAAATCAACTGTACCCGCTTTTTTCAGACGGCAT

SEQ ID 5162

LLIHYNKQYALTGKTSNFIKKSTVPVFFRRH

SEQ ID 5163

ATGGGAATCTCTTACGGTATCAATGCCGTCTGAAAAAGACGGGTACAGTTGATTTTTTGATGAAGTTTGGGGAAGTTTTCGGGTACGGCATATTGCTGTGTA

SEQ ID 5164

MGNLLRYQCRLLKKTGVDLFMKPGEVLPVRYCLL

SEQ ID 5165

ATGCAAAACCGCAACCGAGCTTTATTCACCGCGCTTGGCTGTTCAGACCTTATTGATGATTACCGCGCTTCGGCGGTGATTCTGTTTTTCGCGCGCAACACCGCTTGGGGCGG
AGTTTGCCTATATCTCGCGCTTTGCCGTGACCCGAAAGCAGCGTCAAGATATGCTGCTGATTACGGCAATGTTACGCTGCTGTTAACCGAAGTCCGGTTGAATGTGTGAGTACCTT
CATGTCCAAGGACTTTACGATTTCGATGACAGGATTTGAATGCTTCGGCATTTTGGATGTTTCAGCGATGAACCGCGCGTGGTACTGATACGGCGGTTTAAACACGTCGTTCACGACTTT
CTCGAT

SEQ ID 5166

MONRQTELYSTPSWLLQTLIMITAASAVILFFARNWRLGREPAYILRLCLTPKSTVKVLLILITAMVTLILLFEVRLNVLSTFMSKGLYDSMQLNASAFWMFAMNAGVVLIRAFNVNVND
LD

SEQ ID 5167

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CAGCAATGTCGAGCAGACTTAAAGCCATCTACGAACGCGATCCCGCTCGCAGCAATATTTCGCTGCGCTTTTATATTTCAAAGGCTTCCACGCGATTCAGGCACACCGCATCAAC
CACCAGCTGTATCTCGACGAGCAAAAACGCTGGCGTATTTCTACAAAACCGTATGTCGGAAGTATTCGCGTGGACATCCACCGCGCGCGCTTTAGGATACGGGCTGATGCTCGAC
ACGCCACCGGCTTTGTGCGGAGAAACCGCGCTGTGGGCAACAAATTTTCGATTTTGCACGCGCTAACCGCTCGCGGTTTCGGGCAAGAAGGCGCGACCGCACCCCAAAATCGGCA
CGCGGTGATGATCGCGCAACCGCTCGATATTGGCAATATCCGATCGGCGCAATGCCAAATCGCGCGCGGCGAGCTGCTGTTTTCAGAGCTGCCCGCTCCATCAGGTTGTGCGG
GTACCGCGCAACCGCTGGCGGATCGCTCAAAACCGCTCGCGGATATGATCAAAATTCAGTTTGCAGAAATCGACTTTATGAT

SEQ ID 5168

MKNHLATTFGLMHTIREETAATAAAAEPLASFLHQTVLRHRSLSVLAHYLSSKLGSPIMDVRLFEIYQALGSDTQISKVEADLKAIERDPACDEYSLEPLLYFKGFHAIQAHRIH
HRLVLDGRKTLAYFLQNRMSVFPVDIHPAARLGYGLMLDHATGFPVAGETAFLGNISILHGVTLGGSGKEGGDRHPKIGDGMIGANASILGNIRIGSMARIGAGSVVSDVPPSITVVG
VPAKPVARSILKTPSADMDQNIQFARIDFMI

SEQ ID 5169

TTGAACCAAGAAACATCATCGCCACACCCCTCCGAAAAGCGGTATTGTACAGGCAAAACCGCTTGGGAAACGTGATAAAATCAGGCGGA

SEQ ID 5170

LNQENIIAHTLPKSGIVQANRLGNVKSOG

SEQ ID 5171

TTGGCGATTAAATGGTCCGAACGGCTCAATGAAGTTTTGACTTCGCGCTGGCTTGGCGCAAAAATACTACCGCTGCAAAATGCGCCGCCACGGCCGGACAACATCGACCAGCGTATCC
AACAGGATGCGCAGGAATTCATCGCTTCGACCATCGAATTTGTGCGCGCATGGTCAATTCGTCGTTACTTCTCTGGAATTTGCCGTTGTTTTG

SEQ ID 5172

LAIKWSERLNEVLTSRWLADKNYRLQMRHAPDNIDQRIQDQAEFIASSTIEFVRGMVNSVVTSLFAVVL

SEQ ID 5173

GTGCGGAATGTGCAAGCCGAACACGGTCAGGATGCCTGCCAAGCCCTACAAAAACAAGCGCAAAATCCAGAGAAGTAACGACCGAATTGACCATGCCGCGCACAAATTCGATGGTCGAAGCG
ATGAATTCCTGCGCATCTCTGTGGATACGCTGGTTCGATGTTGTCGCGCGCTGGCGCGCATTTGACAGGCGTAGTAGTTTTGTGCGCAAGCCAGCGCGAAGTCAAAATTCATTGAGCC
GTTCCGACCATTTAATCGCAAGCCTTAATCGAGAAAGTCGTTAACGACGTTGTAAACGCGCGTATCAGTACCACGCGCGCTTCATCGCTGCAAAATCCAAATGCGCAAGCATTCAA
ATCTGTCATCGAATCGTAAAGTCCTTTGGACATGAAGTACTCAACATTTCAACCGCACTTCGGT

SEQ ID 5174

VRNVEAEHQDQACQALQNGKQPSNDRIDHAANKFDGRSDEFLRLILDLTVDVVRVAHLQAVVVFVGKPARSONFIEFFPFPNRQALIEKVNDVVRFPYQYHAGVHRCKHPKRSIQ
ILHRIVKSPGHEGTQHIQPHFG

SEQ ID 5175

TTGGCAGGCATCTGACCGTGTTCGGCTTCGACATTCGCGACGGCATTTGTTGGTTTGTCTTTATTTTCATGATTTTGGCGATCTTTATCGCCATGTGGATAGGCAACCCCTTGATTGCTT
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CCGCTTTAAGCCATTATTCGCAACCGTTGGCGCATCGCGCGGCAAGCGTCTGCTTAAGCGGCTTTAACGATATGTTTACCAACGGGCATCAAACTCTTCTGATTATTTTGAAGCTCCG
CGCTGTTTGGCGGCAAAATCAAAATCGCGGACATCCAGCAGACCGTCCAAGCCTTCGCGGACATGCAAAACGCGCTGCTTTCTTCGAAATGTTCTACAAACAAATTCACCGCTGCCAGC
CCGACTGGAGCGCTCTGATCGTCTTTTCTGCTGAGTACCGAAGAACACACGCGCGCAGCAACCCGAGATTAGCGAAGTTTCAGACGGCATTCGACTGGAAACGCTCGCCCTGTTCGCGCA
CAACGGCGAAGTTTATTTGGACGGCATCAACATCAAACTCAAAAGCGCGGATTCCCTGCTGATACGCGCGCCGAGCGT

SEQ ID 5176

LAGILVVFQFDIPHIVVFVIFMILAIPIAMWIGNPLIRYNYENKKLNGDYRSLILVRDHAESVAFYSGEQHEHGRLSDRFKAIIRNRWRIARQSVCLSGFNDMFTNGIKLFLITLQAP
RLFAGQIKIGDIQQTQVAFARLQNALSPFRMFYKFTACHARLERLVFLSTEBQHAQQPEISEVSDGIALENVALFRENGEVLLDGINIKLSGDSLLIRGPSG

SEQ ID 5177

ATGAACACCTGCGCTTGGTTATCTGATTGACAAATTTGGATAAACAAGCGCTGGCAGCACAAACTCTCCCGCGCAACTGCAACGCGTGCCTTCGTCGCGCCCTGCTCTCCAAGC
CCAAATCGTCTGCTCGACGAAGCGCGCGCGCTTGGACGAACCGCGCAAGCC

SEQ ID 5178

MFTCLGYLIDKLDKTDGQHLSPGELQVAFVRALLSKPKIVLLDEAAAAALDEPAEA

SEQ ID 5179

ATGCCGTCTGAAAACGGCTTCAGACGGCATCGTTACGCCGAGGCGAGCTTCCGACATCGAGGTGCATATTCGGAACGCGTTGAGCGTACTTCGGTGTCCGATACTGATGATGCTGTCCG
GGCAGTTTTGCTT

SEQ ID 5180

MPSENGFRHRSAAGSVADIEVHIAERVERTSVSDTDDAVGQFL

SEQ ID 5181

GTGCTTTTCAATTTGAACGATGCGCTGAAAAACGGCTTCAGACGGCATCGTTACGCCGAGGCGAGCTTCCGACATCGAGGTGCATATTCGGAACGCGTTGAGCGTACTTCGGTGTCT
CGATACGTATGATGCTGTGCGGAGTTTTCGCTTTAAGGCGCGG

SEQ ID 5182

VSFQFERCLKTPASDGIQVQALPTSRCLRNALSVLRCPIILMLSGSPCFKAR

SEQ ID 5183

TATTAATAACGCACTCCGCAAGCAATTTCCCTGCGCTGTTCAGCGCGGAGGCGAGAGCTAGTCAAGTTTGAATTTGATTTTCCGCTTTCGCGCGGAGTAAGACGGCAGCGGAGC
CCCA

SEQ ID 5184

Y*KRTFQSIFPAPVPSRQANVVKFELILFFRRSGKTAEPQ

SEQ ID 5185

GTGAACACGCTTTGAACCAAGAAACATCATCGCCACACCCCTCCGAAAAGCGGTATTGTACAGGCAAAACCGCTTGGGAAACGTGATAAAATCAGGCGGATAAAACAAATCGAATAAATCCT
TACCGCAAAACGGAGGCAAAATGCTCAAAATCCATCGAACTCAATTCACATCCGCAACCGCTTGCAGCATATCTGAAAGCGAGGGTTTGGATTTTCAGACGGCAATGCAGGAAGAAGA
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SEQ ID 5186

VKQLEPRKHHRPHSEKRYCTGKPLGKRDRIIRINKSNKSLPQNGKMLKSIENSHIRNRLAAYLKGRGLDFQTAMQEEGNKEIAIVHSGLPTLVRLKLYSEDKMQKFFWEKRLIADY
ISRRMQG

SEQ ID 5187

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TGGCGCGCGCACGCAAGTAACCGTCGATTCGAAATTTTCGAATACCTGCTCAAACTGCGCGCGGATATGGACAGCTGATGATGATGCTCGACAGCTGGACAACTACGCGGTAAC
CATGGGCAACGCATCACCTCGCGCTGCTTCCGACGCTTTTGAACACAGGAACCCAA

SEQ ID 5188

VNQLIFDFAAHDPSPFKFLGTENALVYVLQHKHDPFTYVWEEGAGKSHLLQAWVAQALEAGKNAAYIDAASMPLEDAFEAYLAVDQVEKLGNEBQALLFSIFNFRFRNSGKGFLLLG
SEYTPQQLWIREDLTRMAYCLVYEVKPLTDQEKIDALANMAAARQVTVDSSEIPEYLLKHWRRDMSIMMLDLDNYAVTMGRITLPLLRQLLQKQETQ

SEQ ID 5189

ATGAAAAACCTCGCATCTTCGACCTCGACAACACCCCTCATCAACACCGATTCCGACCACGCTGGCCGCAATACCTCATCAAAAAAGGTTGGTTGACGCTGCCGAAACCGAAGCGCAAA
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CCCCGATCGCAACTGGAAGAAAGCAAGCAAGAAAGGCTGCCCGTTTGAATTTCAA

SEQ ID 5190

MKNLAIFLDNLTINTSDHAWPQYLKKGLVDAETPAQNEKPYRDYQNGCLDIDAFLLKHLPLARYSKEELAEFHREFMAEYIIPHISPMQRLVQSHQMGDETLLVSSNEFLITP
VCRLPGIANNITQLETPGDRGTGNVIGTSPSLKEGKITRLNQLAERGETLESYGKTYFYSDSKNDLPLRLVSEPVAVNPDAELEKEAKEKGNFVLPNK

SEQ ID 5191

ATGCGCTCGAAGCCGATTCCGCGTTCAGACGGCATTGAGGCTGAAATCCCAAAACCAAGCCACAGGAATTCATCGGGAACCAACAACTTTCCACCGTCATTCCACGAAAGTG
GGAATCTAGGACGTAAATTC

SEQ ID 5192

MPSEARFVQTAALRLKSQPKATGIHREKQSFHRHSHEGSLGRKI

SEQ ID 5193

GTGGGAATGAGAAATTTCAAAGTTATGGCGTTATCGGAAAAACAGAAATCAAAGCCGAGAAATTTATCCAAACCAACCGATTTCAAAAACCAATTCGCGCGGGAATGACGGATT
TTAGGTTCTGTTGTTGTTCTGTTCTGCTCGGAA

SEQ ID 5194

VGMTKQSYGVIGKTENQSRRIYPKQPDFKTKFPAGMTDFRFLMFLFARB

SEQ ID 5195

ATGCGCGCTTTGGCGGAAACCTGTTGTCGGTTTCTGTTTGGGGTTTCGGGCAATTTCTAAGTTGTTATTCGCGAGCAAAACAGAAACCAACAGAAACCTAAATCCGTCATTCCT
GCCGGGAATTTGGTTTPTTGAATCCGGTTGTTTGGATAAATCTCCGCTTTGATTTCTGTTTTCGCGATAACGCCATACTTTGAAATTTGTCATTCACCGCAGCGCGGAATCC
AGACCTGTCGCGCAGGAACTTATCGGAAAAAAGTTTCTT

SEQ ID 5196

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SEQ ID 5197

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SEQ ID 5198

MEFENIISAADKARILAEALPYIRRFSGSVAVIKYGGNANTEPALKEGFARDVLLKLVGIHPVTVHGGPQINAMLEKVGKGEFVQGMRTDKETMDIVENVLGGHVNKEIVSMINTYG
GHAVGVSGRDHPHAKKLLVDTPQNSVDIGQVGVESIDTGLVKGLIERGCI PVVAPVGVGKEGAFNINADLVAGLAELNAEKLLMMTNLAGVMDRTGNLLTKLTPKRIDGLIADG
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SEQ ID 5199

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SEQ ID 5200

MMFSWPKLPHLFPVVISWFAGLFYLPRIFVNMAMIDAPRGNPEYVRLSGMAVRLYRFSPLGFAGVVFAGAI PFAAGRWGSGNVHVKLCLGLMLLAYQLYCGVLLRRFQDYSNAPSHRWVYV
PNEIPVLLMVAALYLIVFKPF

SEQ ID 5201

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CTTCTTTATCCGACCTTCCGCACACGGTTCCCGGAACGTGCATCCCTGCGGATTTTCAA

SEQ ID 5202

KTHSAKHFPACSQPAGAERSQV* IDFAVSARK* DGSGAPSPERKPPENTGITIITRRSRPFRPQRSERGRQTAASIFIAFFIRPFTRFPGTCTIPADFQ

SEQ ID 5203

TTGTCGGAATCAFTGCCGACTCCGCGCTTTACAAGGAAACCGGTTATTTCCGGTTGCGTGGGAATCGGCGTATCGAATAAAGGCAATTTGTCGCACTGATAAGTCCGCGCATCGCG
GCATATTAAGCGCGAGGCTTGAAGCGGCAATGCCGTC

SEQ ID 5204

LSLSLPDSARLQGNRLFPVAVESGVSNKRHFVRLISAGIGGILRRRLLEAGNAV

SEQ ID 5205

TTGTTGACAATTTCCGCTTATGTTAACGCCAAACGCGCTGTAACCAATCTTCAGACGCGCTTTGGCACACCTTCGCGCAGGTTGAAGCTTTCGATACGCGCGG

SEQ ID 5206

LLTISAYVNAKRLKQSSDGVWHFTFGQVEALRYGR

SEQ ID 5207

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SEQ ID 5208

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SEQ ID 5209

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AC

SEQ ID 5210

MI THQFPDVLISIGPLAVRWYALSILGFLPFTFLRRRIAQGLSVPTKESLDDFLTWGILGVILGRLGYVLFYKFSYLAHPLDIFKVBEGMSFHGGFLGVVIAINWLSRKHGIGFL
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SEQ ID 5211

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SEQ ID 5212

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SEQ ID 5213

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SEQ ID 5214

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SEQ ID 5215

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CCGTC

SEQ ID 5216

LFEHMLPIETERRFLIENDKWRQYADEPLLLKQYLSVEKERTIRIRIAGKRAWLTLKGYISEISRSEFEYELPLADEKMMETMCPFKMKRRYPVRNGSLFEVDVFLGENSPLVVAEI
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SEQ ID 5217

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SEQ ID 5218

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SEQ ID 5219

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SEQ ID 5220

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SEQ ID 5221

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SEQ ID 5222

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SEQ ID 5223

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SEQ ID 5224

MSGIAGIEGHPFRMDTVTVYSKATQPLGKGRVLFSGAAEDLLKSRKAGVFIHRDWISITPEIRILLTFE

SEQ ID 5225

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SEQ ID 5226

MSNTQKQALAKAAKSVNTADAEKNRALLAMADSLAAEDILAAANRLDKAAAGKIPDSMTDRILLDGKRICAMADGIRAVAAPDPVGEILETSTLPNGLEIVKRVAMGVIGIYE
SRPNVTSDAALALKSGSAVLRSGKDAFQSAATVAALKTLGATQTRIDPEAVQLIEDTGRGSEYEMRAKDYLDLLIPRGAGLIRAVVENAVVPVITGTGIVHIIYDKDADWDKALRI
VYNAKTRPSVCNMEVLVHIEGIAADFLPKLERLLVGRIEAGLPPVFRIDPQAARYIGGEAAGADDFTEFLDYILAVKTVASVEEAVGHIEARGTHRSIDGIVTENRHAADFTTHID
SAAYVINASTRTDGEFGLGCEHISTQKLRHARGPMGLKELTSYKYIVQGTQVRE

SEQ ID 5227

TTGATTTTTTGCAAATAGAAATGCCGCTGTAAGACTGTTTCAGACGGCATTTTATAGTGATTAAACAAATCAGGACAGGCGCGGAAGCCGACAGTACAAA

SEQ ID 5228

LIFLIQIEMSEDCFRHFYSGLTKIRTRRSRRQYK

SEQ ID 5229

TTGGAAATCATGTAATGCCGCAAGATTAAAGGAAGGGCGGCTATTATACGTGTCGGCGGGGCAAAACCGAAGCGCAATCGTTTCGCGCAGAAITGCGCGCGGTTGTTTTTTTGG
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GTGCGGATGTTCCGACCGCATCCGACGGGTATTCAGACAGTGAAGAACGGGACGGAGAGCGGAAACCGGAGCAGCAGAGCTGCGGAGGAGAGGCTGCCGATACGGAAGACATTGCAAC
TGCGGTATTCGAACACCGCGCATCCCATTCGACCGGAGTATTGCTGAAGGTTGATGAGCTGTAAGGCAAACTTGCCCGTCCGTCGCGTTTAAAGGAAATCACTTTGGAAGAAGCA
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GTTTCAGACGGCACAGCGCTCCGCGATGCCCGCGCGGCTTCCGCTCAATTTGAAAGAACCGGAACAGGCAACGCTTCTGCGGAGGCGCGGATTTGCGCGCTGATTCGGAAGTCCGGA
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CGCGCGGAGGATTGAGCAGGCGCAACGACGCGCATTCGGAACCGGACCATCTTCGCGCTGATGTTTGAATGGAGGTTGCGAGGAGGAAACCGCGCTATTGAGATGACGCGAGTG
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CCGATCCGATGTACGACAGGCGGCTATCTGCTGTCTGTAAGAACCGCAATGCGACGATTTTCGGCGCTACAGCGCGCTTTCGCGATCGGCTACAAACCGCGCCGCGCTCGATTGACCAAAAT
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SEQ ID 5230

LEHNHNAAKIKRGGGYITVGGGKPKAESVSASLPAAGCFILGNKHVKINSVNRSLSCGRHMFIVILVILVILLALAGLGFVRAQSEREMHREVSANQEKKGKQAELEPKDGHDPDFEFSLH
LPHAVKTAVVYVFLVGVVPRPCRNLIHAHESEDPDRPVPASANRADVPITASDGYSDSNGTEEAETFAAAAEAEAAEDTEDIATADVINNRIFPDRISNAGLQMSKTSVPVRPFVKITLREZ
TRALSSAALRETKKRYIDAFENKGTAVPKVRVPTPMEGLQIIIGLDDVFLQRTYSRMFPADKAEFSESADYGEPEFYKQHPASFAVSAKNAEARNAPFRRHAGGKQKQAEAKSPDVSQGS
VSDGTAVDRARRRVSVNLKEPKNATVSAEARISRLIPESRTVGRKDVMEPSETENVPTITVSVGGYQGYDPEADIIHEPAADPAWVVEPEPEVAVPEIDILPPVPVSEIYNRTYE
PPAGFEQAQRSRIAETHDLAADVLNGWGQEETAALADDGSEGAAEERSGGYQLSETEAPGHDSQAVCPFEDVPSESRPSCRVSDEADBGAFQSEETGAVSEHLPTDILLPLFPNPEATQTE
ELLENSITIEBKIAEFKVKVKVVDYSGVPVITRYEIEPDVGVGRNSVNLNEKDLARSLGVASIRVVETIPGKTCMGLLELPNPKRQMIKRLSEIFNSPEFAESKSKLTLALGQDITGQPVVT
DLGKAPHLHLVAGTIGSGKSVGNAMILSMLFKAAPEDVRVMIMIDPKMLEISTYEGITHLLPAPVVTMKLANALNMVNVNEKKYRILSLMSFGVRLNLAGFMQJLARAARAEKIGNPFSLTP
DDPEPLEKLPFIVVVDEFAVLNMTAGGKIKELIARLQAQARAAGITHILATQRPVSVDITGLIKANITRIAPQVSSKIDTILDQGAENLGGQGLMLPLPGTAYTPQRVHGAFASDE
EVRVRYLKGFGSEPDVDDILSGGSGEELPGLIGRSGDQKAPTHIDEAVSVLRTKASISGVOBALRIGTVNARLIDHEAGETVSAPEHNGMRTILVPLVLA

SEQ ID 5231

ATGTTATTCAACGCAACGCAAGGCGGAAGAGCTGCGGTTGCCATCTGTCGACGGACAAAACCTGCTGGATTTTGGACATCGAAAAGCTGGGCAAAAGAACAGCGCAAAAGGCAATATCTACAAAAG
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SEQ ID 5232

MLFNATQAEELRVAITDVGQNLLDLDITFLGKQQRKNGYIKGIITRIEPLSEACFVDYGTDRHGLFPFKEVSRSYFLYGEGRARIQDVULKEGHEVTVQVEKDERGNKGAALTFFISLAGRY
LJLMPNNPRGGVSKRIIEGEERQELKAAMAQLDIPNGMSIIARTAGIGRSABELEWDILNYLKQLWQAIKEAGKAHHDYLLPFHESSILLIRAITDTPRPDITGEILVDNQEVYDQVAEFNSYV
MPGNAGRLKLYEDHTPLFSRFQITQHIESAFSRSVSLPSGGALVIDHTALVSI DVNSARATRGADIEDTAFKTNMBAEEVAEQMRRLRDGLGVVIDFIDIMENPKHQRDVENVNLDALEK
DRARVQMGKLSRFGLELRSRQLKLPALGESSHAACPRACTGVIRGIESTALHVLHVMQVEAMKNTQGEVRAQVPVDVATPILNEKRAELFAMEERLDVNVVLIPINHLHENPHYETNRITP
DDVEEDGEP SYKRVAEPEDESAKPPGGEKAAARPEPAVKGVHTSPAPTAAPKEKTSWSDSKAWLKRIFGGSETQAVPAAETSEKRSSTANRSGSRANRRQNPRRSKREGSKIEVREA
AGKTAQKARADAKETRNNGKRRNRERGRATERANEAEITQSRNVQAPPAADVAAPFETEGQTKRRNRSGSRNERGQTAFETAVAFTAQTAENTPPPYTAEDKSGSKPKSRNRRERDS
RDAKERRENNQRDRQNGKKNRTIPSAKTEQYLIHMDTARVSVAAAHVFGSTADNAPITQVSIADPLIATPVQTTASSAVSNGDALIYDAEKIRRAAADILFEGAAPKAAQJEMPSETAT
FTAAABQARETAOTGGVLIVITETDPAALKAWAAQPEVOAGRLRRSEQPKPSEAAITVPAEMIQVETROG

SEQ ID 5233

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AGTCGCTCAAATTTGAAAAACGAACCGCTCGCGTCCGCTGCGGCTTGCCTTGGAAAGCCTGGGGCCGATTTTCACTAAGTTCGGGACAGTTTTGTCCACACGCCCCGATTTGATTCGCGCA
CGATTACGCGCTGCACTCGCAAAAGCTGCAAGACAAGATGCCGCCCTTTTGACGCGCGGCTTTCGCGTGAAACAAATCGAAAAATCGCTGGGTCAGCCCATGAAAAGCTGTATTCGGGAATTT
GAAACCGAGCCCGCTCGCCAGCGCGCTTCATCGCCCAAGTACAAGCCGCCCTTGCAATTCGGGGCGAAGGATGGCGCTCAAGAGTTCGCGCCCAACCTCTTGCCCTTATTCGACAACAGATCT
TGCTCGTATGCTGCTTACGCGCGGCTTGGGTGCGAACCCTGTGTTTTCAGACGCGCAAGCGCTTGAAGACCGCGCGCAAGTGGTGGGGAGATTTCGACAAATACCTGTGACAGCAAGTAFTGGATTGTAAT
GCGCGAAGCCGCGTATGACAGGACAACCTCGGGCGCAACTTTCCAAAAACGCAATATGCTGATTGTGCCCAAGGTGTTTTACGACTACTGCAACAAGGACGCTGCTGACGATTGAATGGATGGAC
GGCACGCCGGTTTCCGACATCGCCAACTCAAAGCAGACGGCATCGAATTTGCACAACTTGCCGATTACGCGCTGGAANTCTTTTTACGCAAGTTTTCGCGACGGCTTTTTCCACCGCG
ATATGCAACCCGGCAATATTTGGTTCGCGCGCAACCGCTATATCGCCTTGAATTCGCGACATCGTCGGTACGCTGACGATTAACGACAACGCTATCTTCGCCATCAATTTCTCTGCGCTT
TTTTAACCCGAGATTAACCGACGCTGTCGCCACCCGCCACATCGAATCGGCTGGGTGCGCTGCCCGCTGCGGAAGAGTTGGAAGCGCGGCTTTCGCGCGCTGTGCGAGTGTGCTTTCAC
AAACCGATTTCGACAGATTTCCTTCGGCTTGGTATCATGATCGAATCTGGTTTGAAGTCACCGCGCTTCAATGTGGAATACGAGCCGACGCTGGTATTTGCTCGAAAAAACGCTGCTCAACTACG
AAGCCTTGGGCGCGCAACTCGATCCGATTTGGACTGTGGAAAAACCGCCAAACCGCTTTTGGTAAATTCGGAATGAACGGCGACGAGTTCGCTCCCAAGCCCTTTGGCGCAACCTCAAAGACG

AGCCCCAGACTGGCGCAAATCATCCCTCCCTGCCGCGAAATCAATGCCTTGGTCGATGAGCGCGCGCGCAGGAAATGCGCGATGCCTATATCCATTGGTCAAAGTGCAGCAGCGG
CAAAGCCTTGCGCTGGCAGCGATAGCGGTGTGTTTGTCTGCTGATTGCTTTTGAAA

SEQ ID 5234

MRWLKRLTVIVGTTPYRILAGLVSIMGSGWICALIKMMPQSSKLKNEPPAVRLRLALESLGPIPIKPGQVLSRPLDIPHDYAVELAKLQDKVPPFDARLSREBIEKSLGQPIEKLVAEP
ETEPVASASIAQVHKARLHSGERVAVKVLRLNLLPLIEQDLSLMRPGAAWVERLPSDGKRLKPREVVAEFDKYLHDELDLMREANAGQLGRNFQNSNMLIVPKVFDYCTSDVLTIEWMD
GTPVSDIAKLKADGIDLHLADYGVIEFTQVFRDGFPHADMHGPNILVAADNRYIALDPGIVGFLFDYDKRYLAINFIAFFNRDYYRVATAHRSWVPADTRAELKLEAAVRAVCEPVFN
KPIISQISFGLVLMRLFEVSRFPNVEIQPLVLLQKTLNLBGLGRQLDPDLMLWKTAKPFLVKMNGQVGPKALMRNLKNEAPDWAQIIPSLPRKINALVDEARRQEMRDAYTHLVKVQQR
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SEQ ID 5235

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CATTACTCTAAGGGATAACCGCAAGCGAGATGCCGTCTGAAGCCGCTTCAAGCGGCATTTTCCAGCT

SEQ ID 5236

LWRKYAQNNHNCVCGKPVHRGGQCYALAHPRFRIFQSLYLQTRHYGAENVGIPARQTPARTEEHRHQAGGLLRGRNGNGKPGGGIGIVRRRGRSRHYRRADIRTSDAISRFDN
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SEQ ID 5237

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GGATACCTCCGCGCGCTTGGCTTGGCGCGCTGTGATGTGCCCTACTGCTGCTGTTTGGCGGTCTGCGCGCGCATATCCGCGCAACGCTTTGGTGTGATCTGCCGCGCTGTG
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GTATTTTGGATGCGCGAAACGCTTTCCGTCCGAAATATTTGGAGCGGTGCCCTGCCGCTTATTTCTGCTGCGGTGGCGGGAAGCCTTCTCAGCGGCATTTCACTGCCATTTCGT
GGCACTGAAGCCCATTTGGATCAACACTTTCGACGACAACCGCTATCTGAAGTCCGAGCGCGCATATGGCTG

SEQ ID 5238

MIFQTVWFSDVVLVSIVLILILAAAPSAPRSLARYRSALPLCTVIFSAWCLNASVGGGLAQMNHYHLLAVNLVTLMDVTSALMLAALLMLFYLIFAGSAGAYFPNALVLILPALN
VNRLSRMLVNRLPNFIFIPVNGFLASAAGILITGLVLIGILDAANAFPSKILMTVALPVFIILAWAEFLSGISTAFVVALKPHMINTFDNRYLKSERGIWL

SEQ ID 5239

ATGCTTTTCAACATCTCCCTTTCCATCGGTGCAATATTCGGCACAAACGCGCGTGGCTGTCTCAACCTCGCGTCCCGCATCGTTGTCTCCCGCCACAGGCAACCTGTTTGCCTCACT
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CGTAACCTGCTCAATCGAAACCGTCCCGCTCGGCACCTTGCCAATATTTCTACACAGCGAGTTCGCTGCTGACTTGGCTCGGCTGAAGATAGGACGGCAGTCAAA

SEQ ID 5240

MLSNILPLSIGATGTARWLLNLAVPASLSPATGNLFANWTGALLIGIFAETVSHQWKLILLITGFFGSLTTLGFSLETVTLLQSNRPASALANIFLHTAGSLLLTWLGLKIGTAVK

SEQ ID 5241

ATGTCAAACCAAGGAAGCAATTTTTCGGGTATTTGACTGCCGTCCCTATCTTCAGCCGAGCCAAAGTCAGCAGCAGCAACCTGCCGTGTGTAGGAAAATATTTGGCAAGTCCGGAAG
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AAAGATGCCGATGAGCAGCGCGCCGTCCAGTTGGCAAACAGGTGCGTGTGCGGGAGACAAACGATCGGGGACGCGAGGTTGAGCAGCAACGCGCCGTTGTGCCGAATATTTGCACCG
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SEQ ID 5242

MSKPKAIFCGYLTAVPIFSPQSVSSEPAVCRKILASAEAGRFWSRVTVSSNPESVRLPKPKPVISSSFHCGWLTVSAKPMSSAPVQLANLRFVAGDNDAGTARLSSQRAVVPNIAP
MERGRMLESNVLISAYAV

SEQ ID 5243

ATGAATATCTTCGTTACTGTATTTTCTTACTGCTTATGAGTTTATTAAACGCTTCTTATATACCGTCCGTTTCATTTCATCGGATGATGATATTTGTTGGCAAAGGATTATGACGGTTA
CTTTTTTGCATTTT

SEQ ID 5244

MNIFVTFPSYWFMSLLTSLYIPSVHSSDDIDFGKRIINTVTFLLHF

SEQ ID 5245

ATGACGAAAGGTGCTTTTGGTCCCGCAGTGGCGTTATGCGGCAATCAGCGACATTTGGAATCTCTGCGGCAAGCTGGATGTGGCGGGCAGGATATGGCAGCGTGTGCGCTGCGAG
AATGCGCGGAGGAAACGCTTATGTTGCCGACAGCGTGCCTGTGTACAGTTTATACGCGCGTGGTTTTCGAAATGAAAAATGTATCTGTTCGAGGCGGAAGCGTGGCGTTGGG
CAGTACGCTTCTAATGATGAAGATGAAATAACGGAACCGTGTGATGTGCAAGATGAAGTCCGTGAGGCATTGGCAAACGATGAAATTAAGACGTTAAACATTAATCGGTTTGCAG
TACTGGCTGATGAAGGAT

SEQ ID 5246

MYKRSFWCRQWRYAANQATLELPAGKLDVAGEDMAACALRELAZETFPYVADSVRLLYSPYTAGVFCNEKMYLFEAGVRLGSLTNDDEITETVMSKDEVRLQALANDEIKDKTYLIGLQ
YWLAKD

SEQ ID 5247

GTGGATTTGACGGAAGTAAAAATAGGCGCGGAAACCATTTACGAGGGCGGTTTCTGTAGTATCAGCAGGGAATAAGGTGAGCTGCCCAACGGCAATGAAGGCGAGCGCATCGTATCCGGC
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CGGCGAGGATATGGCAGCGTGTGCGTGCAGAAATGGCGGAGGAACGCCATTATGTTGCGGACAGCGTGCCTGTGTACAGTTTTATACGCGCGTGGTTTTTGCAA

SEQ ID 5248

VDLREVLGGFTIYBGFVSI SRDKVRLPNGNEGQRIVRHPGAACVLAVTDDKVVVLVPAVALCGKSGDITGSCQAGCGRGTGVSVCARIIGGNALCCRQAPAVQFLYGRFLQ

SEQ ID 5249

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GGTTTTGGGATATTTCCGCGCGGTGTGGTGCACGTGAAATCTGCAAGCCGGTATTTTGGAAAGCGTGCAGGTTGGAGTGGAAATCAGACCGCGCAAGCGTGAAGAT

SEQ ID 5250

MDKIFLHGMKADTLIGYVGERERLQTLIVDLDIGVPEKAGSDDDIANTVHYAEVCEVLRRLHKEQDFLLLEALAEYIADLVLGYPGAWVHVHVKVPGILEGVREVGVEIERGKRED

SEQ ID 5251

ATGACCGTCAGCGGCTTCAACCAATTCATATATAAAATCCGGAATACAGCATTTATCGGACAATCAAAAAATCTTACCGAGCACATAGCCCATAAAGGCAATCAGCAACCCGAAACCAGC
GGTTTGAATATTCGCGGGCGGCTCGGCTGCGCAATACGAAATATCATCTTCCCGCCCGCGTGAAGTTCAAGATATTCGGGCATTTCCCATCGCGCTCTCTCTCGCCCTCCCGCT
CTCCGCGCGCAGCAGCGTTTCCAACTCCATATACGGGTAATAATATCCAAACCCAAA

SEQ ID 5252

MTVRRPNHFIYKIPNTAFIQGSKNLTEHIAHKNGQOPENQRFDIAGRLGLPTYXNIIFPPAVKFKIFGHFPIRASSFALPLLRREDRFLHRIIVISKPK

SEQ ID 5253

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SEQ ID 5254

VFTQMVWRAQVEIFDAECHKMPSEAFRRHFCENMLKITIIAACAENLCIGAGNMPWHIPEDFAFFKAYTLGKPVIMGRKTWESLPVKPLPGRNIVISROADYCAAGAEVVASLEVALA
LCAGAEAVIMGGAQIYQAMPLATDLRIITEVDLSVEGDAPFPEIDRTHWREARTERRVSSKGVAITTFVHYLKG

SEQ ID 5255

ATGTTCAACATACCGCGCGTCCGCTTATTTAATCGGTTCACTTTCTTCGCGCTCATCGTTTCCAAGTATTACGGGATGGACGACCGCGCACCTACGGATCGGGCAATCCCGCGG
CGAACATGTTTACGACGCGGCAAAAAAAGCGCGCGCTGACGCTCTTGGCGGATCGCGCAAGGTTTGGTTGCCGTTTTGCTTGCACGCGTCTTCAAGAACCGCTCGGTTTATC
CGACAGCGCAATCGCGCGCGTGCATCGCGCGCTGCTGGGCAATATGTCGCGGTGTTTTTCGGATTAAAGGCGCGCAAGCGGTGGCAACGGCATTTGGCGGTCTCTTGGCACTCTCT
CTGCAACTGCTTGGTCTGCGCGTGTATTTGGCTTGTGATGGCATTCGGCTTCAAGATATCTCCCTTCCGCGCGCTGGTGGCCACAAACCGCGCGCCCTTCCGCACTCTTTTTATGC
CGCATACTCTTGGATTTCGCAACCTCGCAATCGCATATTGGTGTGCTTCGCGCATAGAGCAACATCTCAACCTGATTAAAGGCAAGAAAGCAAAATCGCGGAAAAACGC

SEQ ID 5256

MPNIPAVAVSYLIGLSFAVIVSKYYGMDPRTYGSGNPGATNVLRSKKKAAALTLGLDAAGLWAVLIARVLQEPLGLSDSAIAAVALAALVGMWPFVFGFGKGGKVATAGVLLALS
PATALVICALIWLWAFGFKVSSLAALVATTAAPLAALFPMPHTSWIPATLAIATLVLRLHKSINLNLKKGESKIGER

SEQ ID 5257

ATGCTCAAAACACTTCACCTTGTGTTTTAGTGTGCAATATTTCAACCGCAAGACAAGCCCTACTGGTACATCGACACGCGCGCGCGGCTGTGTACAATCTCGAAGGCGAGCGGCGC
AGAAAGTCGCGGAATACCGCAAGGCATCGCCCTGCTCCGACAGCGCAAAACCTGCTGCGCAACTCTCTGACTTTGCGCGGCACATACAAAAATCCTGCCCTCGCCCGAATCTTACTG
CGGCTCTCCGTGGCTGGCGCAATCGCTGACCTGCTGCGGACAAATTCGCGCTGTTGAGCTGCACCCACCGCATTTGTCCATCTGCAAAACAATATGGGCGAAGCGGGATTGGGCAAA
CGCGGACAAGTGTTCGCGGAAGACGGTTACAAAGGGCTGATTTCCCTGCTGCCCGCCCGCGCGCGCGCGCTCTCATCGACCCGCCCTATGAGGAAAAACAGGACTACCGCGGTG
TAACGGAACCGCTGAAAGCGCTTTAAAAACGGTTGAGTCCGCTGTTATCTCATTTGGTATCCTGCTTCAGCGCGGAAGAAAGCCCAAGCTGCGGGAAGAAATGAAAAAATCTCTGCC
CGCAACTTACCTTTACGCGCGCACTGCAGCTCCACGCGCGGAAACCGGAGCGTTTCGGTATGCACGCGGCAAGGAAATGTTGCTGATTAAATCCCTTACCTTTTAGCCGAACAATTTGGCGCA
AACCTCCCGCGCTGACGCGCTGCTTTCGCAAGACGAAGCGCGCTACCTTTTGGACAGCAAAATCGC

SEQ ID 5258

MLKHPFLFLVLYQVFNKDKFYWIDTHGGAGVYNLEGSEAQKVEYRQGIALLRQAQNLPAELSDFAAHIQKILPSPELYCGSPWLAQSLTCVGDRLFLFELHPTDFVHLQNNMGEAGLEK
RGQVLRDYGKGLISLLPPPRRAVLIDPPYERKQDYRRVTETLKAALKRPFESGCLYIWPCLSRRESKLPPELKKLLPDNLYLARLHVHAKPTDGFGMHSGSMFVINPPYLLABQLAA
NLPAFLRLLAQDEGARYLLDSKIR

SEQ ID 5259

ATGAAAACTTGAATAATTTCCGTGTTGCTGTGTGCGGTTTTGCTTGTGCTGCGCTTCTGAAAAATCTGTAGCCAACTATGCTATCGGCGACGATTTCGGCGTAATCAAGGCTG
GTCGTAAACCTGTCGGAAGCGGAATTAGCCGTGCGGAACGCGCAACACCCCGCTCAACGTAAAAATGTTTCTGAGGAGTTGGCTTTGGAACGTGAAAAACGCGCAATAAGCATGACGC
AATCCGTCAAGGTATGGGTACGCTGCGGTGCTGTATGCTGCTGAACGGTGTGTTGTTGTTACCGTGGGTGTAATGAAAGCGGTGTT

SEQ ID 5260

MKNLNISSVAVCAVLLAACASENSVANYAIGDDSAVIAKAGNRAREARI SRAELAQHRRQRKNVSEELALEREKRAKHDAIRQGMGTAAAGLMLLNGVVTGTVHKSVP

SEQ ID 5261

ATGCGCTGTAACCCCTCAGACGGCATCTTCCGTCAAAACAAACAAAACCGGCGGATACACACTCCATATCGTCCGGTTCTGCATAAACACAGTATTCAAAAAACAGAACCGCTTTTCATT
ACACCCAGGTACCAACACACCGTTTCAGCAGCATCAGACACCGGCGCGCTACCCATACCTTGACGGATTGCGTATGCTTATGGCACGTTTTTCAGCTTCCAAAGCCAACTCTCTAG
AAACATTTTACGTTGACGCGGTGTTGCGCGAGTTCGCCACGGCTAATTCGCGCTTCGGCAGCGTTACGACACCGCTTATACGCGCGAATCGTCCCGGATAGCATAGTTGGCTACAGA
ATTTTCAGAGCGCAGGCGAGCAAGCAAAACGGCACACAGCAACCAAGGAAATATTTTCAAGTTTTTCATACCTGTCTTATATCTCAAAA

SEQ ID 5262

MPSEPFRHLPSNKQNRRAIHTPYRFLHRTSIQKSEAFHYTHGNTHTVQHQHTGSRHTHTDCVMLIGTFTTFSQQLLNIFTITAVLRQFRTANSRFGVTITSLDYGRIVADSIYGR
IFRSAGSKQNGTHSNNGNIFQVFTCPILSK

SEQ ID 5263

ATGAAATGAAGAACTGATTTTGTGTCGGTGGCTGCGATGTTGGTGACGGCATGTACTTACGACAGCCCGCTTTGTAACTCAAGAACTGACGCGGAAATACAGCGGAAAGTCTGT
CCATTACAGATAAGCGAGCGTGCCGAGCGTGCCGAATACCGTAAAGAAACGCCGGAAGAAATGATGGATGCGGCACGCGCATCAAAAAGGCAACGAAATTCACCCAATATTTATTTAT
CGA

SEQ ID 5264

MKMKLLILLSVAMLVACTYADRRPVTQESAIEIQAKSRAIQISERAEAEYRKERREREMDAARAIIKANENSPNIYFIR

SEQ ID 5265

ATGTTATCACTATATATATGTAATGTCAATATTTTTAAAAATAAATTTGGCATCTTGTACTTCTCGATCCGCTGCCGCGTTCCGACTTGCCTCCGCGCGCTTTTTCCCACTACAAATC
CCACGGATATCCGCGGAAGCAACCAAGGAACGCGCGGCAATCTGCCGCTTTCAGACGCGCAAAACCTTTCGAAACGAGCAACCAATGACACACTGACCCGATTCCTCCCGA
ACACTGCAACAAAAACCACTGCGCGGCACTCGCGCGGCTTTTGTCTGCTGCTGTTTCCGCTGTACCGAAATCAACGCCAAAGTCCGCTCGCGGCACTTTCGCGGCTATTTGGTATG
GCGGCGACGCGCAATATTTCAGGGTGAAGACCAAGAAAAACTGGATGTTATCCGCAACAACATATGATGATGACACACTCAAGGCCAACCCCTGCCGTTCGCGTTTGGCAAGCGAGGAAG
ACACTTTCGTAAGTCCGGTGAAGACGCGCTATCTCGTCTATTTCGACCCCTTAGACGGATCGTCAATATGATGTCACAAATTTCCGTCGGTAGATTTTCTCCATTCTCGCAAAAC
CGAAGCGCATTTGGCAACCGAATCATTTCTTCAACGGGCGAGACGAGCTTGGCGAGGCTATGCTCTACGGGCTCAAAACCGAGCTGATTTACATTTCGGACACGCGGTGTACGTA
TTTACACTCAATCCGCAAAACGAATTTGTGCTGACCAAGAAAAACCCGAAAGTACCCGAAAGTACCAAGAAATTCGCCATCAATATGTCATACCGCGCGCACTGGCTACCCCCCGTTCAAC
AATACGTCGACGAGCTCTTGGCGGGGAAACCGGTACGCGCGGCAAAACCTACAATATGCGCTGGGTAGCCAGTATGGTTGCCGAAATCCACCGCATCTGATGCGCGCGCGGTGTTCAAT
GTATCTGCAAGACAAACCGACCCGCTCAAACCGGCAAACTGCGCTGATGTACGAAGCAACCCCTATGGCCCTGATCTGCAACAGCGCGGCGCATCGGCAAGCAACGCATATCAAGCC
ATGCTCGATATACCGCGAAAGCGCTGACCAACCGCTGCGCTCATTTATGGCGAGCGGAAGAGTGGATTACCTCAACCGTCTGCATTCAAAA

SEQ ID 5266

SEQ ID 5266
 MLSLYICIMSIFFFNKFGILYFSIRLPRSDLPRAVFSHYNPTRYPAERTKGTGTPRNSLPFRHRHKPFNEQMTDLTRFLPEHLQONQLFEALGGVLLSVVSACTEINAKVRLGALAGVLGM
 AGFGNIGQEDQKKLJVIANNIMIDTLKANPAVAGLASEEDTFVSAGENGRLVLPDPLDGSNNIDVNLVSGTTFISLAKPEGALATESFLQTRGROQLAAGVYLVGQPTQLVFTFGHGIVV
 PTLNAENEFVLTKENPKVPESTKEFAINMSNRHHLWLPVQYVDELLAGETCTRGKNYNMRVASMVAKEIHRILMRGGVFMYLQDKRPDSKPGKLRIMYEANPMALILEQAGASASNAIYQA
 MLDIQPESLHORVAVIMGSSSEVDYLNRLSK

SEQ ID 5267

SEQ ID 5267

GTGAATCCGATATTCAGCATACCCCTCCGGAAAAACAGAAAACTGCCTTTTCGGAACGATAAAAAACCGCTCTGAAAAATTTTCAGACGGTATTTTAAAAATTAAGCTC
AAATTTATTTGCCCGCCGCTTTTTCAGGATGGGTACAACTCGTCTTTTCAGTTCAATTTGGCTTTTTCAGCTCATCGATGGTTTCCGCACCGCTGTGAACCGGATGTTGGCCAGACC
GGTAATTTTATCGTCCAGCTCGGTATGCTCGTCGAACAGACGGGCGAAGCGGGAATTTTCCGTGTTCAATTTTGAAATCAAATCACGGTATTCGGAACATAATCGCTTTCTCTCTGG
TTTACGGTTAAAAAGTCAAAT

SEQ ID 5268

SEQ ID 5268
VNPILRRYFKHTLRKNRKLPRFTIKIPSEKFDGILKIKAIQIYLPAAFCRMAYNSSFSFNLAFFSSSMVSAPLVTGLIARPVILSSSLCSSNRRAKREFSCFNLEIKSEYSGNIYAFLSN
FTVKKSN

SEQ ID 5269

SEQ ID 5269
ATCGAGTTGGAACCGCTCGTCCCGCGGAGGAGGGGAGGGCGAAGGAGGAGGCGCGGATGGGGAATGCCGAATATCTTGAACCTCACGCCGGCGGGGGAAGATGATATTCNGTATGTT
GGCAACCCGAGCGCCCGGCAATATCAAACCGCTGGTTTTTCGGGTTGCTGATGCGCTTTATGGCTATGTGCTCGGTAAAGATTTTT

SEQ ID 5270

SEQ ID 5270
MPTETATPREFEGEGGGADGEMPEYLELHGGRDDISVCWQPEPPGNIKPLVFGLLAFMGYVLGKIF

SEQ ID 5271

SEQ ID 5271

ATGACACACCATTACCCACAGACGATATTAAAGATTAAAGAGTTTGGCCGCGGATTGCCCATCTTTACGAGCTGCCGATTTCCAAAGAGGCTCGGGCTTGGTTACCCGCA
TCCGCCAGGAACCTTCCGATTTGGTTACCGCAGGGACAGGCGCTGTTGGTCATTATCGGGCCGTTTCGATTCACGATCCGAAGCGGCGTTGGAATATCGCGAAGCTCTGTTGAAACT
CCGCAAGCGGATGAAACAGAGCTTTTGATCGTGATGCGCGCTTATTTCGAGAAGCCGAGAACACGCGGTTGGAAAGGTTTGATTAACGACCCCGCATTTGGACGGTACGTTTCGACATC
AATTTCCGTTTTCGCTCAGGCGCGCAGTCTGTGTTGTTCCCTGAATAATATGGGCATGCGCTGCTTACCGAATTTTGGATATGATTACACCCCGATTTATGCCGACCTGATTTCTTGGG
GGGCAATCGGCGCGCGGACGACCGAAAGAGGATCCACGGCGAATGGCAAGCGGCTGTCTGCCCGTCGCTTTAAACACGGTACGGACGCGCAATTTGAAGATTGCGGATCGACGCAAT
CGGTGCGCGGACGACTTCGACATCAATTTCTTGTTATCAACAGGCGGGCATTCGCCATTGTTCCATACCGCGCGCAATCCCGACTGTGATGTCAATTTTGGCGGCGGAAAGAGCGCAAT
TATGATCGGGACACGCTCAGCGAGGCGGTGGAACAACCTGCGTCGCGCAGGGTTAACGACAAGCTGATGATCGATTGACGCCACGCCAACAGCCGCAAGGATTACACCCGCGAGATGGAAG
TGGCACAAGACATTCGCCACCAATTGGAACAGGACGCGCGCAATATCATGGCGTGATGGTGGAAAGCCATTGGTTCGAAGCAGGCAGGACAAGCCGGAAGTGATCGGCAAGACATTTAC
CGATGCGTGATCTGTTGGGCGCGACTGAAGAAATGTTGGCATTTGTTGGCGGTTGCGAACACAAACGTATGGCGCGCGCAGGT

SEQ ID 5272

SEQ ID 5272
 MTHHYPTDDIKIKEVKELLPIIAHLYELPISKEASGLVHRIRQELSDLVHGRDRRLVVIIGPCSIHPKAALEYAERLLKLKRYENELLTVMRVYFEKPRTTVGWKLINDPHLDGTFDI
 NFGLRQARSALLLSIANNMGMPASTFELDMITPQYADLISWGAIGARTTESQVHRELASGLSCFPVGKNGTDGNLIKIAIDAIGAASSHFLSVTKAGHSAIVHTGGNPDCHVILRGCKEPN
 RAGGGRFLLMTDCSHANRKYVTRFMEVAQDIADOLEDDGNGIMVMVESHVBCGRQDKPEVYKGSITDACIGWATEELLALLAGANTKKMARAG

SEQ ID 5273

SEQ ID 5273
ATCGCTAAAGCGGAAGATTGTCAACGATTTTATCGGACGGTGGGGCGGTTTCTCGCGGACGGTGTGTCCGGTGTATACAAACACTGGATAAAAAATATTATCTTTGTATTAAATTAATGTAA
AGATTCAATTGACTTTTAAACCGTAAACCAAGAGAGGAAAGCATTATGTTCCAGAAATACCGTGATTTTGATTTTCCAAATTGAAACAGGAAAAATTTCCCGCTTCGCCCGGTCTGTTCGACGA
GCATAACGAGCTGGAGCATAAAAATTACCGGCTTGGCCAACAATCCGGTTACCAGCGGTGCGGAAACCATCGATGAGCTGAAAAAAGCCAAATTGAAACTGAAAGACGAGTTGTACGCCATC
CTGCAAAAAGCGCGGGGCAAA

SEQ ID 5274

SEQ ID 5274
MRKAEDCQRFYRTVGRFSADGVAVYNKTLDKNIIPVINVKIQDFDLTVNQERKAINFPPEYRDLISKLKQENSRFARLFDENKLLDKITGLANNPVTSGARTIDELKKAKIKLKDELYAI
LKAAGK

SEQ ID 5275

SEQ ID 5275
TTGAATTATTATTAGCCATATTACATACAATAATCAGCATGCTTTGTATGAATTATCAATCAAATCAGGCGAAGGAGTGTCTTGAGCTAAAAATATTATTGACTGCATTGATAATGTCTA
TGGTAATCTCCGGATGTCAAGTCATCCATGCCAATCAAGTGAAGGTTAATCTAATTTCTGCTGTCTATCGCAGGTGCAGACGCTCACACGCCTGAACATGTAAACGGGACTGACCGGAACAAA
GCAGGTGATTTCAAGTAGTAATTTATAGTAGCGTCGACCGCAATTCATTAGCAACACAAAGCTGGCTATGATATCTTAAAGCAAGGCGGTAGCGCTGCAGATGCGATGGTGGCGGTGCAGACGACA
CTAAGCTTTGGTAGAGCCACAGTCGTGAGGCTTGGGCGGTGGTGCAATTTGTGTTGATTGGGACAATACCGCCAAAACATTGACCACATTGATGGGCGGTGAGACGGCACCGATGCGTGCGA
CGCCAGAATTATTTTGGATAAAGATGGT

SEQ ID 5276

SEQ ID 5276
LNYLAILPTLISLMCMNYQSNSSGEGVLVAKTYLLTALIMSMVISGQVVIHANQGVNTNSAVLAGADAHTPEHVTLGLEQKQVIASDFIVASANPLATQAGYDILKQGGSAADAMVAVTTP
LSLVEPOSSGLGGGAFVLYWDNTAKTLLTTFDGRETPMRATPRLFLDKDG

SEQ ID 5277

SEQ ID 5277

TTGCCTTGGGGAAAAATTAFTTGTATACGCCGATCCACTTGGCAAAACAAGGCTTTGAGGTGTGCGCAAGGCTTGCCATCTCGGTTGAGCAAAAATCAGCAGCAFTTGGCAGCGTATCCAAAAA
CAGCGCGCTTATTTTTTGCCGAATGTTGTCGCCGTACAAGCAGGCAGCTTGCTGAAAAATTTAGAATTTTGCTGACAGTGTTCAGCGCTTAGCAGCTCAAGGTGCAAAAGCTCTGCATACTGG
TAAATATGCCCAAAATATTGTTTCAGTTGTGCCAAAATACGTAAAGGTAACCCCGGTCAATTATCTTGCAGAGTTTATCTGATTATCAAGTGGTGGACGCCCGCGCTGTTTGTGTGACTTAT
CGTATTTATGAAGTATGCGGTATGGGTGCACCAAGCTCAGTGGGATTGCTATGGGTGAGATTTTGGGGATTTTAAATGAATTTTCACCAATATCGGGTGGGTGATGATGCTGAAGGTTTGC
GTTTGGCGGATCGTGATGTATATTGGGCGACCCGTGATTTGTACCAAGTACCCATTCGCCAGT

SEQ ID 5278

SEQ ID 5278
LFWGLFDTPIHLAKQGFVSPRLAISVEQNQOHLARYPKTAAYPLFNGVPLQAGSLLKNLEFADSVQALAAQAKALHTGKYAQNTIVSVVQNAKDNPGQLSLQDLSYQVVERPPVCVTY
RIYEVCGKAPSSGGIANGQILGILNEFSPNRVGYDAEGLRLRIVMYINATLLIYQYPPAS

SEQ ID 5279

SEQ ID 5279
TTGGGCGACCGCTGATTTTGTACCAAGTACCCATTTCGCCAGTTGATTTCTAAAGACTACCTAAACATCGCAGCCAGCTGCTTGAGCAGTCGGATAAGGCAATTCGCTACGGCTATTCGACGGCG
ATTTTATTCATGAGTGGGCGTCCTCACAAAGCGATTGAGTTACCTTCTACCAAGTCATATCAATTTGTGATAAGCGGGCAATGTGCTCATCAATGACGACTTCCATTGAAATGCGGTTTG
CTCAACTTTGATGGCAATGGCTACCTGCTGAATATGAGCTGACAGACTTTAGTTTGTAGGCCAATAAGCAGGGCAACAGGTGCCAATCTGTGTCGAGCTGGCAAGACACAGCTCC
TCAATGGCCCAACCACTGATTTAAAGCAGGCAAGCCTTATATGGCAATCGGCTCTCCAGGTGGTAGCCGATCATTTGGCTATGTGCTTAAGACGATTGTGGCACAATAGTACTGGAATA
TGGATATTCGAAGTGCCTATCAGTGCACCCAAATTTATTAATTCGCTTTGGTAGCTATGAACTAGAAACGGGTACAACCGCGCTCCAGTGGCAACAAACATTAATGATTTGGGCTATAAGAC
TGAATGTGGCTGAGCTAAATTCAGTGTTCACAGCCATTATTTATCGAGCCAAGCAGGCTGGTTGGTGGTGTGATCCACGCGGAGAAGGTGAGTGACGGGTGAT

SEQ ID 5280

SEQ ID 5280

IGDDPDPVFPPIRQLISKVDLKHRSQQLLEQSDRALPSVSAGDPTHEWASSQAIELPSTSHISIVDKAGNVLSMTTSIENAFGSTLMANGYLLNNELTDFSPFEPIKQKQVANRVEPGKPRSSMAPTIVPKAGKPYNIAIGSPGGSRIIGYVAKTIVANSDNMNDIQDAISAPNLLNRFSGSYELTGTAVQWQQTNDLGYKTTVRELNSGVQAIIEPSRLVGGVDPREGRVTDG

SEQ ID 5281

ATGGCGGGCAGGAAGAAATGTCTTGGCAAGTGGTGTATCAGCGGGTTATGGCTGATAAAGATGTGGTGGTCTGGTTATTTGATTGATTTTGCACAACTGCCGAAATTTACCATTT
ATGATTTGCTTTGATTAGCTTTGTCTAAATAAAGTGATGAGACGCTAAAAACCGGCATGTAAATAAATTACCTGATAATGCCAAGAAATTTACGCATTATGGGCTATCTGCC

SEQ ID 5282

MAGQEELSWQVYQVRNADKVVVAGYLIDFAQTAENLPFDVLP LLSLVLNKGDETLKTGMLNKLFDNAKENLRIMGYLP

SEQ ID 5283

ATGTTTTCAAAAGCGTTACCTTCGCAACAATATGACCCGATTTGGCAGCAGCATTTGCCCAAGAACGCCAGCCAGCAAGACCACGTCGAGCTGATTGCTCTGAAACTACGTCMAY
GCGCGGTGATGGAGGCAAGGTTGCAATTGACCAACAAATACGCCAAGGCTATCCCGCAAAACGCTACTACGGCGGCTGCGAATACGTCGATATTGTCGAACAATTGGCAATCGACT
CGTAAAGAACTGTTTGGCGAGCCTATGCCAACGTTTCAACCGCCTCCCGTTCCCAAGCAACCAAGCGTATATGCTTCGGTTTTAAACCAGGCGACACCATTTTGGGTATGTCCT
GCGCAGCGCGGACCTGACCCACGCGCGGAGCGTTAATATTTCCGCAAACTCTACAATGCGGTTACTTATGGCTTGGATGAAAACGAAGTCTCGATTATGCGGAAGTCAAGCGCTG
CGCTCGAACACAAACCCAAATGATTTGGCGGGCGGCTCTGCTACGCGTTGCAAAATCGATGGGCAAAATTCGCGAAATCGCGGATFAAAGTCGCGCATACCTCTTTGTCGACAT
GCACATATGCGGAGCTGCTGCGCGGCGGAATATCTTAACCCGCTGCCATTCTGCGACTTCGTAACCACTACCAACCCACAAACCCCTACGCGCGCTCGCGGCGGTGATTTTGTGCG
GACAATACCCACGAAAAGCGCTGAACCTCTTCCATCTTCCCAAGCTGCAAGCGGCTCGGTTGATGACGCTTATCGCGCCAAAGCGGTAGCGTTTAAAGAACGTTGCAACCCGAGTT
AACATACGCAAAACAGTGAATCAATGCTGCGGTCATGCGGAGAGTTGGTTAAACGCGGTTTGGCGATCGTTTCCGCGCGCACCGAAAGCCAGCTTTTCTCTGTCGACCTGCMAT
GATGAAATACCGGCAAGCGCGGAGCGCTTTTGGGCAAGCGCACATCACCGTCAACAAACCGCATCCCGAACGATCCGGAACCGGTTCTTACCTCCGCGCATCCGCGATCG
TCCGCGCCATGACCACTCGCGCTTTAACGAACCGAGCTCTGCTATTTGTCGAATTTGGTTGCCGATGATTTGGCTAATCCCGAAGACGAACCACTCCGCAAGTCCGCGGAC
TGACTGCTTTGCGACAAATACCCGTTTACGGAAC

SEQ ID 5284

MFSKSVTLAQYDFDLAAALAQEDRRQDHHVELLASENVSCAVHEAQSQLTNKYABGYPAKRYYGCEYVDIVEQLAIDRVKELFGAAYANVQPHSGSQANQAVYASVLKPGDTILGSL
AHGHLTHGASVNIISGLYNATVYGLDENEVLDAEVERLALAEHPKMI VAGASAYALQIDWAKPREIADKVGAYLVFVMAHYAGLVAGGEYPNPFPCDFVTTHKTLRGPBGVVLQ
DNTHEKALNSSIYPSLQGGPLMHVIAAKAVAFKEALQPEFKYAKQVKINAAMAEELVKRGLRIVSGRTESHVFLVDLQPMKITGAARALGAHITVKNKAIIPNDEKPFVTSIG
SAAHTTRGPNETDARVLSNLVADVLNPEDEANLAKVRGQVLTALCDKPYVYGT

SEQ ID 5285

TTGTTTCGGTAACATTTCTCTCCAGCAAAATGACCAACTTTTCAATCTGCGATTCTACTATCTTCTGCTGATCAATTCATCTTTGATCCAGCAGCGACCTGAM
TTTTCATTTTCAACACCGCATTTTCATCAGAGCGGATAATATTATGATGGTTATTGGTATTGTCGCGATAGAGAAGAAAAACGATCGGTTCGCTCCGCCAGCAGCTCAACCACTG
TATTGAAATCTGGGCAATCTGGCGCAGCTTTGCGAGATTGATGCGCTTTTCCCGCTTCTATTTTGAATACCGGTAAACGACATTTCAATTTTCCGCCATCTCTTCTCGCGAT
CTGATTGACTTCCCT

SEQ ID 5286

LFSVTLFFFLFQQNDQLFQYCDFTIFLPDQFILCIQORPQFIFPKHQHFI RADNIMMIGIVADREKRSVLLRQQLNHIDIEHLGNLAQLVEIDAFFAFYFRI PVRHFPQFRHLFLP
LIDFP

SEQ ID 5287

ATGGCTTTCCACATCAGGCCATGATATGGCGCGTCTGTTTCAATTTGGTCGCAATGCTCTTGTGCCACTTCCATCTGCGCGGTGTAATCTTGGCGCTGTTGGCGTGGCTGCAAT
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CGGTATGGCAATGGCGGAATGCCCGCTTGGTTACAGACAAGAAATGATGCGAATGGCTGCGCGCAGCGATTCGCTGATCGCAATCTTCAAAATTCGCGCTCGTACCGCTTTTAAAT
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TCGGTAGAGCGAGGATGCCATATTATTACAGGACAACAACAGACTGCGCGCTGACGCAAAACCGAAATGATGTCGAACGTACCGTCCAAATTCGGGTGCTTAAATCAAACTTTCC
CCACCTGCTTCTCGGCTTCTCGAAATAAACGCGCATCAGATCAAAAGCTGCTTTTATACCGCTTTCGCGAGTTTCAACAGACGTTCCGCAATTTCAACCGCGCTTTCGATCGTAM
CGAACACGGCGGATTAATGACCAACAGCGCGCTGCTCTGCGTGAACAAATCGGAAGTTCTTGGCGGATTCGGTGAACCAAGCCGAGCGCTTTTGAATTCGGCAGCTCGTAM
TGGGCAATCGCGCGCAACACTCTTAACTCTTAAATCTTAATATCTGCTGCTGGGTAATGGTGTGTCATCTTGCATCTTCTCTGATGGGTTTTATACGCTGCTTAGGTACATCGT
ACCTTGCAACAAACAGTGCAACATATTACTACAAAGCTATTATTATTCAAAA

SEQ ID 5288

MAFHHHAIDIAVLFLQVGNVLCFHLPGVILAAVGVAAIDHQLVGYPCRTQLPHRLADVSRIIRLFSAAQNDMTVGIAAGMDNGMPLGYRQEMRMARRTDCVDRNLQIAVRVW
DGAGTACQFVADLAFGRPRADCPPRNQVGLILGCNHIQKPRGRHAHIQGGQQTARLTQTEIDVERTVQMRVNVQTFPHRRSRLLLEINAHHDQKLVFIPLAEFQQTFRIFQRRFRW
RTRPDNDQQPPVAVNQIGKFLADAVNQARSLFGNRQLVKMGNRRQQLFNFNLIVCGVMVCHLASFLMGFYTLRLHRLPCTNKNILLQSYFISK

SEQ ID 5289

AAGGCTCGCGCGCGCATCTCGACGCGGCTCCACGCGAGTTATCAGCTGCGGAGTCCGCGCTGCCGTTGCCGCAAAATCGAGCGCGGTGCGCTGATCGACGAGGTTGCGGATAM
GGCAGCGCGCGGCTGATGTTACGCGCTGCCGAGCTGTGTTTCAACACGCGGAGCGCTTGGTCTGTTACATCGCAATACGCGATCCGACCTTCGAGCATAAACGGTTGGAM
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GAGCGCGCGGATAGGATTTTGGGATTTTGTATGCGCAATTTGTGTTTAAAGTCTGATGCAAAATCGCTGCGAGCTTTCAATCAGCGGTTGCTGATGGCGCGGCAACGCTCTTCT
GGCAGGTTGGTCTTACGAGGCGCAGCGCAGGCTTTTCCGCGCAAGCATCATCAGACCTGCGCGCTGCCGCTTTTTCGCGCAGATATTCGGGTGTCGCTGAAAAAAGCTGTGCT
CGCGCGCGGCTGATGATGCTTTTGTGCGCGCGCGGTAACGATGCGCTGCAAAATGCGCTGCAAAATGCTGCGAGCGCGGCTCCAAAGTTGACGACATAGGCGCGGTTGGG
ATTGAGCCACCTGCTTCAACCGCTTCCGCGCGGAGGATGTGCGACACTTCCAGCGCGCTTCTCCGTCGCGCGCGCTGATTTCCGGAATCGAAGTTCGCGAGGACGAGCTTTTGGCG
GCTTCCGCGCGCGCGCAACAGGTTTGTGCGCAATACCGCGCAGCGCGAGGCGGCGTGAACGCCAAGTCCAAACAAATATCGGGCGGATGCGCGCGGCTGCGCGGAGG
CGGCAAAACAGGCTGTTTCACTGCTGTTTGTCTCAACAA

SEQ ID 5290

KAAARHLGGHGSYQAAGVRPAGCRQIERGAVIDGGADKQPQRDVHALPEAVVFQHQPLVVVHRQYGIPTFEHKLRLQCVRRIRAGEVYPPAAQVFERGDNVGVFVSEVSAPAGNI
EPGD*DFGI PDAEFVF*VWQNAADAFNRRLDGGNVFQRQVGRYEGDAQFAGKHHDLPRAAPFRQIPGVSAEKTACARGVDDAFVQRGNDVAVEN* NACERGVQKLQHIQGW
IEPPCLNRFGRDVQHPQPAF SVRAA*FRIEVAQDDAFAGFGARAQVVFVAQYRAAGQACKRQVQTNIGADAGRLAGSNGNRLPHRVCSEQ

SEQ ID 5291

ATGATTGAGATGAGTAAAGATTACCGAAACGATTGTACGATGTATGTTTCTACCGCCCCAAGTGGATCGCGGCTTATCCGGGAGTGCCTTAAGGAGAATCTCGCGCAAGAAAG
CGGAAGGATTGATCGAATCGCTGATTCCAAACCGCAAGTCTGTTGAGGAAAAATGCACCTTGGGCGAAACGGGAAGAGTTCATGATTATTTCAGTATTGGGTTTGGATATTAT
CCGTATATGAGTTGGAACCGGTCGTGCGCGGAGGAGGAGGCGAAGGAGGAGGCGCGGATGGGAAATGCCGAATATCTTGAATTCACGCGCGCGGGAAGATGATATT
TATGTTGGCAACCGGACCGCGCGCAATATCAAAACCGTGGTTTTCGGCTG

SEQ ID 5292

MEEMSKDYRNDLYDVVSYPPQVDRGLIRECLKENLGEKAEGLIESLDSKPQVLVEEKCTWAKREELHDYFSYLGLDITRIWSKRSRRRRGRAKEARMKCPNINLNTAGKNI
YVGNPSRPAISNRWPSGC

SEQ ID 5293

TTGGAGGGCAGGATGGAAGTGCATGACAAGATTCCGACGTTAAGGGAAGTCAATCAGTGGACGCAGGAAGAGATGGCGAAAAATTTGGAATGTCGGTTAACGGGTATTGAAAAATAGAAC
GCGGGAAGAGCGGCATCAATCTCGACAAGCTGCGCCAGATTGCCAGATTTTCAATATCGATGTGGTTGAGCTGCTGCGGAGCAGAACCGATCGTTTTCTTCCTATCGCGCAGCAATAC
CAATACCATCATATAATATTATCGGCTCTGATGAAATGCTGGTGTGTTGAAAAATGAAATTTAGAGTTCGCTGCTGATGCAAGGATGAATTTGATCAGGCAGAAAGATAGTGAATCGCAGTA
TTGAAAAAGTTGGTCATTTTGCTGGAAGAGAAAAA

SEQ ID 5294

LEGRMEVHDKIRTLREVNQWQEBMAEKLEMSVNGYSKIERGKSGINLDKLRQIAQIFNIDVVELLAEQNRSTFFSIGDMTNHNNHNIIGSDEHLVFENEKIRSLLDKDELIRQKDEIAV
LKKLVILLEKK

SEQ ID 5295

TTGGGCAAAAAATATAAAAAACGGTTTTCATCTGTAAATACGTGTGCGGATGTGGAAGCTCGTGGGCAAAACGAGCAATGAGAGATGTTAGGGACATAGAAAGGCTAATAAGCCGAAACG
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GCATCAGGAGAAATTCATAGGATCTTCAAATCATTCGCATCATCACTTCTCCCTTAGCGTTACAACTTTTACAACAGACATGGCGGTGACTCCCGAATTT

SEQ ID 5296

LGKKYKNGFHPVNTCADVEARWANGAMRDVDRDIERLISRNVLRRIGDAIQNMCMETVNSIRMYRQBCRSSESDFYDEMLBHEHNFIGSSKSFASSLLPLSVTNFTTDMACTPEF

SEQ ID 5297

ATGAAAAAGCACTGCTTGCACTGACTATTGCCGCCATCTCCGGTACTGCTATGGCCAGTTGCCCCGACTTTCCTGGGTAAAGGCGAATATACCGTCCGTACAGACATCTCCAAACAAACGC
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ATTTGGGCGGCGGCTGGTATCTGAATCCTTGGGCGAGGTTAAGGTTGACCTGGACGCCAAATGAAACACACGCAACTGTAGCCGGTGTCTCAGCCGACATTAACGCAAAAAACACGGG
ATGGGGCTGGGCGCTAGGTGCGAATATCGGCAAAACAAATTACCGATACCGTGGCATCGAAGCGGCGCCGTTCTACAAACACCGTCACCTTCAAAGCATCCGCGACGCTCGTTTAGACGGC
GGGAACATCCGAGTCGATCTTACCAAAATCAACGAATACGGTGTTCGTGTGCGGCGTGAATTC

SEQ ID 5298

MKALLALITLALISOTAMAQLPDFLGKGEVTVRTDISKQTLKNADLKEKHVKQKNIGFRADMPDDIHHGMRFEVSHSRDKKDMYVVTBSTTKPPGKDVEEKRDTVYAGTYTQPISEATK
LRAGLGLGYEKYKDAVANERKFTSTEREAPYTKAHADLTSLDGGGWLNFMAEVKVDLDKAKHNAITVAGVSADINAKTRGWSGVGANIGKQITDTVGTGAPFPYKHFHFKASGSPVLGD
GNIRVDPTKINEYGVVRGVGTF

SEQ ID 5299

ATGCCGTCGAAAAAGTTTCAGACGGTATTAGGGTCTGCTACAACATCAAAAACCCCAACCAAAAGGCTTTCGGGTTTGTGTCTGGGGCATATCGCCCGCAT

SEQ ID 5300

MPSEKPTVLGSATTSKTANQKACGFVSGAYRRD

SEQ ID 5301

GTGCTTGCTTCTGTGATTGATTATCTCATATCGACCAACACCTGCTCAGCCTGTCGGCGCAATACGGTGTGTGGATTATGCGATTCCTGTTTGTATTGTTTTTGGGAAACCGGTC
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TGTGGGTATCTCTGTTTTCTTACGCGGGCTATTCTTTGCCAACTTCCCGCTGTAATAAACCAATCTGGGCTTGGTGTGGGCGGCATCATATTGTTTCCGCTCTGCCCGCATCATCGA
AATCGCCCGCGCAAACTTTCGGCAAAATCGAACGT

SEQ ID 5302

VLASVDFILHIDQHLLSLSAQYGVWYIAILFLIVFCETGLIVTFFLPDGLLFAAGGIAALGMDIHLWVALLSLAAILGDALNFTVKGYPGRLFANPDSKIFRCEYLKTRTRFYEHK
GKTIILARFVPIVTPAFPVAGMKMHYAKFIRYNIIGLLWVILFSYAGYFANFFVVKNNLGLVMGGIIVSVLPGIIEIARAKLAASER

SEQ ID 5303

TTGTGGAAATTGACATTATGAATATATTATCCGTAGAAAAACGCTTCTTTGCCGTCGGACATGTGCCCTGCTCGACAAAAACGCTCTTCCAACTCGACAGCGCGGAAAAAGTCGGCTTGA
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SEQ ID 5304

LLEIDIMNLSVENASFAVGHVALLDKTSFQLDSGEKVLIGRNGAGKSSFLKILITGVQKLDGQIIIVQNNLKIVYVQESFFDKDATVFDTVABGLGEITDRLRRYHVSHELENGSSEL
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SPSKYSBKQAQELAVEAENHRLFDKFAHQBEAWIRKIEARRTRNEGRVRLBELRQRAERNVQGVNFKLDSGKSGKIIAELEHASFAYDDKVINDFPSAILORQDKIGLIPNGIG
KITFLKILGELQPTYGRIRIGSKQEVATFDQFRSALNENDTVFTLQGMNDYVEVGGKKHVMSTLEDLFPFPPARAQSPVSSLSGGERNRLLLAKLIFRPNILVLEPTNHLIDIDTQEL
LEDLLRDYQGTFLVSHDRMFLDNVITQSVFEGQRLKEYIGGYQDYIDAKSREDKIQTASAPKASDVEPAKEKPKANRTVKLSYKEQRELDALPDEIAALETEQAEINAQLSDPGIFPD
YERAGALQNAEIEIMLLEKLERWELLETRQNGNAV

SEQ ID 5305

TTGCAATGCTCTGCTTTTTCGTAATCTTTGAAATTCGCGGATCGGAAAGCTCGCGGTGATTCTGCTGTTTCGCTTTCGAAGGCGCGGATTTTCGTGCGGACGCGGCTCGAGTTCGCGC
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TATAGTCTGATAGCCCGGATGATTCTTTCAGACGCGCTTGTCTTCAAAAACAAATGCTTTTGGTAAATTTACATTGTCGAGGAACATACGGTCTGCGAGACGAGGAAGACCGCTGCTTG

SEQ ID 5306
LQCSCFVPIFENSIGIKLRVDVFCFLFGQGGDFVVGQVGFALFVVGKFDRTVVGPGFFGGFDIGCFGCQGRINFIIPRFVCDIVLIAADVFPQTALSFENNALGNVIVEEHTVVRDEORAL
VIAQQIFKQFLGVDVQVGRFVNQNIGGTSKEPCQQKAVAPAAGE

ATGCCGTCCTGACGACGGCATAACACAAACACCGCGGTACACGGAAAAACGACGATCCGCAACCGCAGGTGTGTTCCGCATTCCGATTGCGGATGACGAACCTGCGAACCCCTGCAGA
CTTTTCGTAATAGTCGATTTCCGCGACCGACAGATATTGATAGCTCATCGGATCGACCAAAAAGACCAAAACCGTTTTCTCAATTCAAAATCGTCGTCGTTTTTGATTTCTGTCAAAAGTAA
ATCCGTACTGGAAGAACCGAACAGCGCGCGCGGTGACAAAAACCGCAATTTCAANTCGGGATTGTTTTCTTCGGCAATCAAATCGGCAACTTTGGCACACAGCTGTCAAGTAAATAAT
AGGGCTTTCTGTCGCACATGGTGTATTCTCT

SEQ ID 5308
MPSESDGITOYSRSHCKRRSATAGCFRIRIADDELRLTQTFRIVDPRTDQILIAHRIDQDKQTVFLNFKIVVVDFVKSXSVLETRTAAAVDKNPQFIGIVFFGNQIGNFGTAAVSKN
RAFVREHGVIP

SEQ ID 5309
TTGATAAAACAAATACCCGCCATTTCATTCGGGCAAAACCGCAGGAACATCCGTTTTCCTCGTTTCCACGACAATCCGGTACAGGACACCCCGCTGCGGATTCCGCTGCACATCCGGCAAA
ATTTCATCGCAAGGAAAATGTTTGA AAAACAAAAAGAAC

LIKTI PAI HSGKTARNIRFPVSTTIKYRTPRCRFLHIRQNFIRKENVENKKN

SEQ ID 5311
ATGTTCAAACGACCTGAAGAAATCATCGTCTCTGATACTTGGCGCTCTCGGATTGCCGGTAGCTATTTCCTGCCGCCCTGTTTGGAGCGGATGCTTATACCGTGTTAAAAATCACTGCCCTTACACCTGCTTTGGTCTGCGCATCATTCCTCTCTTTGGCAAAAAAACCTCAGCCGGCATATCTGGCGCTGCTGCTCGGCTGCCGTACCACTGTTGGTGGCCGTATCTGAATCAATCGGTCGCACCCGGTTCTTACCTTGGCATGCATCATGGACGTTTCAAACCATCTTAGCCCTGATTCCCGCAACCCGAGGTATCTGTT

SEQ ID 5312
MFKRPEEITVLILAVLNIAAGTYFLAALFGADAYTVLKITALTLLWSAASFLWQKKPQPAYLAAARLPDHLVAVSESIGRTRFFTLACIMDVQNHLSPDSSNRRLSV

SEQ ID 5313

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SEQ ID 5315

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AAATACTCCCATGTGATGCACATGTTTCCCAACGTCGAAGGCTGTTTGAAGAGGGCGTTACCAATATGGACATCTCGCGCCGCACTCTTCGTCGGCGGCACTCTCGCGCGCGCAAAAG
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SEQ ID 5316
 MISKQEQYQAQAQGYNRIPLVQELLADLTPLSLYLKLANRPYTYLLESVVGGERFGRYSGFGLPCSHYLKAGGKHVDVYNGEIVEQYDGNPLPPIEAFHNRFKTPETPSLPRFTGGLVG
 YPGYEVYVNFHEFAHRLKNTAKANPLGTPDILLMSQELAVIDNLSGKIHLIVYADPQSPDSYERARERLEDITQQLRQSCAIPLSLGSKQTOQVSEFSGEEPFKACVDKIKDYIFAGDCQ
 VVPQSRMSMEFTDNPALYRALRTPLNESPYLFFYDFGDPHIVGSSPEILVRREKDDVYVTRPAGTRLRGKTPAEDLANEBQDLSDAKEIAEHVMLIDLGRNDVGRISKTGEVAVFDKNVIE
 KYSHVMHIVSNVEGCLKEGVTNMDILAAFTPAGTILSGAPKVRAMEIIEBIEPEKRGYIGGAVGWGPNNDMDLAITARTAVIKNNFLFIQSGAGVVALSDPTSESEQETQNKARAVVRAAQ
 VQGLGR

SEQ ID 5317

ATGCAATTACATCATTTAGAAATTTGTGCCGGAGCAGCGCGACAGGCTTTGGGCTTAGAAAGGGCAGGCTTTTCCCATGTTGCGTTAATCGAAATCGAACCGTCGGCTTGTCACAAACCTAC
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SEQ ID 5318
M Q F T S L R I C A G A G G Q A L G L E R A G F S H V A L I E I P S A C Q T L R L N R P D N V I E G D V R L F Q G B Y D I G D L L A G G V P C P F F S K A G K Q L G K D D E R L F P E A I R A K E T D F K A I M L E N V R G L L D P K F
E N Y R N H I T T E P A R L G Y L G Q W K L L Y A A D Y G V S Q L R P R V L F V A L K N E Y T N F F K W P E P N S E Q P K T V G E L L F D L M S E N N W Q A G H N W R L K A A Q I A P T L V G G S K K H G G A D L G P T R S K R A W A E L G V D G
S G L M S A P P E S G S G H P R L T V R M T A R I O G F P D D Q F F G K K T P M Y R O I G N A F P P P V A E A V G R Q I I K A L K K E N

SEQ ID 5319
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TGA AAAAATTCGACGATATCAGACCCGGGCACTGGAATTCGTAAGCAGGTCGGTTCCTCGCAACCGCTCTGGAATATCGCACGTTATCAGCAATAACGCACATCTGACAGCCTTAGCCAAAGCTGCC
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ATTTGGCATT

SEQ ID 5320

MNPLFTQERRIRHKKLLDGNILATNNRGVVSMDGNSNRSFNIAKGIADLLHSEFVSRILPGQTSNFAEAIKSEFVQSAPEKLQHIRPGDWNVQVGSNRRLKLIARYQQYVHL/FALAKAA
EENPELAAALGSDYTTIPDIIVTRNLIADEINRNEFLVDENIATYASLRAGNGMPLLLHASISCKWTIRSDRAQNARSEGLNLRNRKRLPHIVVVTABPTPSRISSIALGTGEIDCVY
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SEQ ID 5321

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SEQ ID 5322

MNTPILPPMILGILGGQIGRMFAVAAKTWGKYVTVLDPDPNAPAEFADRHLCAPFDDRAALDELAKCAAVTFEFENVNADAMRSLAKHTNVSPSGDCVSLAQNRIOEKANIRKAGLQT
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DELDYVGLVALEMVVGDTHELIVNETAPRTHNSGHHTIDACAADQFQQQVRIMCNLPADTKLLSPCCMANILGDVWQEDGGEFDWLPQSRPNHLHLQKRAQGRKMGHPTVLTDD
SDTAFQRAKHLQSL

SEQ ID 5323

TTGAAGATGCTTTGCGAGTCTTGCACGCTGCGCGGCGGTAAACAGTGTGACAGGCTCATGGCGGTATGTCGCGCGCTTCAGACGCGCATCTGTCCGCTTGGTTCGGAFTA

SEQ ID 5324

LKMSLQSCFVAGRNSVSRILMAVCRRLQTASVPLVGL

SEQ ID 5325

TGCTGTTTGTCTCAAAACAAACGCGATTCTAACGCCACAGCGCGCGCGGATGTAATTTTCTGATTTTGTGACAATCTGCTAGAAATGGCGGTTTACAAAATTTAAACCTGCTTCAT
ACCGCAT

SEQ ID 5326

SCLLQTKRDSNATGARRCKFF*FC*QSARMGVYKI*TLAYRH

SEQ ID 5327

ATGTCGGACGAAGCCCTATTATTTTACTGACAGTGTCTGCCAAAGTTGCCGATTGATTGCCGAAGAAAAAATCCCGATTGAAATTTGCGGGTTTGTCAACGGCGCGCGCTGT
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AATCGACTATACGGAAGTCTGCGAGGTTGCGAGTTGCTCATCCGCAATCGAATCGGAAACAACTCGCGTTGCGGATCTGCTTTTCCGTG

SEQ ID 5328

MSDESPIIFDSCAKVADLAEENNPDLKLRVFNVGCGSGFYQYGTTFDEIKNDDFEIEKNGLVFLVDPMNSYQYLVGAEIDYTESLQGSQFVIRNPNAETTCGCGSSFSV

SEQ ID 5329

ATCCTTCCTTTTTCAGATAGGTACTCAGATAAATACCTGAATAATAAGAAAAAAGCATCAGCGCAGTGAACCGAATCTTATAGTTAACCCATTGCGCTTCAAACTAGTAACACA
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TCCGACCCACTGCATCTATCCAGCTTTTATGCTTCCAATAAGGAAAGCGCTGAAACCAACCGCTGCAACCAAGCAACCGCGCAGCGCAATCATATTTTGGTAACGGTATAAGTA
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SEQ ID 5330

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SEQ ID 5331

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GTTCCAAATCTCGGACTGGGCACTGCCGTGCTCGGTGAGGAGAAACATCGCCACAAATCTCGGTTGAGCTTTCTGAAACTCTACGCATCTCTCAACTCGCTCCCGTTTACCTTCTC
AACCGCTACGAATCGCTCGGTTGCGGAGTATTGCACTTGACCCGACATCAAAATCAATGCGAACTGATGCGCAACACCTC

SEQ ID 5332

VQDCKDIFKVLHVSQYTCILSYNEHALKWEGLLNTPESYLPITSDPKALNVAEYKNGIQGFPQIDCQEAQLDALYVHPLFHNILGLTALLRQAEITIAHKSGLSFLKLYASLNSVPFYL
NRYEISLGSVQLDPSIKIKCELMRKL

SEQ ID 5333

ATGCTTGTCTGTCGGTTGGTAGATGGGCAACTTTATACGGCTGTCTGCGCTTGTGGAATAATGTTGATTGAAGATTATCAGTTTGTGTTATAAGCGGGATTAGAGGTGTTGCGC
ATCAGTTGCGAATTGATTTGATGCTGCGGTCAAGCTGCAATCTGCCAGCCAGGAGATTCTAGCGGTTGAGAGGTAAAAACGGGACGAGTTGAGAGATGCTAGAGTTTCAGAAAGC
TCAAAACCGGATTGTGCGGCGCAGGCGAGTGCCTGACGAGTCCAGATTTGTGGAACAGGGGGTGGACGTAAGCGCATCGAGTTGTGCTTCTTGGCAGTCTGATTG
GAAAAATCCCTGTATGTTGCTTTGTATTGCGCAACCCAAAGTCTTTGTGCGGATCGGAAATGTCGCGAGGTAGCTTTCTGTGTT

SEQ ID 5334

MLVLSVGRWGNFIRLSALVEIMFDLKIISFGYKAGLEVFAHQFAPDFDAGVKLQYCRTERFVAVEKVKRDGVERCEVFQKAQTGFVGDGFLTEQGSQSEIVEQGVQVVKRIELCFLAVDL
EKSLYVAFVFGNPKCFVIGNGRQVAFV

SEQ ID 5335

ATGAAAACTTACGACAGGCACTCTATACCGACGCGCTGCTCACCGCTGACGCGCGCAGCGGATTCAAACCATCCGTCGCGCAAAATGCCCGGCAATACCGAATCCGACGAAAAA
ACATTACCTGCTCAATGCTCTATAGATGTGACAGGTATTTTACAAAGAAATACCAACCTATTATTATCAAAACATACCAATCCGAACACCCCGGCACATCCGTCAGCATCCCAACATC
CCAGCGCGCTCAGCAACAGGCATTATCCGTAGCCAAACCGCTTCAAGCGGATTCGTAACCATGAACCAATCTCCGACATCGACCTGCTCGAAAAAAGGACTGG

SEQ ID 5336

MKTYAQALYTAALLTACSPAADSNHPSGNAPANTESDGKNTILLNASTYDTRYFYKEYNHILFKTYQSEHPGTSVSIQQSHGGFSKQALSVAQLQADVVTNNQSSDIDLLEKKDW

SEQ ID 5337

ATGTTTTCCTTGTGCGAAAAACAACCCCAACAGATCCGCGATTGGAACGACCTTGCCAAAGACGGCGTTAACATCGTCATCGCCAGACCTCGGGCAACGGAGCTACGCCCTCCTCG
GCGCATACGGTTACGGTCTGAAAGCCAAACCGCAACGAGCAGGAAGCCCAAAACCTCGTCGATCATCTCTCAAAACACACCCGTTTTTGAAAACGGCGGACGGCGCGCCGCCACCAC
CTTACACAAACGCAACATCGCGGACGTAATCTATCTTTTGAAGCAAGCCAACTACGTCAGCAAAAAAGTACCCCAAGGACAGTTTGAATTCGTATCCGAGCTACACCAATTTCCGCC
GAAAGCCCGCTTGCGTCTCAACAGCGTCTGCGGAAAAAGGACGCAAAAAACCGCCCGCCCTATCTCGAATACCTTTGGAGCGAACCGGGCGCAAGAACTCCGCCCTCACTCTACC
TGCCTCCCGCAACCCGAGTATTGGCAGCAGCAAAAGCCGACTTCCCGACTTAGACACCTTCCCTCCCGAAGAAAAATTCCGCGGATGGGACAAATCATGAAAACTACTTCCCGCA
CGCGCGGCTATTCGACCGCTGACCCGCAAAAA

SEQ ID 5338

MVFLVRKNNPKQIRDNDLAKDGVNIVIAKTSNGRYAFILGAYGYGLKANNENQEAQKLVASILKNTVPFENGRAAATFTQRNIGDVLITFENEANYVSKKLQGGFEIVPSTYISA
ESPVAVNSVVAKKGTQRTARAYLEWLSEPAQELAAASLYLRPNPEVLARHKADFPDLDTFPPPEKFGGWDNIMKTYFPADGGVFDRLTAQK

SEQ ID 5339

ATGACCATTATGCGCTCTGAACCGCCTTTCAGACGGCATTTACACATCAAAACAGAAAACCGCACCCAAATCATCATCAAGACACAACGGCAAAACCGGATACAAAACCAACACCGC
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SEQ ID 5340

MTIMPSEPPFRHFTQNRKPKPKSSQDTTANRIQNPTPPKCRKPSAQPSLSGARLIKGAHNP

SEQ ID 5341

ATGTTCCGATACGAACCGCAAAATATTTGGTTTGTCTTCTGACAGGCAAAAGCACTGTTTATTTGGCTGTCAAAAGGGATGGTTAAGGAAAGTTATGCGCCCTTTGATGAGCGCGCCCCA
GA

SEQ ID 5342

MFRYEPQNIQFVSDRQKHCLFGCQKGLRKVMRPFDEARFR

SEQ ID 5343

ATGTTTTTTGAAAGTGATGTTATATCAAAAAGAAATGCGGCAACCGTCGCGAGTGTGATTGCGCGAAATCGGGTGGTGAACCGATATGCTGCAACCGCTGATAAAGTTTAAAAA
CCTGCTTGGCAAGCAGGTTAATGGTTTGTCTAATCTTGAATTCGCGGAAACGCGAAGACCGGAAATC

SEQ ID 5344

MFPESVIVYQKMRQPSAVLIAGNAGRSNRYARTPDKVLKTLAKQVNGPANLELPETRMTEI

SEQ ID 5345

ATGAATACCGACTTCCAAAGATCTCAAACTGGGCAACAGGCCAAAAAGAGCGGCAGAAAAACAGGAAGCGAAAAAACAAGCAAAACAGGATTGGATTTTTCAC
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SEQ ID 5346

MNTDFQKILKQLKQAKKEAEKQAEKKNQKQEQDLDLFSQAVGVSLPNKQOYYAQSDKTPIKARPKDNRTEZENYFYIGSTYNDPPSPCKNGQSKNDIQRLKNGYPPVTVDLHYG
TQBEAQKVLNEFIATFQKRGVCGEIIHSGSLGSKGYKPVILKNTFRNMLMQHPDVLAYVEPREGNDGCVRIILKRLRQDD

SEQ ID 5347

TTGAGTTTTGCAATTTATGGGGTAACTTTGGGGTAACTTTTCAGGAATCACCTTAAAAATATCTTAAAAATACAAAAGCCATCACGATTTTTT

SEQ ID 5348

LSFRNLWGNFWGNFSGITLKNILKIQKPSRI

SEQ ID 5349

TTGCAGGCGTTTGACCAACAGATTTTCATTAATCCGCAACATACAGTCCGTCCTCGGCGTATTTTCCCATGATTGACCAAAATCGAATCTCCGTCATTTCAAACCCCTCCATCGAA
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CCGCGCCGCGCAATATCATATCTCGGCACAAAGACAACTCGTCCGTATCACTTCAATTTCCCAAGGTATCGTAAGCAAGGATTTTTTTGGGGCTTATCCGGAACCGGATTACCTC
CCCTGTCAGCAGCCCAATCGATACACCCCTTCACTGCTTAATTTTTTTCAATGTTTTCAGACTTCGCGCAGCCGCTTCAFTCCATATCTCTGCTGAAGCCCGCAATCGTCAATTCATA
TCGGATGCGATTTTTGCTCGCTCGCTTCACTTTTCCA

SEQ ID 5350

LQAFDQIFINPOHIQSVSRRIIPMIDQNRISVIONPLHRIPLDGNRYQVFRISGNIILNPMPSERHKYRFLMTDKLPVSRSRPNIISRHDKLVRINFI SQGIVSKGFFWGFIRKRI
PCQPIIDTTPPLQLLNFQCFRLRQTAIPYSAERNRHFNIGCDFCLPRFTFP

SEQ ID 5351

GTGTCGCGCGTACGGTAGCCGATATCCCGAGTCTAACGGCAAGGCGAATACAAAGCTTTTACCGCTTATGTTAAAGGCAAGGCCACTGCGCGCAATTTGAAAGAAAAA

SEQ ID 5352

VSAVTVADIPESSNGKEGYKVFYAVYKATAGNLKEK

SEQ ID 5353

TACTTGGTTTATATGCTTTTGGGTACGGGGCTTTTCTTACCCTAACCAAGGGCTTTGTCCAATTCGCGCTGTTGGGGCGCAGCATCAAGAAATGCTCGCGGGCGCAACAGGGGAGC
ACCTCAC

SEQ ID 5354

YLVMYLLGTGLFTTTFVTFVQFRLPGRSIEKLGGRKQGDDPH

SEQ ID 5355

TTGATTAAACTGTCCGACTTTTTGGGGTGCACTGAGCTTCGGCAATTTTTATCCGTTTGGGGTAACTTGTGTTGAAAGCTGCAAGCCTTATAAA

SEQ ID 5356

LKLSDFIGCSSAFFIRLVTCLSECKPYK

SEQ ID 5357

ATGCCATCCGTTGAACCTGCTGTTGGGGATTGTCGAGTGCACGACGACCTTCTATTACCAATTTGGCGTCCAAATCGGCAGAGGCAAAATATGCGGATTGAAACGACATATCCATGATA
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SEQ ID 5358

MPSEVLELLGIVLPRSTFYQLAVQSAEGKYADLRHIDHDIYQRYKGRYGYRRIAAIRHAGIPVNHKKVSRIMAKTGLKAVIRRRKYSRPFGEVGVKAPNIIQRCFPHSEKPNKWKVTDVT
KFDVGGKTYLSPIMDLFNGEIVSYRIQTRPTFDLAGELKGAPEKPGSEKPNLHSDQWQYQMFYQKQKGNGLVQSLSRKGNCLDNAAMESFPGLKSECFHTKYDSVTESEAAIH
EYIRYNNDRILKLGKLSVPVQYRIQSLKAA

SEQ ID 5359

GTGACGGGGCAGGAATGTCCCAAAAAGCTGCCGACGACCACTGAATCTGCCCGACTGCTCCGTTTTCGCCCAATGCTTGGCGCTCTACCGTTGAATGGTATTACCGTTTAAAGCCCA
AACCCAAAGGAAGAAGCCCGTGAAAAACAGTATCCGCCGCAACGAAAAAGCCGACTATCTGAAACCAAGGAAGAACTGTTTCCGGAATTTGGCTTACCTTAAAGCGGAAGCGCTGT
CCTAAAAAGCTCGATGCTTGAAGAAGTGCAGGAGAAAGCACTCGTCGAGGGT

SEQ ID 5360

VTGQMSQKAAADQLNLPDCSVLPQWLRLYLRLNGINGLKPKEPKGRKPKVKKQYPPQTKKADYLTKEELFAELAYLKAEAAVLKLLDALKEVRQKERNSSQG

SEQ ID 5361

ATGCCGCTTTCACCGTGAATCTGTATCTTGCACCCCACTTTCGCTACCAATGAATCGAAATGGAATAATATAGTGAATTAACAAAAATCAGGACAAAGGCGCGGACCGCAGGCAGTACGA
ATGGTACGGAACCGGTTCCGCCGCGCTCCATCACCTTAGGGAATCGTTCCCTTTTGGGCCGGGGCGGGCAACGCCGTACCGGTTTGTGTAATCCGCTATATTACGGAATGCAAAAAAC
ACCGGCCAAACCGCAGCAACGTTTAACTTGTCAAGAAACACGCTTTACCTGCGGATTCGCTTAAAAACAAACAGGCAGCC

SEQ ID 5362

MPLSPCNLYLATHLRNTESEMEKYSKLTIRTRRTAGSTNGTPEVPRPALHHLRESFPLRGGATPYRLLIRYITDNAKTPAKPQRLTCQETRTCTGFPALKNKQAA

SEQ ID 5363

ATGCCGCCAAATCCGATAGGCAAAAACCGGCTCGATATGTGCGGCGCATCCGGATGCTGTGTCATGAATCGCCAAACATTTTGTATGACGCGCGCGCGGTTTGCCTACCGCCCA
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AACAGGATTTCGACCGCGCGCTGTCCGCCCTTATGCCCGCAGCCTGAAAGGGCAATGGCGAAAGCGCGGATAAGTGGGAAAGATAACCGCGCTTATCTGCGGAACACGCGGAGGATT
TCCAAGGGTTCGCGCTCCGCTATATCAGCAATCCAACAG

SEQ ID 5364

MPPNRIGKNRLDMSGIRMPVCMKSPNILLVRQPPFAMRPNRCGWRAKTAAYKQDPAKVTHYLTRPAGFSDCQRVCPDETGFDRRLFRPYARSLKQMAKARI SGKRYRLSAEHABGF
SKGCGCRYITKSNR

SEQ ID 5365

GTGCGGCTGCGCTATATCAGGAATCAACAGGTAGAAATCTTCTTTGCCACGCGCGATTTCGGGCAATTTCCAGTCGTCGGGATGTCTTCAAACCTTTTCCCGGGGCGGATGCGGT
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TGCCGTC

SEQ ID 5366

VRLPLYHEIQQVEIPFAHAAGFAPFVVGDFVFLCPGDAVFRVAEFFIVNPAAGAAHLSHLCLVCTVLFCSGPPFGSDAV

SEQ ID 5367

ATGAAGGGGAGCGGAAGGATATTTATGAAACCTTTAAAGACAGACTGCTTTTTTATGAAAGTGAAGCGGAGGCAAGAAATCGCATCCGATATTGAAATGACGATTGCGGGCTTCA
GCAGATATGGAATGAAGCGGCTCTCGCAAGTCTGAAACATTTGAAAAAATTAAGCAGTTGAAGGGGTGTAGTATCGATTGGCTGTGACAGGGGAGGGTAATCCGTTTCCGATGAAGC
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GAAACCGGATTTTACAATGGCGTTTCAGACGGCATTTGAGATTATGTATTACCCGAGATACGAAAACTGTCTGTAATTTCCGCTCAAGGGGATTCGATGGAGGGGTTTGAATGACG
GAGATTTCGATTTTGTCAATCATGGGAAATACGCGGAGAGACGACTGTATGTGTTCCGGATTAATGAAATCTGTTGGTCAACCGCTGCAAAATCGTCCCGCGCGGATTTCAATGAT
CATTTCCGCAACGAGGCTTATCTGCTTTTGAATCAATTTGAACGACTTGACCGATGATGTGGAGATTATCGGGCGTGTGAGTGTTCGCGAGGACGGTT

SEQ ID 5368

MKSGRIFMETFKDRLVPLWKSEARQAKIASDIEMTIAGFSRINNEGGLPKSETLKKIKQLKGCSDIWLITGEGNPPFDEAPKSLAYDTLGNEDVTEDEFVFPVYD IRAAGYQGFVGH
EPVTFMAFRHWIENYVTRDTKNLSVI SVKGSMEGVLDGDSILVNHGEWPPRDGLYVLRINENLLVKRLQIVPGIINVISANEATPAPEINLNDLTDEVBII GRVWFPGRV

SEQ ID 5369

TTGACGGGTGAAGCGTTGCTTTTGGACAGCGGTAGCCGACGATTTTTCCTCCAGATAACGTTTAACTTGGACACGCTCCAAACCGCCACGGAACGCTGTGGATTGCGCGCGGTTGG
GTGTAGGTATAACCGCATACACGGCAGCCATTTTGCTTATTCGCGGTTAGCGATGTGTGATTCCTCTTTTGTCTGTGATCGTTTTCGTTCCGGCGTACTCTGCTTAAACGCA
TATCGTGGCGTTCTGAAACGAAACCGATGGACGCTGCGCTTATTTTCTTCAAATGCGCGGAGTGGCTTTGCTTTAACA

SEQ ID 5370

LQGEAFAPWTVGAAFFSQITFNLDLQATATETCGFAARLVGVTGSHFAYCAVSDVCIPSPVVCIVFASGVLCKTHIVAFVERKPHDGVRYFSFKLPAVALEFLT

SEQ ID 5371

ATGCGCGCGCGCTTCAGACGGCATCCGAACCAACCCCGCGCGCGCTGCAAAAAAGCAGGTACAAACAGGAAACACAAATGGCTCAATATATGTGCGGCGCTGCGGCTGGATT
ACGATGAAGAACTCGCGACCCGGAACACGGCATCGCCCCGGGACAAAGTTTGAAGACATCCCGAGCAGCTGAAATGCCCGGAATCGCGCGTGGGCAAGAAGATTCTACCTGTGGA
TTTCTGTGATA

SEQ ID 5372

MRRPASDGRTRPRRPAKKHGTNKTQMAQYMCPCGWYDEELGDPHEGSIAPGTFEDI PDDMKCECGVKEDFYLLDFVI

SEQ ID 5373

GTGGGAAAGATACCGCGCTTATCTGCGGAACACCGGAGGATTTTCCAAGGGTGGCGTCCGCTATATCAGAAATCCAACAGGTAGAAATCTTTTTCGCCACGCGCATTCGGG
GCATTTCAGTCTGCGGGGATGTTCTCAAACCTTTGTCGCGGGGCGATGCGGTGTTCCGGGTGCGGAGTTCTTCATCGTAAATCCAGCCGCGGGGCGACATATATTGAGCAATTTGT
GTTTCTTGTGTAACCGTCTTTTTCAGCGGGGCGCGGGGTTTGGTTCCGGATGCGCTGAAAGCGGGCGCGCATCTGCCGCTTGGGCGGTTTGTGCTTCAGACGGCATTTTC
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SEQ ID 5374

VGKDTGAYLRNTPRDPFRGAAAISRNPTGRNLLCFRRIRGISRRGCLQTL SRGRCRVPRRVLHRKSSRRGRITYIEPFPCLYRAFLQRAAGWFGCRKLRAAASVPPWAVCASDGI
RLFILRLRLFLCRGV

SEQ ID 5375

ATGAACGCCCAACCTGCTTGCACACTGTCGCAAACTGCTCAAAACCAAGCTCAAAACCCCTGTCGACGACATCGACCGCAAGGATACCTACCCGAAGCAATTTATGCGCAACTCGGG
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GGCGGCTGCGCGTGGTATCTGCACAAACGCCCAACCAAGCGCTCAAGACAAATACCTGCGGACATCTGCAAGGCAAGGATTTGGCGGGCACGGAAATGCAATACCGTCAACAC
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CGTATTATTCCGACGAGACATCATCGCTGCGCGGCAACAGTTTTCGCGGTACATCAAAAGCATCAAGACAGGCTTCATCTCTGCAAAATCGGATTCGCGCGGGCGGATTTGAAGCGC
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CCGGATTGGCGTGGGACAACACGCCGACAACTCGCCACCCCTCAAGCTGCGGAGCGCGCGTACTGCGCCCTTGGCGCTGCGCAATCGCGCGCTGCATTCGCGCGCGAAAGGCTA
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SEQ ID 5376

MNAQTLLANVAELVKTKLPLVDDIDRKGYYPEAFMRGELGAVGIEABEGNGLGLATRIAVLREIGKECGATSPSAWQAAACAWYLHQTPNQAVKDKYLADILQKVLAGTGMNIVKH
LAGIEKHNLAECVGGYTVNGALFWVSNIGEDHIMANTAQITGGYVMFTGGQREBVSQNCPEFCALBHTTFSLAFKDVFPIDEDILAAPQFAGYIQTIRAGFILLQIGIGAGVIDG
SLGIIRLVNVNAEVNSYLLDDGYSLKARLDGANWATERLAGLAWNDTNDNLATLKLREAAVLALAAAQSAALHSGAKGYLHRSQAQRVRGEANFVATVTPAIKHLCKEIAAIEAAK

SEQ ID 5377

TTGTTCCTTAAGGTTTTTGGGGGAAATCGGGGGCACGCTGATGCGCGGCTGCTTTTCCCGCGCTTGGGCGGCTTGTITTTTGTGAGGGGTGTITTTGAAAAACCGCCTGCATTAG
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GCGGTTGTAGCCGCTTCGAGGAAGCGTTGAGTTGCTGCTGCGATACTGCGCCCTTTTTCGCCATTACGCTTGGGTGAAGGCGGCAAGCGCGCGAGTTTGGCATCTGCAGATTAC
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TGTITTTGGGTAGCGCTTACGCGCGGTTTGGCGGCTTCGCGGGCGGTTTCGAGGTTGTACGTT

SEQ ID 5378

LFLKVPFGKSGRMRGCFRRLLGGFLFEGVFLKRLHSGGFVCLGVCLQFGVDFGLGEVGVVAAQSCQGYAHYDFDCLLPVVARFEEGVFVVGCAFFRHYGLGEGGKRAEFIVRFT
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SEQ ID 5379

ATGGCAGCTTTAAACGTACACACCCCTCGAAACCGCCCCGAGCGCCCAACCGCGCTAGAGCGGCTACCCAAAAACAACGGCTTTATCCCAACCTCATCGCGGTATTGGCAACGCC
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SEQ ID 5380

MARLTVHTLETAPEAAKPRVEAVPKNGFIPNLIGVLNAPLEALFYQEVGKLNAAASLTAGEVEVIRILAVRTNQSPCVAGHTKLATLKLKLSSEQSLNARALAAGKSDDAKLGALAAP
TQAVMAKGAUSDDELNAPLEAGYNRQAVEVVGVALATLCNYANLQAQTEINPKLQAY

SEQ ID 5381

ATGAACGAGAACTTTACCAATGGCTGCACGCGTGGGTGGCGCCATCAACGATCCGATGTGGTCACTATGCTTTTGGGTACGGGCTTTCTTACCCTAACCGGGCT
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SEQ ID 5382

MNENFTWELHGWGAINDPMSYLYVMLLTGLFTTGTGVPQRLPGRSIEKMLGGRKQDHPHIGITPQAFVTGLASRVGVNIGAVAIKVGPGAVFMMVNTALIGHSSAFVSSSL
AQLPKVRDCDNNHFRGGPAYITYTHGLGQKWLGLVLFALSLIFCPGFVFAVQNTIADTVKANGWEPRHYVGVVILPAPIIFGQIRRIKAAAEIVVPLMAVLYLFIALLTNPILPD
VFGQIPSGAFKFDAAAGGLGLISQTMMGIKRGLYSNEAGNGSAPNAAAAEVKHPVSQMIQMLGVFVDTIIVCSCTAFIILITYQPYGDLGSAALQAAIVSQVQWAGAGFLAVILF
MFAPSTVIGYAYAESNVQPIKSHWLIATVFRMLVLAHVYFGAVANVPLWMDMANGIMAWINLVAIIILSLPFLMLRDYTAFLKMGKDFEFLKSEHPLKRIKSDVW

SEQ ID 5383

ATGCGTTTTAAGCGAGTACGCCCGAAGCAAAACGATGCAGACGACAAAAGAGGAATGCACACATCGCTAACCGCGCAATAGGCAAAATGGCTGCCGTGTATGCGGTTATACCTACA
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AGCAGATGTTGAAATCCGTCAAACCTTGGCGAAGGCTGTTTCTGAAGCTA

SEQ ID 5384

MRPKAEYARSKNDADDKRGNAHANGAIGKMAAVYAGYTTTQPGGESTFRGGLEVRVQVKRYLGEKCCGYACPKSERFTLQADGEIRQNLGEGNFKL

SEQ ID 5385

TTGCTGTTTTCTTCATTTTTCTATCCTTTTTCTGTCAATTCGGGATTAACCTATGGAATATCTGAAAAATTTATGTATGGATAAGAAAAATCATATTTAAATTTAGTTTATCATAGTT
ATTCGTTTTTGGGATAGCTAATGTAAATATATTTCAATGTTTACTT

SEQ ID 5386

LIVFPFIFLSFPQPGIKPMENLKNYVLDKKNNHNLNVHSYSVFGIANVKYISCLL

SEQ ID 5387

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ACTGCGGTTTTAAGTATTTGGTTTGGCGGTTTCCGTCTGGTTCCGCGCAAGGCGAACAGCTTTATGCACGCCACTTTTATCGCGCGCTATACCGAATGGCCGAACAGTGAAGC
CGCAACCCCGAAGCGCATTTGGCGCAATATTTCCGCGCGCGGGCGG

SEQ ID 5388

LFGTLWACFKRMWGLGHTGAMPVLAVFAQLVYGDTPATDSAFNVGLAVSVWFGAKGNSLYARHLISRGYTELPEVVEANPQAALQYFGRGG

SEQ ID 5389

TTGTTTGAAGGCTTGGGCGCGGAGGCGGATGGGTGTAGATTTTGTATGTTTTCATGCTGTTTCTTTTCGTTGAAACCTGCCCTTTGGGAAGGAGGATCAGACTTTATTTGTGAGA
CGCGCGCGGTGTGAGACATACGCTTGAACATGCCCTCGGGGAAGACAGATCCGACAACTCCGCTC

SEQ ID 5390

LFDGLRGCGMGVDVFWFHRVSFVETLFPFGKVSDFICETRARVQTYGLNMPVGEDRSINAV

SEQ ID 5391

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CCGACGGCAACGATTACGACCGGACATCGTGAATGTGAACACCATGCGGATGAACATCATCCAAACCATCAACAAACGAACAGTGTGCTGCGCTGCCCGCTCGACCTGAAACGAGT

TGAAC TGCTGCTGAAACCTTTGGGACGAGAACCGCATTCGGT CATCGGCTCTTC TTGTCATCGCGCGTCCGTTT TAGCGCGGTGTGCAACAAC TCCGGCGCGCGTGTGGTACAGCGCGG
CCGGCTACACCGAATGGCGTTGTTCGCCAAATCAACGAAGAGCGGAGTGTGGAAC TGCTGCTCAACCATCTGGGCATAGACTTGGCGACACAGCCCGAAGAAATCTTGACCAACCTGCAAG
GTCATCATTTATCAGAAAAAGACCATCAAGACAAGACGCGGCAAGGACATGACCACGCTATTGCGAACACGTCGCCCACTGGAAGAACCGACCGCGCGCGCTTCAATGCCGACCCCGC
CGCCATTCAGAAAGCCTTCGGGCTCGCGGGGCAAGCTGATGGTTTTTGCGCTCCGTTTGGACACTTCCCGCAAGAAAAACAACCCGCGGTGTTCTACATCGGCACGAACGACATCAACGAG
CTGACCGACATCCGCCCGCGCCCTTTGGCGAAATTTGAAAGCTGCGCGCTTTCGCGGCAATACATCCACGCCACGCTTTGCACATTCCCGACAGTGTACCGCAAGACACGTTCTACGTC
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ACGAATGTGAGGAGCATTTGGTGGCGCTGATATTGAGCTGCGCGCGCGACACCGCGACTGGTTTGA AAAATCGCCCGGAAATGCACAATTAATTCATTAATTTGATTTACCGGCATTT
TATGTGCAACGCTTTTCCATCAGGATTACATCATCAAAAAAGCAACGGCTGTATGGCTTGGAAACAGAAATGTCTACATCTCTTAGACCAACGCGGCGCGCAATATCCGCGCAACACAAC
GTCGGCCATTTGTATGAAGCCAAGCCCGCGCTCAACAGTTTTACCGCAAACTCGACCGGACCAACAGCTTCAACCCGGGTATCGGCCAAACACGCAAAAAGAAAACTTGGCGGAA

SEQ ID 5392

EQ ID 5392
LAVVRPGSILEMWRKILQACVEADVIVITQAAFTGLTGGSTPDGNDYDRDIVIVNVMRMIQITINNNEQVCLPGSTLWQLELLKPLGREPHSVIGSSCIGASVGLGGVCNNSGGALVQRB
PAYTEHALFAQINEEGRLELVNHLIGDGLDTPBETILQDQGHYQKKDIQDAGKGHDHAYCEHVVRQVDEPTAARFNADPARHYEASGCAGKLMVFAVRDLTFPQEKQTAVFYIGTNDINE
LTDIRRAALGEGFESLVPVSGEYIHRHAFDIADVPYKQDFTFVILKPGTHQLPKLFDLKRVDPRGKVSFLPKHFSOKAMQVFSKFLPDHLPKSMRDYRDKYEHLLILKMGGGGVDEARAFLE
EYFSSHGGGAFFECNAEETQAAMLERFAVASAAIYRSVHDEVEDVALDIALRRDDRDWFELKLPPEINDKILHLYYGHFACHVPHQDYI IKKNGCNCALHEHLEHLILDQGAQYPAEHN
VGHLYEAKPALQYFVKLDPTNSFNPNGIGKTSKKKNAB

SEQ ID 5393

SEQ ID 5393
ATGATGTAATTTTCGCTACGGTTTGGGTCAGGCTGCTGATTAAATTCGGAGGCGTTCAACAACCTCTCCTATCGGGATAAGCGCGCGCAAAATCCCGGTACGCCGCCGTATGTTCAATTT
GCAATATTTTGGTGGCGCAAGTTGCACGCTGCAAATTAATTTTGGTTAAAGAAA

SEQ ID 5394

MMYPSPTVWVRLLINECAFITLSYRDKRRRSRYAAVCSIWIFWCGKLHAANYFWLKK

SEQ ID 5395

SEQ ID 5395
ATGAAAAAACTTCTAATGATAACCCCTCACCGGTATGCTTGCAGCTTGTTCACAGGTGTCAATGTGCGCGGTTGATGGTTGAAATGCCGACAGGAGAACGCCCTGTTGTGCTGCAGGTTTC
CCGCGACGAATAAACCCGCTTTCGATGCGGTGGCTGTCCGAATGATTAACAATCCCGGATCGCCTTCGGCATCAAAATATGATTGAAATGCTCGCGCGGACAAATATCAACGTGCGCGTGGC
GGGAGGCAGCCAAATGTTTAATAAGGCGACCGCACTTTATTCCCTTAAACATGCAAAAGAAATCGGAAATAATGTCAGTGTCTATATGACGGGGCATAGCGAAAGGCACAAGGCCGATTTG
GAAACCGCGCAAAATGCCAAAAATATTAATATACATTATTCTTTAACCAAAA

SEQ ID 5396

SEQ ID 5396
MKKLLMITLTGMLAACSTGVNVRGLVEMPQGERFVVVQVPATNNPLSDAVAVGMKITSGPSASNNMIEMLGADNINVGVAGGSQMFNKAPALYSLNHAKKVGNVSVVNTFGDSSESKADL
ENAAANAKNIKLYHFFNQK

SEQ ID 5397

SEQ ID 5397
TTGAANTGAACCATACTTCCATTTTATGAAGCCGGTTCCTCATTTGGCCCTGTATGGATACATTGTAATGATGCGTTATGGCAAACTAAAGGAAATGCCGTC

SEQ ID 5398

LKLNHTSIFMKPVLHWPVWTHCNDAL#QSKGNAV

SEQ ID 5399

SEQ ID 5399
ATGAAGAAAACAGCAAATATCTTATCTACTGCGGCATTACCTCATCTGCCTTTGCCTTCCAAGAAAACGGTCTGAAGCAAACAGCCCGACATCACTTTATCCGCATCCCTGTGCG
AACAAATTCACATGCTGAAGCCAAAGATATGGATACAGAACAGTCTCCCTTTCCAAGAATGCGACATCATCGAGTCTTCACACGACTGGGAAAAAGTAGTCGGCAACTTGAACGAACA
GGAAATGCTCGCCGGCGTCTATGAA

SEQ ID 5400

SEQ ID 5400
MKRTSKYLIIYTAFTSPCFAFQENRSEAKQPDITLSASLCEQFMNLNAKDMITEQVSLSKCEDTIESSHDWEKEYGNLNEQENLAGVYVE

SEQ ID 5401

SEQ ID 5401
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CCGGCAGTCTCGGCGTAGAGTTTGACCCATACTACGCCACCGCGCAATCCGCAAGTCTGCCGAATTGTCTCGAACACTACCAAAACCAAAACAGACAGCGAAAAGTTTAACGAG

SEQ ID 5402

SEQ ID 5402
MSGVAVYL R N K N R I A I A S O D A N L N S K G R F V S S G L N V G K Q L T G S L G V E F D P Y Y R H R A I R K S A E F V S N T T K T K T D S E K F N E

SEQ ID 5403

SEQ ID 5403
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AAACACCGCC

SEQ ID 5404

SEQ ID 5404
MPSERLSDGIGAIRRRNIEAPAFQIGRRTKPPALAHRSGLLASAFDPVFRFAMRGDPQRRNGIITGFLKNSTVLIRSYAGNTA

SEQ ID 5405

[illegible]

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ACGGCATCGGCATCACCAAGCTCGAATTCCTCACCAGTGAAGATTTGCAACCGTTTGGAACTACAAAAACCAAGTCGACCCCAAGCACACCTTCAACCGCCACAACTGATGAAGGTTTC
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SEQ ID 5406

LNYYIAPSPNETDFSNIGIQTAKHGHMTTTTTAPQRIRIEIPYNTSYTDREIVIRLLGDEAHILQLDRGQRKTGRSARMLFEVLGDIWVVVRNPFYVDDLLHEPKRRAALVREMRHL
NEIRKRRDDNQADVLAAAEKAVERFDGSDFTETQRKRQILERLSKITPHNINFDGLARVTHVTDATDWRVEYFFVVPVNDTEAEVAPLVRALIELDLVII PRGGGTGYTGGAAPLDAN
SAVINTEKLDRHGRVEYVELAGLYGRHPIIRCGAGVVRVEETAHQAGLVFAVDPTSDASCVGNNVAMNAGGKAVLWGTALDNLAYNNMNPQGEHLRIERVHRNFGKIHDEETAVID
VHTLSDGINIVKTERLEIPGHKPRKVLGKDVTDKPLSGLPGVQKBTGDIITGVAVLHKPKYTRTCMEFFCTAATATPSIVEIRDPLLAHDSVRLAGLEHLDRYVRAGVYATKAA
GKGRPKMVLADVVSDDEAAVEAAAEHICELARARDGEGFLAVSPARKFTWLDLRSTAAIAKHNAFKNEDVVIPLERLGEYSDGIERINI ELISIQNKLLCAALEQYLSGLPLIDKHG
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NVHTNIPVNSDDAEMLQTAYSVERIMKIARSLGGVISEGHEGIGITKLEFLTDEDLQFFWNNYQVDPKHFTFNRHKLKMGSDLRNATPSPPELLGAESLIMEKSDLGTIADSVKDCIRCGK
CKPVCSTHVRANLLYSPRNKILGVGLLFEAFLYEQTRRGVSVKHFEELMDI GDHCTVCHRCVKPCFVNIDPFDVTVAVRNYLADSGHGRFPAPASMGMAFLNATAGGCGACCTGCTG
GFPANFAYKIGKLLPIGTKKQAEPRATVKGAPIKBQVIHF INRPLPKSVPAKTPRSLGIEDGKSIPIIHNPAAPEDAFAVFPFGCGSERLFSQIGLAVQAMLWHVGVTQVLPFGYSC
CGYPODAGNKAEMSTNNRVAFHRMANTLNLYLDIKTVVSCGTCYDQLEKYRFEIIPFCRIIDTHEYILLEKGVKLDGVKQYLYLHDPCHTPIKTMNATQMASSLMGQKVVLSDRCC
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SEQ ID 5407

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ACCGTCAACAAACAAAGGCGGCGCAATCTTCTGAAAGAGCGGAACTGATATTCACATCGTCAAAACGCTGCGCGGACGTTTGCCTGCACATATTCGCTGACGGGGAATGCGGC
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GGTCCGCGTTCGCGTTCGCGCGCAATTCAGCAATACGAGAACCGCGGACCGGTCAAGAGACACGGATTTCGCGAAGTTTCCACATGATAGGCGAGTTTTCGAGC
TGTGCTGACAAAGAGGCAAAACAAATACCCGATCGCGCTCTTAAGCAATGGCTGGGCTGATGAAAAACGTTGACCGCGCGCAACGCTGTCGACCGCGTCCGACGTTAA
AGATCGGATGAAGTCCGCGCAATCTGAACGCATTTGACATGAGATGATGTT

SEQ ID 5408

LNQIPTRIMIDGQTFEPKQRTIIPAFMRGLVDDVMRDLITRIGGYDECVSEFVRITHTVHSRISWLKYVPELANGNKTFSGTPTCTVQLLGSADNMMAALEAVRFGADKIDLNFGCPAP
TVNRHGGAILLKEPELIPHIKTLRGLPAHILPTGKRLGYEDKSPALECACALAEAGGACGLVTHARTKAEGYEPFAHWEVIRKIHDTVNIPTVANGDVSLQDYITGIRPISGCNSVML
GRGAVIRPDLARQIKQYENGFPVKDITFAEVSTWIGQFFELCLTKBANNKYPIARLKLQWLMKMTFDPAPQTLFDRVTVKDADEVRIILNAFHEHDV

SEQ ID 5409

ATGTTTGTGATATGTAATCGGCTTTTTCGCGCTTTGTGCTCGCGCTGCTGCTGCTGCGTCAATGCCGCGCGTTCGGTATGCAGGAAGCAGATACCCCGCAATCGGATTATGAAAAACGTT
TGGGTTTGGGGCGCAAACTGAAAAACAAAAATACACCGAAGCAGGGGAAAAACGGCAA

SEQ ID 5410

MFVYVIGFCFVVALLSLVNAGAFGMQEDDTPQSDYERLGLGAKLNKNTPKAGEKQ

SEQ ID 5411

TTGTATCTTTATTGCGCTTTTCCCTGCTTTCGGTGATTTTGTGTTTTTTCAGTTTCGCCCCCAAAACCAACGTTTTTCATATCCGATTGCGGGGTATGCTTCTCTGCATACCGAAC
CGCGCGGCAATTGACCCACAGCGACAGCAGCGCAGCAAAAGCGCAAAAGCGGATTTACATACCAAAACATTCGCCCTCCAAATTTGTAAAAATCATATCAATACAGTCCGCAATTTATC
ACAAGCGCAGGACAAATAATCTTTCGACCGCAGTATTTTCATTATTTACCTTGAABACAAAAAGGGCAC

SEQ ID 5412

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SEQ ID 5413

CCGAGCGCTTCCCGCGAAGCGGCTTTCCCTTTCCGCGCACTGATAAAACAGGGCGAACAGCGCTACATCCCAACCCCTTACTTTTGAATCGGTTTCGTTTTCAGACGGCATCCTG
CTTGAATCCGCTTGAAAAACCGATAGGCAATACACACATGACCCACAT

SEQ ID 5414

PEPLPREAAPPFRITVKTGRTGVQSQPTTFESVSFFRRHPAMNAV*KTDRQYTHDPH

SEQ ID 5415

TTGGTGTACCTAAGTCGATACCGATTACTTTTGCCATGTGGATACCTATTGTGATTTGCTTATTTTGAGAAATATGTTGGAACATTTTGTCCGATGGGCTG

SEQ ID 5416

LWPKSIPITFAMWILLDFAYFEKYVGTFCPDGL

SEQ ID 5417

TTGATGAGCAAGGTTGTACGAAGGTTGAAGGCCAACCTGTGGGTGTTTGTATGTCGCGCTTGAAAAACGTTGTTTAAAGGACAAATGCCCTCTGAAAAATGTTTAAAGCGCAT
TTTCGGTTTGTGTAACAA

SEQ ID 5418

LMGRLYEGWKATCGCLWWSRLKKRVLRDKRLKIGFTAFSVCRQ

SEQ ID 5419

EQ ID 5419
ATGAGCGAAACCGGAAATCAAAC TCAACGACCGGTCCGAAATGCAGAAAAACCAACGAAAAAGTCGAAC TGCCATTGTCGATAACGACAAAAAGGCGGACACGGCGAAGCGGGTT
GCTGCGGC

SEQ ID 5420

MSETAKIKLNDRSENAEKPNEKVELPIVDNDKKGGHGECCG

SEQ ID 5421

SEQ ID 5421

TTGCCGAAAAACGTATCAGCCGCAGCAACCGCCTTCGCGGTGTCCGCCCTTTTGTGCTATCGACAATGGGCAGTTCGACTTTTCGTTTGGTTTTCGCAATTTCGGACCGGTGCTTG
AGTTTGATTTTCGCGGTTCGCTCAATTCCTACCTCATTTCGAAACCGGTTTGAAAGATTCAAAATATAGCATGTTTAATCCGAATC

SEQ ID 5422

SEQ ID 5422
LPKNVSAAATAFAVSAFFVVIDNGQFDFFVWFFCFIFGPVVEFDPRGFAHFLTSPGKRFRERFINIACLRIR

SEQ ID 5423

SEQ ID 5423
ATGTTTAATCCGAAATCTGAAAAGGAAGCCGTATGCCAAATCCCGTCTGAAGCCCAATCAGGGCTTCAGACGGGATTTGCTATCTTTATTCGCCGCTTTCTTCGGTATCCGGATTTTGTGTTGGGGCTGAAGCAGATTGCCAGTCAGATTGCAATCGAAGAA

SEQ ID 5424

SEQ ID 3424
MFNPNLKREAVCEIPSEAQSGLOTGFAIFIAAFLPYPDFCLGLKQIGSQIAIEE

SEQ ID 5425

SEQ ID 5425

TTGGCAGGCGAANTCGGCAGGCGCTCGCCGGTCGCGTTGCGAATCCGTTTGGCGATGCCAGCAAGCCATTGATCCCTTGGGACAGCAATAATAATGTGGCTTCGCAATTGGGTATTTTCA
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SEQ ID 5426

SEQ ID 5426
LAGEFTGALAGRANPFGDASKAIDPWSNNNVAQLGIPKRRHDMFVSVRYDSPGSGSGSIQFVPSQNSKSAYTPATFTLESNQMKPVPAVVGKPGSDVYYAGLNKYNGGGFFGNLYALK
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SAAWLKRTGTGIGNYTOINAASVGLRHKF

SEQ ID 5427

SEQ ID 5427

TTGCAATGCAAGAATGAAGGCAAGCCATCAAAAACAAAGCTATCCGCTTACC GCCCGCGATATTTAGAATTTGTGGCGCAGACCAACGGAGCGCGCATTAATTTGAGTGTAGTTGCCGATG
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SEQ ID 5428

SEQ ID 5428
LQSKNEGKPSKTKLSASPPRYLEFVAQTNGGGINLSVVDAGISFQPSGRHDGGSALGKIVIDTGDDLLIAGMFAFLTAPDKVETNGIADARDCITEAVGSSGGNGFGRTVFGVFGIPIQIQ
LSRQGEIQAAPIIARQAVLVMVPQWIGITRSABEQEKSEIMPLIGVFRIFPKGIISEKAAIFVIQTGIIHIRPLADNSRWNPHLITPQRESSRIGGLAVLTRNKLANAAATGKSGGIVT
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SEQ ID 5429

SEQ ID 5429
ATGTCCTGCGCTCCACACCAGCTTTGACTTCGCCGTACAGGCTGACATCGGCAACTGCCGAAACGGCAGTCGCGACAATACGAGGGCGGTAAGTTTTTTTCGCATATCGGCTTCCTTTT
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TATTCAATA

SEQ ID 5430

SEQ ID 5430
MFLPSTPALTSPLYRLTSATAANGSADNTRAVSFRRISASFCKFAKNIGQTPNQSPITPRKKKTIIFRNKFEVNFNGIFILKNNSI

SEQ ID 5431

SEQ ID 5431

TTGGCCATTTCGGAACCGGTCAAAACCAAGTCATCGAAAAACGAGAAGCGCACGCCACCGCGTCCATTATCGCTTATTGGACGGCGCGGAATCTCGTCGGCGCGCTGCCAAACGCCAACGGTAACCAACGCCAAAACACTATTATACGCGCCCAACGFTTGTATCGGTACAAAATTGAAGACAAAGAAGTCCAACGCGACATCGAATCTATGCTTTCGAAATCATCAAGCGCGAACCGGACGATCGGTGAAGCGCAAGGCAAGAGAGCTGTCTCTCTCAAAATTCCGCGAGAAGTCTGCGTAAAAATGAAGAAGCGCGCGGAGAGCTTACTTGGGCGAAAAAGTAACCGAACCGGTATTACGCTCCCTGCCTACTTCAACGACAGCCAACGTCAGGCCACAAAGACGCGAGCGCGTATCGCGCGGTTTGGACGTAAACGCGATCATCAACGAGCGGACCGCAGCGCTTGGCATTCGSTATGGACAAAGGCGACAACAAGACCGCAAAATAGCCGTATATAGACTTGGGCGCGCGTACCTTCGATATTTCCCATCATCGAAATCGCAACCTCGACGGGACAAACAAATTGAAGTATTGGCTACCAACGGCGATACTTCTTGGGCGGTGAAGACTTCGACCAACGCTTGATTGACTACATCATTTGACGAGTTTAAAAAAGACAAAGGCATTGATTTGAAACAAGACGTATGCGCTCGACAGCTGTAAAGAAGCTGCCGAAAAAGCCAAATCGAAATTGTCTCAGCGCGGACCAACCGAATCAACCTGCCGTACATTACCATGGACGCAACCGCGCGGAAACACTTGGATGCGCTCGACAGCTGTAAAGAAGCTGCCGAAAAAGCCAAATCGAAATTGTCTCAGCGCGGACCAACCGAATCAACCTGCCGTACATTACCATGGACGCAACCGCGCGGAAACACTTGGATTTGGTTCGGCGCTAGTCGCGGTATCGCGGAAGCTACCAAGACGTGAAACCGTGAAGAGATGCCGCGCTTGAGCACCGCGGACATCGACGACGTCGAATGAAATATTACCCGCGCCAAATTGAGAGCGCTTGATGAGACCTTGATTCGCGCAAGAGACCTTCCTCGGCAAGAACCGCGCAAGACGTGAACCGTGAACGAAGCCGTTGCCGCTAGGTGTCAGCGATTGATTTGGTTCGGCGCTAGTCGCGGTATCGCGGAAGCTATCGGACCTTGATTCGCGCGCTCTATCGAGCGCTTGGCGCACCGCAFTGAAAGATGCCGCGCTTGAGCACCGCGGACATCGACGACGTCGAAGCGGAAGTATTGAGCGGCGCGCGCAGCGACGTATTGCTGCTGGACGTAAACCCCTCTGTCTCTTGGGTATCGAAACCATGGTGGTGTGATGACCAACGCTGATTTCAAAGAACACTACTACTTCCGACTAAAGCGCTCTCAAGTGTTCTCTACTCGCGGAAGACAACCAAGCGCAGTAACCATCCAGCTACTGCAAGGCGAACGCGAACCGCTTCTGCCACAACAACTCTTAGGTCAACTACTTCAAATTGGGCGGACATCGCACCGCGCACCGCGGTATGCCGCAAAATGAAGTACTTGAACCATCGACGCGCAATCTCTGCAAGTATCTGCAAGTATCTGCAAGTATCTGCGCTTCCGCAAAAGACAAAGGCACTGGCAAAGCGGCCAACCTGGAAGCCCTGATTACTCTCGTGAAGAAATCTTTTGGCGGACTATCGCGGCAAACTTCGACGCTGCCGAGAAGAAAAATCGAAGCGCGCTGAAAGAGCGCGAAGAGCCGTGAAAGCGGACGCAAGCCGATCGATGCGTACCGCAAGCGGACGACTGGGTACAGCGACGCAAAATCTGGCGGAAATGGTTTACGCGCAAGCGCAAGCGGCAAGCGCGGAGGCGCACAGGCCAATGCTTCTGCAAGAAAGACGATGATGTCGTAGATGCCGACTTTGAAGAAGTAAAGACGACAAAAA

SEQ ID 5432

SEQ ID 5432
LAISENGQTKVIENAEAGRTTPSIIAYLDGGEILVGAPAKRQAVTNARNTIYAARKLIGHKFKEDKEVQDIESMPFEIIKADNGDANVKAQKELSPPOISAEBVLKRMKEAABAYLGKEVT
EAVITVPAYFNDQRQATKDAGRIAGLDVKRIINEPTAALAFGMDKGNKDKRIAYVDLGGGTFDISIIETIANLDGDKQFEVLATNGDTPLGGEDFDQRLIDYIIDEFKKEQGDILKQDV
MALORLKEAAEKAKTELSSGOQTEINLPYITNDATGPKHLANKITRAKFEIIVEDLIARSTIEPCRTALKDAGLSTGDIDVILVGGQSRMPKVQRAVKDFFGKEPRKDVNPDEAVAVGAAL

QGEVLSSGRSDVLLDVTPLSLGIETHGGVMTLQKWTITPTKASQVSTAEQNSAVTHVLQGERERASANKSLGQFNLGDIAPAPRGMPIEVTFDIDANGILHVSADKGTGKAAN
ITIQSSSLSEEEIERMVKDAEANAEDKLTFLVASRQARALIHVSVKSLADYGDKLDAAEKEKIEAALKEAPEAVKGDOKTADAKAELGTASQKLGEMVYAQAQAEQAGBAQAN
ASAKDDDDVVDADFEVKKDKK

SEQ ID 5433

ATGTTTGATGGAGCAAGGTTGTACGAAGGGTGAAGGCAACCTGTGGGTGTTGGTATGGTCGGCTTGAAAAACGTGTTTAAGGGACAAATGCCGTCTGAAAAATGGTTT

SEQ ID 5434

MFDGAKVVRVVEGNLWVFGMVALEKTCFKQMPSENNF

SEQ ID 5435

ATGTTGCGGGAAGCAACATTTTCAAAAAAGTTAATTTATTTGTTTATATTGAATAATTATTTTCAAAATAAAAAATCCAAATTTACCCGAAATTTGTTCCGAAAAATGGTTTTTTTTT
TTCGGGGGTAATTGGAGAC

SEQ ID 5436

MLRESNIFPKVNLFPYILFPKIKPKFTRNLPRKVVFFRGVIGD

SEQ ID 5437

ATGCTTGCCCGCGCAAAACCGGTGTCCGGAATATGGAGAAAAAGACCGGATGCAAAAAATCCCCCTGACCGTACCGCGTCCGGAATTGCTGAAACAGGAATTCAGCAGCTCAAAAGCGTGG
CGCGTCCCGAAGTGTATCGAAGCGATTGCCGAAGCCAGATCGCACGCGGATTGTCCGAAAAACGCCGAATACGAAGCGCCAAAGAACGCCAAGGTTTTATCGAGGGCGCATTTCCGAGTT
GGAACACAAATTTCCGTTCGCCACATCATCAATCCGCCGCAAAATCCACGCCGAAGGCAAAATCGTGTTCGGTACGACGGTTACGCTGGAAGATTGGAACCGGAAGAACCGTTACCTAT
CAAAATGTCGGCGAAGACGAGCCGACATCAACAGGCAAAATCTATGTCGGCTCTCCGATTGCCCGCGCTGATCGGCAAGGAAGAGGGGATACGCGGGAAGTTACGCGCACCGGGCG
GCGTACCGCAATACGATATTATCGAAGTCGGTATAFT

SEQ ID 5438

MLAAANRCAGTWRKRPQKIPFVRGAELKQELQKLSVARPEVIEAIAEARSHGDLSENAEYEAKEKQCFIEGRISELEHKLVAHILINPAKHABEKIVFGTTTLEDLETEHVY
QIVGEDADIKQKITYVGSPIARALIGKEBGTAEVQAPGGVREYDIIEVYI

SEQ ID 5439

GTGTGTGAGTGTATCGAAATCAAGCCGANTCAAAATATACCGGACTTCGATAATATCGTATTCGCGTACGCCGCCCGGTGCCTGAACCTCCGCGTATCCCTTCCTCCTTCGCGATCAGG
GCGCGGCAATCGGAGAGCCGAGATTTTGATGTCGGCTTCGCTTCGCCGCAATTTGATAGGTAACGTGTTCTTCGTTTCCAAATCTTCACGGTAACCGTGTAC
CGAACACGATTTTCCCTTCGCCGTGGATTTCGCCGCGATTGATGATGTCGGCAACGGAAGATTGTGTTCCAACTCGGAAATCGGCCCTCGATAAACTTGGCGTTCTTTCGGCGCTC
GTATTCGGCGTTTTCGGAACAAATCGCGTGCATTCGGCTTCGGCAATCGCTTCGATCACTTCGGGACGCGCACGCTTTTGAGCTGCTGCAATTCCTGTTTCAGCAATTCGCCACCGCGT
ACGGTCAGGGGATTTTTGCATCGGTCTTTTCTCCATATTCGGCACACCGGTTTCGGCGCGCAAGCATACCGGTACCGTCTGTTTTCGTCGCGGATATTAATA

SEQ ID 5440

VCRVYRNQAESNIPDFDNI VFAYARCLNFRRI PFPLADQAGNRRADIDFALDVGFVADNLIGNVFRPQIFQNRNRTEHDFAFGVDFGRIDVGNKGFVPLGNAALDKTLAFFGGF
VFGVPGQIAVRSFGNRFDFHGFTRHAFELLQFLFQQFRATAYGQDPLHRSFSPYSGTPVCGKHTAYRLVLCVRLK

SEQ ID 5441

GTGTGCCGAATATGGAGAAAAAGACCGATGCAAAAAATCCCCCTGACCGTACCGGTGCGGAATTGCTGAAACAGGAATTCAGCAGCTCAAAAGCGTGGCGCGTCCCGAAGTATCGAA
GCGATTGCCGAAGCCAGATTCGACGCGGATTTCGCCAAAAACGCCGAATACGAAGCCGCAAGAACGCCAAGGTTTTATCGAGGGCGCGATTTCGAGTTGGAACACAACTTTCCGTG
CCCATCATCATCAATCCGCCGCAAAATCCACGCCGAAGGCAAAATCGTGTTCGGTACGACGGTTACGCTGGAAGATTGGAACCGGAAGAACACGTTACCTATCAAAATGTGCGCGAAGACGA
AGCCGACATCAAAACAGGCAAAATCTATGTGCGCTTCGGATTGCCCGCGCTGATCGGCAAGGAAGGGGATACGCGGAAGTTACGACCGCGCGGTACGCGAATACGATATT
ATCGAAGTCCGGTATATTGATTTCGGCTTGATTTTCGATACACTCGACACACGAGGAATTAAGCACCGCGTGTGTTTTTTATGTTGTTTT

SEQ ID 5442

VCRMEKKTDAKNPDRTRCGIAETGLAAQKRGASRSDRSQIARRFVRKRRIRSRQRTPRFYRGPHFRVGTQTFRCPHHQSGRNPRRRQNRVYDGYAGRFNGRTRYLSNCRER
SRHQTFQNLRLSDCPRPDRQRRGYGGSSGTGRRTRIRYYRSPVYLIRLDFDLDTRRLKHRVCFPHF

SEQ ID 5443

TTCGCGCGCAAGCATACCGGTACCGTCTGTTTTGTCGGTCCGATATTAATAAAAAATACAAGCCCGCGGAAAAATCGCGGCTGTCTGTGTTGAACAGCGGCTATTCTACCAAA
TTCTA

SEQ ID 5444

LRRQAYRVPSCFVRPDIKIKIQAARKIGLSVVEQRLFPYQIL

SEQ ID 5445

TGACACCGCGTATTCTACCAAAATCTATGAAATGGCAATCGTCCGTCGCGCGGCAAAACGCGCTATGTCGCAACAAAGCCGAAAAATATCGCGCAAAAAAATTTAGAAACAAA
AATTTAAAAAATCAATTTTCGGCA

SEQ ID 5446

LNSGYSTKFEIGNRAVPANALCPQQKPKICRQKNFRNKKPKKNQPSA

SEQ ID 5447

GTGGAAGGTTTGGCGAGGCGCGGGGAGCGGACGGATTCCGTCATGCGCAAAACGTAAATATAAGATAAAAAACAGCCTGCATTATATCGTGCAAATCCGCTCTGAAAAATCTCAGGTT
TGGCAATTTTCGTTTTAAAGTACGTGAATTTGGTTTTTTATGCCGAAAAAT

SEQ ID 5448

VEGLGEAAGRRTDSVMKRYKDKNSLHYTGNAVWKISGLAFSVLKYVNLVYAE

SEQ ID 5449

ATGCTCGAAGCACTCGATAAACTCGGCGTTCAATCGAACATCTTCGCCGAAGGCGCTCTGAAAGTACACGGCACGGCGGACGCTTCCCCAACCGCTCTGCGGATTTGTTTTGGGCAAG
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TGCGCGCGCGGATGCAATATCTCGCAACGAACATATCGCGCTTCATATCGGCAAAACGTCAAGACTGCGGCGAGCGCGTATCTATTAAAGGCAATGTGTCAGCGCAATTTCTG
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AGGTTGCCAATGAAGGCTACCGCGTTTTCAAAATCCCTGCGGATGCGCACTATACGCGCGGCAACACTTGCACGTGGAAGCGATGCTCCGCGCGGCTCTACTTCTCGCAGCGGTT
GATTGCGCGCACGCGGTCGCGTTACCGCATCGCGCAACAGCATACAGGCGGATGTCGCTTTGCGCGCAACTGGAATAAATCGGTGCGGACGTGTTGGGCGGAAAAATTCGTC
GAAGTCTGCGCGCGAAAGGACGCGCGTCCAGCCTTTGATTGGATGCGAACCATATCCCGGATCGCGCGATGACCTGGCCATGTCGCGCTTGCACAAAGGCAAACTGCACGCTA

SEQ ID 5450

MLEALDKLVQIEHLAEGRLKVHGTGGRFPNRSADFLGNAGTAFRPLTAALAVLGGDYHLHGVPRMHERPIGDLVDLRIAGADVEYLGNEHYPLHIGKQDCGERVPIKGNVSSQFL
TALLMALPLTGQAFIEIMVGEELISKPYDITLKLMAQPGVQVANEYRVFKIPADAHYHAPEHLHVEGDASGASYFLAAGLIAATPVRVTGIGANSIQGDVAFARELEKIGADVVGGENPV
EVSREFGRAVQAFDLDAHNPDAANTLAIVLATRQCTL

SEQ ID 5451

SEQ ID 5451

ATGACCACCATGATTATACCCCAAAACCTACAGATGTCTATCTGCTCGGCGCGGCACACGCCGGCAGGAAGCCGCGCTTGCCGCCGCCGTATGGGCGCGCAGACGCTTTTGCTCACACACA
ATATCGAAACGCTCGGACAAATGTCGTGCAACCCCTCTATCGCGCGCATCGGCAAGGGCAATTGGTACGGAACTCGACGCATTGGGCGCGCGATGGCGTTGGCGACCGACAAATCCGG
CATCCGTTTCGCGCGCTCGAAGCCGACGAAAGCGCGCAGTACGAGCCACGCGCGCGCAGGCAGACCGCATCTCTGTATAAAGCCTCCATCCGCGAAATGTTGGAAACCAAGAAACCTC
GACCTTTTCCAACAGCCGTCGAAGACGTAACACTCGAGGGCGAACGCATCAGCGCGTGATCACCGCGATGGCGCTGGAGTTTAAAGCACGCCCGTGGTGCTGACCGCAGGCACGTTCT
TGTCCGGCAAAATCCACATCGGTTTGGAAAACTACGAAGCGCGCGCGCGCGACCCAGCCCGCAAAATCGCTCGCGGCAGCTTTGCGCGAATTGAAGCTGCCGCAAGGCCGTCTGAAAA
CGGCACGCGCGCGGTATTGACGGACGACGATTTGACTTTTCCCACTTACCGAACAGCCCGCGCAGCCCGGTTCCCGTCAATCTCGTGGCGCGCAACGGCGAAATGACCCGCGCAA
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CCAAATCGCGCTCGTGGCGAGTATGAAGGCTTTGAAAGACGCCCATATCTCGCGCCCGGCTACGCCATCGAATAGACTACTTTCATCCGCGCAACCTCAAAGCAGCTCGAAACCAA
ACCAATTGAGGAGCTGTTTTCGCGGGGCAATCAACGCGCAGCAGGCTATGAAGAAGCCCGCGCGCAAGGATTGCTGGCGGGCGGAACGCCGTGCAATAGCTCGCGGACAAAGATCCGG
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CCTGATGACGCTCGAAGCGCGATGCGCTCTGAAACCTCTTCGCGAAGTCTACGACGATTTGATCGAATCCGAATCAAACTACCAAGGCTATATCGACCGCCAAAAAGAAATTCGACAG
CGCGCGCGCATCGAAACCTTTAAACCTTCGCGCAGCGATGATTACGGCAGAGTCAAAGGCTTGTCCGCAAGTGCACAAAGCTCAACCAGCACAAACCCGAAACCGTTCGCGCAGCA
AGCGCATTTTCCGCGGTTACGCGTCCGCGCTGCGACTGCTGATGGTGCATTTGAAGCGCGGTTTAAAGACGCGAAA

SEQ ID 5452

SEQ ID 5452

MTHTMPTKTYDVTIVVGGHAGTEAALAAARMGAQTLTLLTHNIEFTLGQMSCNPISIGGKKGHLVRELDALGGAMALATDKSGIQPRRLNASKGAAVRATRAQADRIILYKASTREHLENQENL
DLFQQAVEDVTLLEGKRSVITAMGVFEKARAVLTAGTFLSGKIHI GLENYEGGRAGDPAAKSLGRLRELKLPQGRLLKTGTPPRI DGRITDFSQUTFEQPGDTPVPVMSVRGNAEHMFQ
VSCWHTHTNTQIHTDIRSGFDRSPMTFGKIEGVGPYCPYSIEDKINRFADKDSHQIFLEPGLATHEYYPNGLISTSPFDQIALVRSMKGLENAHILRPGYATEYDTPDPRNLKASLET
TIEGLFPAGQINGTGYERAAAGQLLAGANAVQYVRQGDPLLLRRBQAYLGVLVDDLITKGLNEFTRMFTSRAEYRLQRLEDNADMLTDEGYKILGLVEGAKQWFMNEKRRAVEREITQRK
TTWYTPQKLAEDQIRVFGQKLREAHLDLIRRPNLDYAALMTLEGAMPSENLSAEVIEQVEITQVKYQILQDRNERIDSRDITETLKLPGDIDYGRVKGLSAEVQQRILNQHPKPTVQQA
SRI SGVTPAAVALHMLVHLKRGFKDAK

SEQ ID 5453

SEQ ID 5453
 TTGTCATCGATTTCATCCCCGATATAGCGCAGGCTTTCTCCAGCCATTTCCTTCCAAACAAGAAACAAAAAGCGCGCGGCAGCGGATGCCCCCTCCTTTACAGGTTCCCCCTATTTT
 TAACCCGAGGCAGCACCGGTTTGCGGGGGCTTTTGGTGGCGGGCGCGCGAGCGAAGCTGGTCTTTCAGCTTCGCGCAGCACCGCGGACCGATGCCCTTCACCTTGATCAAAATCGTCCAC
 AGACTTGAACCGCGCGTGTTTGCGCGCGGTATTCGCGAATGGCCTTCGCGGGCTATGCCCCGCGAGCGCTCCAGCTTCTGGTGGGAAACCGATTTGAATGTTAACCGCGGAAAGGGAGAA
 GCGCGCAGGAGAACAGCATACAGAACAATAACAACATTTTTCATGGTTTTCTTTTAAAGGTTGCAACAACAACCGCATCTTCGCGAGCATATGCGCGAT

SEQ ID 5454

SEQ ID 5454
LHRFIPRYSAGLSLPAISLPNKEQKSAGGSRCPFLYRFPYFLTAGSTGLAGPFGAGAPTEAWSFSFASTAGMPFTLLIKSSTDLNAPPCARYSAMAFAGMPGSASSFWWETPLNVNRRKGE
GAGEOHTEOYKHFFHGFSFKGCKQOTASCDDMAD

SEQ ID 5455

SEQ ID 5455
ATGCGCAACGAGTTGCGCAAACTCGGTGCAAAAGTCGTGCAAGAAGCCGAAGCGATTACATTATCCCCGCCGAAACGCCGACACCCGATGCCGTCATGCACACTTACGAGCACCACCGCA
TGGCGATGTGTTTCCTGCTGATTTCGCTGTTGGGAGTACCCGCTGTCATCAACGACCCGAAATGCACCCATAAAACCTTCCCGACTTATTTTGAAGTGTTTCATCACTGACCGAAACAGC
GGAA

SEQ ID 5456

MANELRKLGAKVVEEAIAIHITPPETPTPDAVIDITYDDHRMAMCFSLISLLGVPVVINDPKCTHKTPPTYFEVFFSSLTETAE

SEQ ID 5457

SEQ ID 5457
ATGAGCCGCCCGCCGCCGGAATCGCGCAAAATGCCGTCGAGGCCCTGTTTTCGGGTTTCAGACGGCATTTTTCGGCTTATTCCGCTGTTTCGGTCAG

SEQ ID 5458

MSRPPRRNRGKMPSEALFSGFRRHFSAIFRCFGQ

SEQ ID 5459

SEQ ID 5459

TTGGAAACGCATCGCGCGAAAAATCCTATCCCTGCTGCCCATCGAAGGTTTATTATAGAAATGCCGCTCTGAAACACCTTCAGACGGCATATCGAACCCGCAAGGAAAAAACCATGTTTT
CCCCGCGACAAACCCCTTTTCTCTGTCTCGCGGCACTGCTCTCGCCTCATGCGGCACGACCTCCGGCAACACCCGCCAACCGAAACCCAAACAGACAGTCGCGGCAATCTCAAGCCGCTCG
CATCAGCCACATCGGCCGCACACAGGCTCGCAGGAATCTATGCTCCACAGCCTCGGACTCATCGGCAGCGCCTPACAAATGTGGCGCGGCACGACGACCCGCAACCCGCTTGACTGCGAGCGG
ATGATTCAATTCGTTTACAAAAACGCCCTCAACGTCAAGCTGCCGCGCACCCGCCCGCAGCATGCGCGCGGCAGCCGCGCAAAATCCCGCAGCAGCGCCTCAAGCGCGCGGACCTCGTATTCT
TCAACACCGCGCGCGGCACACCGCTACTCACAGCTCGGACTCTACATCGGCACCGCGAATTTCATCCATGCGCCCGGCAGCGGCAAAAACCATCAAAACCGAAAAACTCTCCACACCGCTTTTA
CGCCAAAAACCTACCTTGGCCGACCATGTTTTTACAGAA

SEQ ID 5460

SEQ ID 5460
LETHRRKNPIPAHRRFIIEMPSETPSDGISEPAKEKTYMPSDKTLFLCLGALLLASCSTTSGKHRQPKPKQTVRQIQAVRISHIGRTQGSQELMLHSLGLIGTPYKMGSSSTATGFDSCG
MIDYVYKVAI.VVVLPTARDMAASRKIPDSRLKAGDLVFPMTGGAHRYSHVGLYIGNGEFTHAPGSGKTIKTEKLSPTPYAKNYLGATFFTFE

SEQ ID 5461

SEQ ID 5461

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CCCCACGAGGAGCTTTGGCCGCGCCGCGCCCTTATCGAATCTGCCGAACACAGCCTCGATTGCAATACTACATTTTGGCGCAACGACATTTCCGGCAGGCTGCTGTTCAACCTCATGTAC
CTTGGCCGACGAACGCGCGCTGCGCGTACGCTGCTGTTGGACGACAAACAACGCGCGGCTTGGACAGTCTCTGCTGCGCCCTCGACAGCCATCCCAATATCGAAGTGCGCCTGTTTCAACC
CCTTCGTCCTACGCAATGGCGGCGACTCGGTACTGTAGCGGACTTCCCCGCGCTCAACCGCCGATGCAACAACAAATCCTTTACCGCCGACAAACCGCGCCACCATACTCGCGGACGCA
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CGGAGGCTGCAACAGCGCGCTCAACAGCGCCGAAAAAGCGTCTATCTGGTTTCAACCTATTTCGTCCTTACAAAATCCGGCACAGCGCACTGGCAAACTGGTGACGAGGCGCATAGAC
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TTCGCGACGGCTCAATACCGAAATGGGCGTCTGTCATCGAAAGCCCCAAATTCGACGAACAGATGGAGCGCAACCTCGCGGATACCAACCCGGAATCGGCTTACCGGCTTACCGCTGACAAA
CACAAACCGCTGCAATGGCACGATCCCGCACCGGAAAAACCTACCGGAACGAAACCGGAAGCACTTTGGAAACGCACTGCGCGCAAAAATCCTATCCCTGCTGCCATCGAAGGTTTAT

TA

SEQ ID 5462

MHTDPKIQAMPSETISPMKTRSLISLCLLCLSCSSWLPLEERTESRHPNTSKPVLLDNILQIRHTPHNNGLSDIYLLDDPHEAFAARAALIESAHSLSLOQYITWRNDISGRLLFNLEY
LAERGVRVRLILLDDNNTRGLLDDILLALDSHPNIEVRLPNPVLRRKWRALGYLTDPPLNRMRHMKSPATDNRRATILGGRNIGDEYFKVGEEDTVPADLDILATGSVGEVSHDFDRYASH
SAHNATRITISRGNIAGKQALGYNDETSRHALLRYRETQVSPPLYQKIQTGRIDWQSVQTRLISDSPAKGLDRDRKPPIAGRLQDALKQPEKSVYLVSPYPVPTKSGTDALAKLVQDGDID
VFLVTHSLQATDVAAHVSQYRTRKPLLLKAGIKLYELQVKNHVPATKDKGLTGSSVTLSHARTFIVDGKRPIGGSFNLDPRSARLWFMGVVITBPKIAEQMERTLADTTPPYAYRVTLUK
HNRLQWHDPAKTRKTPYNEPEAKLWKRIATAKLSLILPEGLL

SEQ ID 5463

ATGATTTCCTCGATATATAATATATCAATTACAACATGCGAATGCGGATTCGTTTGGCTTGTGAACATTCAGGATGCGGACTCTCGCGGGCATTGAGACAGCATCTGAAAACAATAACGGCACAAGGATGG
GGTACAAATCACCCCTATGGAAAAAACACCCCTGTCCGCCGCCGCCACCATCCCTTGGCTTGGCCGCTCTTCTGCTGGCAATTTGCCATTTTATATGCAGATGTTGGATGCGGCACCAATTTTAAATACCGC
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CGATGCTGGTTCCGATACCGGCTCTGACCAATCTTTCGGTGTATATGAAAAATCGAAGCTGCTCAACGCCATCAATTTATGCGGTCATGCCCTGCATGATCGGCCCTGCGTTGGGACCTCTTGGC
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SEQ ID 5464

MIFDNNYHYNAMP IRLLVNIQDASAGIQTASENNNGTRMGYNHPEKNTLSARAPSPWLPILLALAIIFMQMLDATI LNTALPREIAADLNESPPDMQQAUVAYTFLVALLIPLSSYLADKF
 GTRKVPFGSIAVFMLGSAIGAASGSLPELTSRVVQIGGSGMLVPIPRLTILKRVKSKLLNAINYAVHPALIGPALGPLAGGYLVEYASWHWIFLLNLPIGLLGPVLGRNIMPVYKGNDF
 ALDFKGYLTFSSVAACLLLLAEESLHALPFPYFALLPLCGGLLPARRYFRHMKTASKPIYSADFLIRTFRLGLAGNLFPSRLGISSIPFLMPLMFQVAFGFGASLSGNLVAVPVALSSLLVEP
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SEQ ID 5465

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SEQ ID 5466

MSATIPPKIIRYDSNPTDYVFFPGTCVLDLMPAEGMDALALIEQOGIRVHFVMAQSCCGGPAYSSGHPTEAFDVAKVQLDLFPKFWPIVIVPSGSCGGMKHHWPTLTKNTEYESKAVDCAN
RIIEFTHFLAIGYKPEDKGEPVKVAHVTSCAARREMNVLHSGWQLIDGMENVERIVHDHESECCGGTGVSVKQADISGAMVTDKVAALKETGATEIISADCCGMNIGGKIAKDEPDHP
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SEQ ID 5467

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CAGCAGTTTTCACGGCAAAGCTTTTACAACCTCCGTTACCGCGCAAGCACTCGGGCGAAGGTATACGGCGTAGCCAACCTCAATCGCACCAAGGCAACCGGTACAAAGATGGCGGTGGG
CGCGACACTGATTGTGAAATACAGCCGCTTCAATCAGGCTTTGGTATCTCGTTCGTCGCTTGATAAATCAAGAATACCGCTCACTTATCTGCACGACGATCAACAACGACCGCCAGC
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CCGCGCCCATTCGAGGCAATCCCGCTGCTGAAAAAC

SEQ ID 5468

MKLNTLTLWALMTVPFVSPAPSWAQBPANTEEQIPVKTFSPPKIAPTAAGQYPPEQFDRSDRSDYFVFTENIQDAFRPLKANSSFYGKSFYNSVTAQALGAKVYGVANLNRTKANGYKDGGG
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TAAVSYRNSQNGERNTHAMCDFLNGYRFADVHIDRWCIADTFSYKFDDRHKLGLGLSYELNEADIRKNTAQPENPIKPGFPASSQQITWKTHYGYDFNGKVRRHASGELKYDFTPSET
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SEQ ID 5469

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SEQ ID 5470

MSARENIIAKLKGAGALMPEEPVAFDYRERKGVSDSEARLKHMAAMRAVKTETYYWTKSNHMQVFREAERGKGLKNTLLPLATEHGQIARAALAGSNDIPAFEREIDTWKTEPFTTH
DAGFSGAQCIGIARTGTLMFSSPEEPRTLSLVPPVHFLCDFTSKMYNEFHNAVEGKGLVENGMPTNWTLISGPKTADIQLTAYGANGPRDLVILAILPDHISPADLEENA

SEQ ID 5471

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SEQ ID 5472

MTTQYIKPHMKPTFKQNAALSLQDKPLKSLRTAMDMIMTKRKAVIDEELQSLRDLCEHTRQSLSKLPALLEQLEENLTKLGKVVHWAETPAEACQIIRDIITAKNGKLMVKKSMV
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SEQ ID 5473

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CGTATACCGGCTATTTTGTGGCGGATGTGCGGTGTCTCAATCCGTGGCAGAT

SEQ ID 5474

VMILLDTNVISEPLRPQPNRUVVWLDLSILEDVYLSAITVAELRLGVALLNGKKNVHLHERLEQSILFLFAGRIILPFDEPVAATYAQIRSYAKTHGKEIAADGYIAATAKQHSILTVAT
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SEQ ID 5475

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CTGCGGCTCGCGCAGCAAAAT

SEQ ID 5476

MDCSKRSCSTFFFLPLSNATPKRNSATVMADKYTSSNIKLSNHATTSGLCGRGKSEITFVSSKIITKKPRYQYDRVRLPAQHILRFPALLMPTLT/PNVQFVVLWRCYPKLSGFLRLRYCA
LRLAHGI

SEQ ID 5477

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SEQ ID 5478

LFQTFVQHILLFLAIEQQRHTQTQPCNSNGRIHIHQYQTIQPCHTTIFGLWAQRGMHVRVQNMHKKETSLSVLRPRTSSSTPPISCPIDANIDPKRTVCCALANLSKIKRISASVLRPA
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SEQ ID 5479

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TACTGATAACGAGGTTTCTTTG

SEQ ID 5480

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SEQ ID 5481

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CAGGCATCCGAGCGT

SEQ ID 5482

LILSDFLGSSRAATVYFLSERGRGDVFLDVKKRLRPPEFSGIRRR

SEQ ID 5483

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SEQ ID 5484

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SEQ ID 5485

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SEQ ID 5486

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SEQ ID 5487

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SEQ ID 5488

MSVELLLGLVGLPRSTFYQLAVQSAEGKYADLKRHIHDIVQRYGRVYRIRAAIRHAGI PVNHKKVSRIMARTGLKAVIRRRKYSFKGEBGVKVPNLQRCHFSEKPE

SEQ ID 5489

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SEQ ID 5490

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SEQ ID 5491

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SEQ ID 5492

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SEQ ID 5493

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SEQ ID 5494

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SEQ ID 5495

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SEQ ID 5496

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SEQ ID 5497

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SEQ ID 5498

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SEQ ID 5499

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SEQ ID 5500

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SEQ ID 5501

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SEQ ID 5502

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SEQ ID 5503

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SEQ ID 5504

EQ ID 5504
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SEQ ID 5505

SEQ ID 5505
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SEQ ID 5506

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SEQ ID 5507

SEQ ID 5507

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SEQ ID 5508

SEQ ID 5508

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YHVTKPRGVITPTLDPGHEAFTAMRARGAKATDILVILVVAADDGVMPTTIEAIIHAKAAGVPIVVAVNKIDKNGEAPERIRQELTQVGVFIDPWGGVQVQFIDVSAKKGTINDALLEAVLLE
AEVLELTAPVDAPAGKIIVEARLDKRGAVATLLVNGTKLKGKMDLLAGTAFAGKIRAMVDENKPSITGASPTVPEILGSLVDVFNAGEDAMVLADEKKARETALFRQGYKRDVRLAKQAA
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VGVHPIRQVIVSVSKVGNIAAGMVTGVDGVRKDSHILIRNVVITHTGELASLKRYKDQVKEVRNGFECGLMLKGYNEIMEGDQLBECFDIVEVATFL

SEQ ID 5509

SEQ ID 5509

TGTTGTGGCGGCGCAAAGCGTTGAACAACAACGCCGGAAGCGCGCAGGGGTTTGCATTGTTTGTGTAACGCCCGGTTGGGTACGATTTCGCCGTGGGCTTCCAAGCGACCAATATCGCGG
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SEQ ID 5510

LLAASQVDETPFEAREGLHLFLVTPRLGITSIPWASKATNIAENCLAGIERIERGMVAVLEALTOEQKQQAALLHDMTESVLPDPQTASKLPHHLKSETPTSTDVLLGGGKEALVKANTE
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 FHTALAPFAGAATGAGGEIRDEGATGKGRSPKAGLTGFTVSNLNIPLDKQPBWQYDKRPEHISPLDINTEGPIGGAAPNFNFGRPNNLGYPTTPEKPDGQVRGYHYPKPHIAGGLSTQA
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 DSEFALIGDNERSAIPADVKFDVNEIDIAAPTINSGKAPAILREQNMVNGVHPIQEMAAFPTRAGTADTVHSNLSLMAGRFRILADFKMLAACGGPSYGDVLGAGEGHAWSILFHPALRDQFAAF
 PADPNTLTLGCNCGQMVSNLARIIPGAFTVWPFPKKNLSBQFEARLNNVHVPKKSASLILNEHQDSSLPVVVSHGEGRADFLHGGNTSADLGLIALQYVDGQNVQTVTYPLNPNGSPQSLAG
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SEQ ID 5511

SEQ ID 5511
TACAGGCAGAACCTATCTTTGCACCTGCAAAACCAACAAATTTTGTTTTGATTAAATGCAAATATGCACAGATGTTTTTGAAAAAAGATGGAAATATGTCAT

SEQ ID 5512

YRONPIFAPAKPTNFVLINANMHRCF*KKMEICH

SEQ ID 5513

SEQ ID 5513
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SEQ ID 5514

SEQ ID 5514
MFRELRLFLIYNSVRQTAFITPIMNKEIVGIPFIPMGIIISMCAALNQMYVMMTETETLNRFKDKELVWRVALLFISFSLAVYLLCPNSRKKGIVVFFILGGGGAVMYILLARMNLPTFSK

SEQ ID 5515

SEQ ID 5515

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SEQ ID 5516

SEQ ID 5516
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IELGKVIKIDTISKGGKSVSVAIYETAAGEAKTEVFVDKLIVIAIGRIPNTKGLNAEAVGLEKDERGFIKVDGECRTNLPNVWAIQDGVVRGPMALHKAASDEGVAAERLACQRPIDFNWVPFVITY
TDPKIAWVGKTEBQLKABGEVYKKGTSFGFGANGRALAGKAKGTVKVLADAKTRDRLGVHMTGPVVSSELVTBGTALTEFPASSEDIAIRI THAHPTLSEVVHEAALAADKRALHG

SEQ ID 5517

SEQ ID 5517
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SEQ ID 5518

INDCVLMVLRKSRLLKVHICRFIRIKCFRRPOSFVEPIVARYYITLHLNKNSDGLFINK

SEQ ID 5519

SEQ ID 5519

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SEQ ID 5520

SEQ ID 5520

MIIDVKPMISSESVEGSLLEKKKVGAEVARDEILIDIETDKVILEVPSQAGVLVEIVAQDGETFVADQVLARIDTAATVAAEAPAAAPAEAAAPAAVPAQAQNNNAAMPAAAKLAETGV
DNNVLOGSGRDGRVLKEDVONAAKPAAAVAPAVAPAGARPERVPMRSLRVARERLLASQOENAILTFPNEVNMKPIHDLRAKYKEKFEKEHGVKLGMSFPFVKAATVALKKYPVWNA

SVDGKDIVYHYGFDIGIAIGSPRGLVVPILRDADQMSIADIEQAVDVYAKKAKDKIAIEDLTGGTFSTNGGTFGSMSTPIINPPQSAILGMHATKERAVVENGQVVRPMYLALSTD
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SEQ ID 5521

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SEQ ID 5522

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SEQ ID 5523

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CGGTTA

SEQ ID 5524

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AL

SEQ ID 5525

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SEQ ID 5526

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SEQ ID 5527

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SEQ ID 5528

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SEQ ID 5529

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SEQ ID 5530

LQAIPLLKTEKHNRILPADSRNDYNGYMNLAGAGMNVGGLVADKVDLIIFDRAHGSGTASDKGGIITRNVDARLFTAQAYARYNFPNPHAAIKAAANYNHNETDGRPPYQIRFP
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SEQ ID 5531

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SEQ ID 5532

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SEQ ID 5533

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GCA

SEQ ID 5534

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SEQ ID 5535

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SEQ ID 5536

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SEQ ID 5537

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SEQ ID 5538

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SEQ ID 5539

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SEQ ID 5540

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SEQ ID 5541

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SEQ ID 5542

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SEQ ID 5543

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SEQ ID 5544

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SEQ ID 5545

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SEQ ID 5546

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SEQ ID 5547

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SEQ ID 5548

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RKPFA

SEQ ID 5549

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SEQ ID 5550

KKPKIRHSRAGGNPIRPVSVFILNPR*LPNRH

SEQ ID 5551

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SEQ ID 5552

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SEQ ID 5553

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SEQ ID 5554

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SEQ ID 5555

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SEQ ID 5568

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SEQ ID 5569

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SEQ ID 5570

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SEQ ID 5571

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SEQ ID 5572

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SEQ ID 5573

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SEQ ID 5574

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SEQ ID 5575

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SEQ ID 5576

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SEQ ID 5577

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SEQ ID 5578

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SEQ ID 5579

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SEQ ID 5580

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SEQ ID 5581

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SEQ ID 5582

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SEQ ID 5583

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SEQ ID 5584

LAERKCKSGYGLIEDTNDVIAAMSRGVNVUQADLEGLTAFNDQSFVIVLSQTIQAMQNTKILRLCLMLAKQAIVSFPNPGYWRNRVQIALGGHBPVSEMPYHWYDTPNIHNCFLKDF
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SEQ ID 5585

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SEQ ID 5586

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SEQ ID 5587

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SEQ ID 5588

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SEQ ID 5589

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SEQ ID 5590

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SEQ ID 5591

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SEQ ID 5592

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SEQ ID 5593

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SEQ ID 5594

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SEQ ID 5595

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SEQ ID 5596

MEQERRLREATLMLTQGSQKTRGQGEPRKARYFEVSATSAYLNRHNNGLGNFQYIGQLPGYLKMHGEMLENQSLFRLSNRERNPKPFLDIHFDENGKIRIVVYEKNIYSGLNLNQDK
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SEQ ID 5597

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SEQ ID 5598

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SEQ ID 5599

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SEQ ID 5600

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SEQ ID 5601

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SEQ ID 5602

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SEQ ID 5603

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SEQ ID 5604

MAFCFFESLMSRNLIVRLAVCLIPLATLAVFAANPPEDKPOHLINGIILACEATFLFKFVLFETIKHHLKQGFDLKQTMFLFIPITVLLVVYLFHYFGAF

SEQ ID 5605

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GCCGACACCGAACCTT

SEQ ID 5606

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AAPFNL

SEQ ID 5607

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SEQ ID 5608

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SEQ ID 5609

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SEQ ID 5610

LCLNPAFCVSLSRYNHHPNMFVPSLARGFYPLQRIKQNKLIIVFC

SEQ ID 5611

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SEQ ID 5612

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SEQ ID 5613

ATGCGTCGGGCTTCAATATGCCGCGCGCGATGCGCGCTTGTTCGCGAGGCATCGCGCGCAGCGTCCGATTTCTCGGGGAACGCCGTCGCGGTTATTTAAAGGTTGCGTGGTGGCGG
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SEQ ID 5614

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SEQ ID 5615

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SEQ ID 5616

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SEQ ID 5617

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SEQ ID 5618

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SEQ ID 5619

ATGATGATTTTCGCGCCCTGACCAAGGTTTGAACGATTTGCCGGAAGCGGATGCTGCTGCGTGGCGACTTGGACGAACAAAAACAGATGTACGTTTGGATTTCCTTACCGCACCC
TGCAAAAGTCGACCTGAAACAGCATGCGCTTGAAACGGAACGACAGCCAGCGCATCGGACGCGCTTGAAGTCTATTACCTGACCGGAGCGGATGAGCGCGCACTTGAACGAGCA
GCCCGAATCACACCTGCGCTTGAACCTTACACCGCGCGCTGATTCGCCGAAGACGCGCGGACTGCAAGAAACATCGCGCTTCCACCTGATGCTTGAACAGGGCTTTATCGGC
GAAGTAGAAAACTGCGCGCGCTATCCGCGCTGACCGCGGACTTCCCGGCATTCGCTGCGTGGCTACCGTCAGGCGTGGGAACACCTTCAGCGGTGAACCGACAGACAACTTCA
TCGAAAAGGCAATGCGCGCACGCGCAACTTGCCAAACGCCAAGTGGTTACGCAAAACACCTTTAGACTGCGTTGCCGACCGGTTTTCAGACGGCACTTCAGGACGCGCGCTGAT
TGAGCGCGCAACCGTTTTTCGCGGA

SEQ ID 5620

MMYFRALTCGLNDLPEADACLADLDEQKQMYGLDFLYRTLQKVPETACRLKPNDSQRIGRALEVVYLITGRPMASHLNGQPEHTLPPELYTAALIPEDRARLHENTIALRFHLMLEQGFIG
EVENLRRRYPGITADSPAIRCVRQANEHLGDATDRQTFIEKGIAATRLQAKRQLTWLRKTPDLCVADPPSDGTSGLRIIEAKRFPGE

SEQ ID 5621

ATGTCGGCCACGCCCGCTCGCCCCAAAACCGTCGCCCGCTGCACAGCGTCGGTATCCGTACGCTCGAAGAACTCGCGCAAAACCGTTTCGGTCAAGCCCTTTCGCTGCTCAAGCAT
CGGCTTTGACCTCAGCAAAAGCAGCTGTGGCACTCGAGTCGCTGTAACGCGACGCCCGCAAGAAATGTCCCAAGCGCAATAAGACTGCTGCTTCCGAGTTGAAAAACCATCC
GCCCGTCGCCCGCTTTCGCCCGCAGGAAGAAATGGGATATTCATCGCGCAAGCACTCGCCCAAGCAGAAATCCGCCCGCAGCGGAAATACCGCTCGGGCAGTCATCGTTTCAGAC
GGCAAAATCATCATCGGCACACAACACCTGCAATGCGGACTGCAATGTGAGCCGACACGCCGAAATCAACGCTTGGCACAGGCAGGCAGGAAATGCAAAATACCGCTTTCAGCGAT
GCGACATCTACATCACCTCGAACCTCGCCATGTGCGCGTCGCACTGATACAGGCAAGAAATCAGGCGCGTATCTACGCTCGCGCAGAACCCAAACCGCGCGGCAGGCAGCATCGT
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SEQ ID 5622

MLATPPLAPKTPVAALHRLGIRTLLELRQNSVKAFLLLKASGLTLTKSTLWQLESLLNGTTPQEMSOAHKDCLLAELKNHPVAAFPQEMGYPMREALRQAEQSAADGEIPVGAIVSD
GKIITSAHNTCTIADCNVSRHAENALAQAGSEHONYRLDGCIDYITLPCAMCASALIQARIRRVYGAAPKTAAGSIVNLPADKRLNTHITARGILQEBEAVLSRFPQNRKG

SEQ ID 5623

ATGACCGCCCTACTCGTCATCTCGCCCTCGCCCTGATAGCGCTCGGCACGGCAGGCATCGTCTATCCCGCCCTGCGCGGCTTGGCATTGATGTTTCCCGGAACATGGCTGCTTGCTATG
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ACTCGCGCTCCGAGGTGCAATGCGCGGCAGCATCATCGGCATATTTTCTCCCTCCCGGACTAATACTCGGCGCCCTTTATCGCGCGCGCGCAGCGGAATGATCGGCGCAATATG
CTTCAGCGAGGTAAAGCGGCTTGGGTACGCTGTTGGGCTTGTCTGCGCAGCGCTTCAAAATCGGCTCGCGCTATCATCTTGTATTCTCTGTGTGTAATACATCGCATACCTGT
TT

SEQ ID 5624

MTALLVILALALIAVGTAGIVYPALPGLALMFAGTWLLAYAGGYQIYGAGILWTVGLISLGGILADYMGHNGVKYTGAGKLAVRGALAGSIIGIFPSLPLGLLGPFGAAAGELIDRRNH
LQAGKAGLGLLGLVVGTAFIGCAVSLIFILLVKYIAYLF

SEQ ID 5625

GTGTCGCGCTGATGTTGAAAAAAGAAAAACAGTCGGAATTTTACCTTTATCCGCACAAAAAGGTATTCATGCCGCTGGAAGCGCGCTCAACGCTTGCTCAGGATGACGATATGGCGT
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GAACCGCATTCAGCATCGTCTGTGCGCTTCGATATAGGGCAGCAGCTCAGGCTGTCGCAAGATGATGGCAATCATTTTTCCTGCTCGCGCAGGCGGCTGATGTTAGGTTTGT
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GCGGCTCAGCGCTTTCGCGCAGCTCAGCA

SEQ ID 5626

VSRMLKKRRTVRNFTPIRTKVFMPSEARSTLAQDDMAFRIQARHVEPLDFDAHILRQAADFPLRIYALHRRPVAAVFPQVRRPRHKIRQFRKTAGNHVGTHTVRNLHAPRHHATV
QPQLDSRLPQKSAFTLRIQGYLHIRTAAHRRNAGLAAARTDIQHRLCAPFDIGQQRQAVQKMDNHFLVAQGGQIVGVPLFQIHIQKQKVLRRFRNIRPHRGNACTQAFFTFHICFL
SIFRRNVSGRTCLRIPIGQPTAFPRPIFSCGTPQAAPARASGVSAASA

SEQ ID 5627

TTGGTAGAGCACTGCTTTTGAAGCAGGGGTTCATCGGTTGATTCGCTTTGCTCCACAAAACCTTTACAAATGAAGCAAGTTTGTCTGTTTATAGCAGCTTATTTGATTTCGGAAGTA
GAATAACGACGATCGATCTTTAACAATTTGAAAGCGGAAATCAACAAACAAAGACAA

SEQ ID 5628

LVEHLCKQGVISIPFASTKTLQMKASLLFLAAYFDLRSRTTHRSITNNKAEINKQKQ

SEQ ID 5629

TTGACAAACACCAATATGGCAAAACCAAGACCAATCTACGGCTTCCACGCGCTCAACGCCCGGATTGTGGCAAAACCCCAAAATCGATTACCGAACTCTATATCCAAGAGGCAAAATCCGAG
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GAAACCGCGCGCAACCGTAATGAAACAAAGAGC

SEQ ID 5630

LFWTIMANQRPIYGFHAVNARLWQNPKSITELYIQEGKSDARTREVLEKAANENIRVYPADADRLNAISKARHQGVVGFIDASKNHVLEDVLENLEPPLLLILDGITDPHNLGACLR
ADAMGVHAVIAPKDKSAGLNAFVSKVACGAATFVPTITVTNLARTLRELKEYGIWLTGDMGGDADLYHCNLPDSTAWVMGNEGDMRRLTREHCIMLVSIPIMGTVESMNVSVSAGHVLS
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SEQ ID 5631

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GGCGACCGCACTTTACCATTTGCAATCTGCGCGACAGCAGCGGTGGTGATGGGCAACGAAGCGCAGGTATGCGCGCGCTCAGCGCGCAACATTCGACATGCTGGTGTCATACCCA
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SEQ ID 5632

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SEQ ID 5633

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GCCACGGCATCCGACGGCGCGAGGCGGTGATTGCGGCAACGTCGGTGGTGTGGGCTTGGCGGTGGGTTTGGAGCGGAAGTGTAAAAACCTGCCGCTCTGTTCGCAAACTCTATTTC
CGGCGCGGCGATTACGCGAGTCTGTCTGAATTTGGTCTTCCCGAAGATAAAACCGAGGCGCGGTCAAGTTTGATACCGACCATTTGGAACAC

SEQ ID 5634

MKEGGLSEGANVSTLLGVSFAGAFVCFSAWLLPYLKKVITPTVSGVVMLIGLSLVHVGLADFGGFGAKADGTFGSMENLGLASVLLVLIPLFMCKNPLLRMSGIAGVLIAGYITVALF
LGKVDPSALQNLFPVTLFPVFKYGFADWHAFLAAGAFLLGVFEAVGDLTATAMVSDQPIBGEYTKRLRGVGLADGLVSVIATAGLSPLTTFQNGNVQIMTVASRHHVGYIAVLLV
LLGLFPVVGRAFTTIPSPVLGGANVLMFGLIAIAGVRILVHGIRRRREAVLAATSVGLGLGVGFEPFVKNLPLVLFQNSISGGGITAVLLNLVLPEDKTEAAVKPDTDLLEH

SEQ ID 5635

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CTTCGGGTGCTGCGCTCGGGGATGCTGTCCATCCACGCTTACCGTCAATGATGCGCTCGCGCGCGGATGAAAGAGGGCGGTTGAG

SEQ ID 5636

MAETHKKQADSPDLVYGLEDRPPFGNALLSAVTHLLAIFVPMITPALIVGGALELPVEMTAIVLSMAMVASGVGTYLQVNRFGSVSGMLSIQRYREDCARREDGERGRFE

SEQ ID 5637

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CGTACACCAATCAGCGGAATCCGCTGTCTTTTCATGTTTCAGCATTTGAAGTCTTCTATCGGTGCCAAACGTTAAAAAATTTTAAAGAACGAAATTTGTAACGAATCAAGGATTCCTT
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SEQ ID 5638

MTVTLDGQHRADRPFAVDLQISADTRNRHRRHQIRRHHRQFQRAAHNRGRNRHNRQKMGNAQERITERRPVFQTVHQIRRIRLFPHCFSHWLSLRQCTLKNFKNEIVNQRF
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SEQ ID 5639

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SEQ ID 5640

MLQGSVALITPMNQDSIHYDQLRLIDWHIENGTDGIVAAGTTGESATLSVEHLSVIEETVKHVAKRVPIAGTGANNVTEALIALSQAARKAGADYTLVSVPPYNNKPSQBYMYRHFA
VAAAAIPMLLYNVPTTGVSMNNEITILRLAEIPNIVGVKEASGNVSNIELINRAPEGFAVLSGDDHTALPFLCGGHGVITVAANAAPKLFADMCRALQGDIALARELNDRLIPIYDT
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SEQ ID 5641

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SEQ ID 5642

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SEQ ID 5643

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SEQ ID 5644

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PERVGLVLRGILPCRPSETANLNEAGGVSRIYPEQWQKFPVPIAENRRNRLIYAYHGLLFHQDEEVLCSAAKAWADWESYLIRFEPEGVDEDAYSLAIALEHNYFVNGWMLQDKAIL
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SEQ ID 5645

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SEQ ID 5646

VLDLRAGACAILNQAALPRRLRGLTVRKQWQSGFLSDIVWVFFSMIYFRLEPMQYFPIDGPTDRFSAPAFRGGLCFVRDVAACRDVRIVRSMNGEDV

SEQ ID 5647

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G

SEQ ID 5648

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SEQ ID 5649

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SEQ ID 5650

MGASLIQPCRVSEGLRVKDFCQGRKRCQYRRPMTVPPE

SEQ ID 5651

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SEQ ID 5652

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SRFKPYAGVRVSYGBVRHSIDSTKKTVDVITAPPTSDGAPPTYNANPQTQNPYHQSISRVRVLGVIAVGDFDITPNLTLDYGRYHNWGRLEWRFKTHESLGRYRF

SEQ ID 5653

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SEQ ID 5654

MTGFKIAVLSDGRDYIVGNDGSGILLRPPRACKRQVHQKRLKQVTSASVNGQR

SEQ ID 5655

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CCAATGCAATCAATACCGTTTCGGCGCGCAATATACGGCTTATTCGGCTCGGAAACGAAATTTAAGCGGCGATTTCGAGAAAACTCGCGGCAATACAGGAACATTCGACCCGAGCTG
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GTTT

SEQ ID 5656

LFIVEENMRSSFLKPICFYLMGVNLYHHSYAEDAGRAGSEAQIQVLEDVHVAKRVPDKKVPFTDARAVSTRQDVFKSGENLDNIVRSIPGAFTQDKSSGIVSLNIRGDSGFRVYTHV
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VGGGGQHIGNFGEYLERRKQYFVQEGGLKFNAGSGKWERDLQRQYWKTKWYKYEDPQELQKYIEHDKSWRENLAPOYDITPIDPSGLKQSGAGNLFKLEYDGVFNKYTAQFRDLNTR
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GDKGLLPQKSTIVPQAGSQYFNTFFDAALKDILYRLNYSNAINYRFGGEYTGYYGSENEFKRPAFGENSPAYKEHCDPSCGLYEPVLKYGKRRNNHVSISADFGDYFMPFAGYSRTH
RMPNIQEMYFSQIGDSGVHFAALKPERANTWQGFNTFYKGLLQDDILGLKLVGYSRSTINNYIHNVYKWMDLNGDIPSWVGSTGLAYTIRHRNFKDKVHKHGFELNLYDYGRFTNLISY
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SEQ ID 5657

ATGCCGCTCTGAAGCCCTTCAGACGGCATTGTGTTCCCAACCGCATCATCTGCCGCAAGCCTATGCCAATCCGTTTATCGCATCGGCAACTCAAAGAAAATCCATTTTCATCCACG
CAGGGAAGCCGGTTTGTGATTTCGGTTATTTTGGTTGTTTCGGGTAATTTATGAGTCGTCAATCCCGCAAAAGCGGAATCAGTTTTTTT

SEQ ID 5658

MPSESPDGICFPKRILLPQAYANPFYRIGNSKKNPFHSHAGKPVDFGYFWLFRVIYESSFPQKRESVFL

SEQ ID 5659

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CCTATTACATGTGTAACACCGGCGACCTTACGATGCGGAAGACAC

SEQ ID 5660

MPALCAIRFNAPKILINLKKAGKPKMVIIVAIMRKLAKPATYIVKTGQPYDAERH

SEQ ID 5661

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AATTAACATATATGACAAATTGAAA

SEQ ID 5662

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SEQ ID 5663

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CAAAACCGATACCGCCACACAAAGCCCGCATAGAAAGCATTGATGACGAAAAATGCGCGCGACCTCGCCCGCGCAAAAGTCGTATCGTTGCCGGCTTCCAAGGCATCAGCAGTGAA
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SEQ ID 5664

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GNI STLGRGSGTSAVALAAALKADECIYTDVGVVTTDPVVVPEARRMDVTTFEEMIELASLGSKVLQIRSVFAGKYKVLRLVLSLQDGGNGTLITFEEDNMRRAAVTGLAFDKNQ
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SEQ ID 5665

ATGGCTTATGTGGTGTGGTCATGTTATTTGTGTCGCTGTTGAATACCTGATTCCAAGCCTTTGTAAATTTTGTATTATGCCGTGGAGGAGATGATGATCTGTCT

SEQ ID 5666

MAYVVLVMVFSLSLFEYLIPSLKFLCRGGDDLS

SEQ ID 5667

GTCCGAGGCCCAAGGCACTCACACTATCGGTAATCTGTTTGTAAAGAGCGTTGCGAAATATATAAGTATCCCTTCGCCCTGTCTAAGATATCTCTCGATATTTCGACATTCGCTGT
ATACTTTTCAGTTCTGTCGCGCTTCGGCAGCGCGGAAGAACCGAATATACGCCCGAGGGGAAACAGTCAATACTTTACGCGGATTTTTCGGGAAATTCGTCTATGTCGCTGTGCG
A

SEQ ID 5668

VRGPRHSLSVICFVKERCEI IKYPRLSKISLDISIPCYTTPQFVRRFGSGEEPNTYFAGENSQYFQDFPFGRIRHVAVG

SEQ ID 5669

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CCCCCTCTCCGAAGCAGGCGCATATACCGCGCACCGCTTGCGCCCGCGGAAAAGTTCGACAA

SEQ ID 5670

PPVVEHRLHRRARQAFRQQRHHPHGRIFRHLPAQPAQGGTAQQQLENP SHRRASRHRQKQVRTRMPPHLFRVQFQARRHNIQKRKHTEHKPNSAVPTATPAESAVRHRHQF
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SEQ ID 5671

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CTATTTTTTACATGAAGTTCAAGAAGGACTGCGCTTTCCCGCTGCGCTTTGACAGCGGTGACGAAAAAAGCTGTTCTTTCAGATTTT

SEQ ID 5672

MRSGRPTDVPPYLCTINAMPHALCIGRAAWFAGKAALITIFYMKFKNGLRFPACRLTAVSEKPVLSDF

SEQ ID 5673

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SEQ ID 5674

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SEQ ID 5675

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SEQ ID 5676

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IQADGGTTFASITGAFVALQIAGKLVSDGILSENPLLEAVAAVSAGVNVGVLDDLDYPEDSGCSDVNVMTASGKI TEIQGTAEAGAPPISDELGLKILVALAKGIGELLYQQNALSVA

SEQ ID 5677

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GGGAAATACCGTCAACACCTGCTGGTTCGCAATAAGGGTGGCGCGGAAATGGCGAGGATTTGGTCGATTATGCCGATGAAAACGGTCCCGGCTGCTGGTGTGGGCACGACGGGCGC
ACCGGCTGATGCACCTTTTATGGGCGAGTTTCGCGCAACGGTAATGCCCAAGCCACCTGCGGCTTTTATTATCCGTAGCAAGCCGAGAGGCG

SEQ ID 5678

MYKHLVAVDGSSETINALKHAELAGVNGARLTLVHVANPAEYMALAPEFLQHSYEAATAVQNEVLDAERTARELVGNTVKHLVANKGAREMAQDLVDYADENGAGLLVLGTHCR
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SEQ ID 5679

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SEQ ID 5680

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SEQ ID 5681

ATGCCCGGAGCGCTCGCGAAGAGGTCAAAGCGTTGTCGGACATGGTCGAATCTCGCAAGATTGGCTCAAATCAAAAAGTGAACGAAAGCCGGCAAAAAATGCC

SEQ ID 5682

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SEQ ID 5683

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SEQ ID 5684

LTSSRRPFGGIARLYGDSALTHFSQAHVGVVGVGGSWAVEALARTGIGRLTLIDLNVAESNANRQLHALTGDGPKAKVTALRERTIQINPQCEVFEIEDVFTEDNLPEYPGKGFDFVID
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SEQ ID 5685

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SEQ ID 5686

LQVQTEIADGVAEDFKTHVFKTDHLLHGIKIKYKLGESGIQTATQIP

SEQ ID 5687

ATGCCGTCTGAACAGGATTCAGACGGCATTTGAACAAACGCGCAATCAAGCTGTCGGTTAGAAAAACCAACATCGGCACGCTAAACCGTATTCACAACTACTCTTTTCAAATA
TTTGCAAT

SEQ ID 5688

MPSETGFRRLNKRGNQAVGSEKPTSRALKPYQSSTPFQNICI

SEQ ID 5689

TTGCATTTAAAGCCGTATAATGCCGTCCGAACATCTGCCGACCATATGCGTGAATGCCGCGAGATTGTTTCTTTTGTAACTTATATTAATAATCACTTACCAATTCACGCCAT
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SEQ ID 5690

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SEQ ID 5691

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SEQ ID 5692

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DGIFGTGGGRDVF

SEQ ID 5693

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SEQ ID 5694

SEQ ID 5694

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SEQ ID 5695

SEQ ID 5695

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SEQ ID 5696

SEQ ID 5696
MKFGLSVKPSGGILKDFMRRKQELYAFSAGLRKRSRFGYAEHLAQVGECAVVGHPARRUGELGDGLPVAFDQFQHQDIQGRMPHIVGEGVADAEAGFEAAFEILVQCPRAFDVQPVGEGQ
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SEQ ID 5697

SEQ ID 5697

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SEQ ID 5698

SEQ ID 5698
 INLTETPNFMNLHQTFVEHEAAAAFAAAGIAGSPVVLQPTKNAEHGDFQINGVMGAAKAKQNPRELAQKVADALAGNAVITESAEVAGPGFINLRLRHEFAQNIHAALNDARPGVAKTAQP
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 SLSHAQAVYDTGLGLKLRPEDEVAGSKYNDLLQVADDLVQKGLAVEDGKAVVFLDEFKNKGEPEAAFTVQKGGGFLYASTDLACLRYRIGRLKAGRLLYVDHQRALHFEQLFTTSRKA
 GYLPEDAKAEFIPGFTMMGKDGKPFKTRSGDTVKLVLLTEAVERATALVKEKNPELGADEAAKIGKTGVI GAVKYADLSKNRTSDYVFPWDAMLSFBGNTAPYLQYATYRVQSVFRKAGE
 WDATAPTVLTPELEKQLAAELLKFENVLQSVADTAYPHYLAAYLYQAATLFSRPFYACPIILKABGASNRSLQAKLKTGNLQKGLDLLGLDVLDM

SEQ ID 5699

SEQ ID 5699

TTGCACAACAAACCGTTTATATATATATACATAACGAAAAACGCCGGTGTAGCTCAGTCGGTAGACGACGCCATTCGTAACGCGAAATGTCGGGGGTCGATTCCCTTCTCCGACACCAATACCA
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SEQ ID 5700

SEQ ID 5700
LHKQPFYIITKNAGVAQSVQRIRNANVGSGSIPFSGTWTKHRPSLGKPVLFHISASDGIYIELATQTTPFRPLAQLRLTLP PPPHTCRAARRNRPVHRTRPATPPTTRMDRDDRLLR
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MIQNPFRCRLNASDGLIFAKELQAGFNDDVEAFQLVAFHDFVVAFEHQTALEAHADFFYVVFIAFQRSQFARVDDHVVADADMGLAFDHAVGHDTACNVADLGNGGDLTDFDRTGNLFF
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SEQ ID 5710

SEQ ID 5711

SEQ ID 5712

SEQ ID 5713

SEQ ID 5714

SEQ ID 5715

SEQ ID 5716

SEQ ID 5717

SEQ ID 5718

SEQ ID 5719

SEQ ID 5720

SEQ ID 5721

SEQ ID 5722

SEQ ID 5723

SEQ ID 5724

MSEVRGFSNKGNTMNIHALLSEQWTLPPFLPKRLLLSLLILLAPNAVFWLALILATARTPTVNLVLPAAILLIALPWRPVKIGVLAFWPAVLFDGLMNVQLPFFMDLIGAINLVPTILT
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SEQ ID 5725

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SEQ ID 5726

VCDSELFGEVSAPFKKHDKGLFYWMTLTSHADYPESDIFNHRKCTEYGLPAETDLCRNPSLHTQFPDQLADLIRRPDMKGTEVIIVGDHPPFVGMLNETFRYLKQGHVAVLHFKIK

SEQ ID 5727

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SEQ ID 5728

LLLFDPEVQPGDVSLEFVAEGFIEVADGRMVADDDDFRAHFHGASDQIRQLVEELGVQAKIAAEVFGGQAVFGAFEPVVENVGFGIVGVAGQRHPVKQSLVVFPEKCRHFABQLAVAHA
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SEQ ID 5729

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CCCGCTGCGCAGGAA

SEQ ID 5730

MPSERTNSLQAFCRQTDLLKPTFFIISDKLLCKNPKIQNHRKLSKKQKPSAVVPAKAGIQTRKPKFKFIGKTETRKQRTFFPPAQE

SEQ ID 5731

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SEQ ID 5732

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SEQ ID 5733

TTGGAGTCATATCAACAAAAAGCTGCCCGGGTATTCATTTGGGGGGGCTTTTTTGTGGCAAAATTTAAATTCAAAGAGAAAACGCCCTATGCCGTC

SEQ ID 5734

LESYOOKAARVFIWGGFFVAKFKFKERTPYAV

SEQ ID 5735

TTGTGGCAAAATTAAATTCAAGAGAAAACGCCCTATGCCGTCTGAAAGTCCTTCAGACGGCATCTGTCAGCCTCAGCAAGAGGGAATCCAGCTGTTGGTTTCAATTTTTTTTGGG

SEQ ID 5736

LNQNLNSKRKRFPMPSESLSDGICOPHARGNPSCLVSIFFG

SEQ ID 5737

[illegible]

SEQ ID 5738

MFLYGALITLGLTVVATAGGSLVGLLLALALRLHLEKAGAPMRLVLAALRKVSLLYVTLFRGTPLFVQIVIMAYVWFFVFVHPSDGLVSGEAAIALRRGYGPLIAGSLALIANSGAYICE
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SEQ ID 5739

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SEQ ID 5740

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SEQ ID 5741

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SEQ ID 5742

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LHLHQVQIGFAGGYLRHFPALIAVGFPHFYTDFTPLRRRAQVARTCTVSLPHLRCDVIRHPNFMFRAVAVDDVKGIAVIDFGHRACVAVAGFRRCPSANGRVETHVPCSAEYVEYGNRRPH
RLTVISRTIQRAQKRGDGKPFHDFNLHIFQMPMPSEHL

SEQ ID 5743

GTGCGAAAGTCACTATCCCTGCGAAGGGTAATCCTGACGTTAAGATGCCGCTGTAATCCGGTTCAGAGATGTTACAGCGCATCGGCATTGAAAAATATGCAGAT

SEQ ID 5744

VRKSSIPAKGNPDVKMPSEIRPRDVQTASAFKAYAD

SEQ ID 5745

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SEQ ID 5746

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SEQ ID 5747

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TACACCACTTTTACGCGCAACCAATCTGCGATGTCCACGGCTTGAATATCGATCAGCGCTGACAGATGAAGATGAATCAACAAATCACCGCGCTACTCGAAAAACGGCATATTCGCC
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SEQ ID 5748

LGRSGKIKGAVSTSKSGELLARYDIPVSVINEVSLAVYIDGADEVNHALQMIKGGGAHLNEKIVASASEKPVCIADSKYVSRIGKPLPVEAVESARSLSVRKLLANGGQPELRIG
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SEQ ID 5749

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SEQ ID 5750

LKKPKQCGGRGPFIMRCFMFSTVITAVALYIATAVDLLVILLIFPARANTRKRYRDIYIGQYLGSVILILVSLFLAFVLNYPKMWLGLLGLIPTYLGIKVAIYDDCEGEKRAKKELDEK
LSKLVGIVALVTVASCGADNIGLPVPYFVTLVDLLVTLVFLVLLIFVLVYTAQRLANISGVEIVEKFSRWIMAVIYIGLGLFIIENNTIRTIISI

SEQ ID 5751

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SEQ ID 5752

LCAGQHIKSVKACPKRGFYNSNVKSSNIS

SEQ ID 5753

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SEQ ID 5754

MPSEIQFTSGTQTMNIRIGQGYDVHQLTEGRKLILGGVEIPFEKGLLGHSDADALLHAVTDLALGAAGLGDIGSHFPDTAAEFKDADSRVLLRAAYQSVQAGWQVNVDTTVLAQKPK
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SEQ ID 5755

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SEQ ID 5756

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SEQ ID 5757

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SECD ID 5758

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TTTLNANREMPGQKASLDALCNRFSDVRSKRVLHGALIDCELLGDEVYLANTRRQFDLMGETEEBEP TAKPVASAEMKLGAKLKVIKADEAELAAHEEYLDGLGEACIWRKEAVPSENQGE
NA

SEQ ID 5761

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SEQ ID 5762
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GISWFPVFGAVITTLQLEPTTQTHLGGNDNVNMLALFSGIAAGSVLCARFGRERIMLAWVTVGALGITVCGILVLVVLTHGHRFEGNLGIPWFLSQGWAVPVMAMVTLIGFGGFFSVPL
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SEQ ID 5785
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SEQ ID 5766
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SEQ ID 5767
GTGATGGAAAGTATGTTTATTCTGGTGCCCATCAGCATTATTTGGCATTGTGCATCGGCTGGTTTTCTGGTGGTCGGGCAAAAAACGGACAGTTTGACGATTGGAAGGACCGGGGCACC
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SEQ ID 5768
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SEQ ID 5769

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SEQ ID 5770
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SEQ ID 5771

[illegible]

SEQ ID 5772
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SEQ ID 5774
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SEQ ID 5775
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SEQ ID 5776
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SEQ ID 5777

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SEQ ID 5778

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SEQ ID 5779

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SEQ ID 5780

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SEQ ID 5781

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SEQ ID 5782

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SEQ ID 5783

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TGGGAAGAGAAAGACATATCTATAATTGTCGCGTCTG

SEQ ID 5784

MNIIDAIINLANPVVGVNSHSQSNRANQAGDALEEVKDLFSGSFNLNETQRIARHAKVFSYLGNNSNPPDAMLRNGDAIEVKKIESKDSALALNSSHPSKLSVDDSMITKAKDAEK
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SEQ ID 5785

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SEQ ID 5786

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SEQ ID 5787

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SEQ ID 5788

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SEQ ID 5804

SEQ ID 5805

SEQ ID 5806

SEQ ID 5807

SEQ ID 5808

SEQ ID 5809

SEQ ID 5810

SEQ ID 5811

SEQ ID 5812

SEQ ID 5813

SEQ ID 5814

SEQ ID 5815

SEQ ID 5816

SEQ ID 5817

SEQ ID 5818

SEQ ID 5819

SEQ ID 5820

SEQ ID 5821

ATGCAAAACCTCATCACCTACCACATTATAATCCTATGAAAACTATTAGTTTGTTTAGCGGTTGCGGCGGTTTGGATTTGGGTTTCGAAAAAGCGGGATTGAAATCCCGCCGCCAACAAT
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SEQ ID 5822

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SEQ ID 5823

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SEQ ID 5824

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AYAVSGDLNLLRAQVHLNMAAVMFVSVRVSLLTGETLKECRKDPVFI PNVTYKNIAITLLHAAEIMLPAQTAGFTALAVGFI LLAKLRELHHELLKHYVETTYILLQLFAAGYLH
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SEQ ID 5825

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SEQ ID 5826

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SEQ ID 5827

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SEQ ID 5828

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SEQ ID 5829

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SEQ ID 5830

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SEQ ID 5831

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SEQ ID 5832

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SEQ ID 5833

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CGGTAATTTGAACCTAATTAGGTGTAGCAGCGAAAACTCAATCTACTTTAACTTGCAAGCGCTCAATTCACCGCCCAACAGCAAACTATCATCAGCTAAACAAGGTCGCTGTAATTTACA
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SEQ ID 5834

LGAELEITNSLWKPWNNSNIDYLTKNAEIRFNTKNESLIVKEDYAGGARFRPAYDLKDKVPEIPVLTPEKNITGTPSDIIFEGKALINLKHLDGHEQIVKVNDFADKDAFRLSSKYRKGITTL
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TGNVKGFGAGVYATWHQLQDKTGAYVDSMMQYQRPFRHINTEYATERFTSKGTASIEAGYNALLAEHPTKKGNSLRVYLQPAQLTYLVNGKPSDSENAQVNLGSRQLQSRVGVQAK
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SEQ ID 5835

ATGCGGAATGTTTGGATAAGTTCGCCCGTTACTTTTATGTGATAAGTTTCTTCTTCTTCAATATTCACATTTCTATCGCGGAGTTTAAAAAGCGATAATTTATCATCAGTGAGCT
TGGTTTTGTCT

SEQ ID 5836

MRECLDKFARYFLCDKFLLSNIHYFYRGVFFKRIISSSVSLVLS

SEQ ID 5837

TTGTTACAGTTTATGCTAAAAATCCAGCCCTATTTATTTTACTTGACAAAGGAAATTTATATGAACTCGAAGCAAGCAAGCAGAAGTTAAAAAATCATTTATATTAAGTCTATTTT
TTCTATTTCTT

SEQ ID 5838

LFSPMLKSTPYFLFLDKGKPKMKLEASKQKPKSFIIISLFFSIL

SEQ ID 5839

GTGGATTTAGCATAAAACTGAACAAAAATGTCATTTAGTTCAAAATTTCTCTATTTATTTCTTATTTATTAAGTAAACGTTTGTCTTTTGTCTATTTTGTCAAGCCGTTTGAAGATG
TGTATAATTTGCCCTCGTTATTTACAAAAATTTACGAAAAA

SEQ ID 5840

VDFSILNKKCHLVQIFSTYFLFIKSKRLIFAILSSRFENVYNCPRYLQKQEK

SEQ ID 5841

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CTTTTGGACGCGCGCACCATCGCGCTGAAACCGTTTGAAGGCAATATGCGCGCAAAAGTTCGAGAAAGCCATCCGCGATTCAAACTTGGGACTGAACCCGCGCAGCTGTGCGCGATTTGATC
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AGAAGACCTGATGGCGTT

SEQ ID 5842

NPSEILGARSNGCPPTLSYRKNMINDIQKTAEGKQMSVEVLKENLAKVRTGRAHTGLLDQVEVYWGSMVPSQVANVTLLDARTIGVKPFEGNMAAKVEKAIKDSNLGLNPAAVGDLI
RVPMPLTEERRKDLIKVVRGEAEGRVSIRNVRDANDHLKLLKDKELSEDEARRGEEAVQKLLDKYIAEADKVLAAKEEDIMAV

SEQ ID 5843

GTGTGTACCTTTATGCGGACCTGCATGTTGAAACATAAAGGAAAAATCATGAACCGTCTCAATTTTGGGACGCGCGCTGCCGTCTCTTTGGCTTCCGCGCGCTCTTTCCGCGTGC
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GCCTGTCCCTGTCTACTCAGGCGACACGCTATGTCCGACTGTGCGGTTCGCGTGCAGATGCTTGCTTATGCGCGCGGTGCACGACCTTGC CGCACAAAAATCCCTCTGACACG
CGACGCGCAAAAGTGTCCCTCGAAGCGTGCAAAACGCTGCCAAAGCGCTG

SEQ ID 5844

VCTLCRTCLMKHKGKNEPSSIFGQRRCLFGFRRLFRACARTRLPPSSRYAACRRIRLHRRFPNCRTLSGCTGLDPLVPVPHSGRHHVYVRLCGCRAPDACLMRRGARPCRTKFPSDT
RRGKSVPSVQTVQSL

SEQ ID 5845

ATGTTTATGGCTATTGCGAACAATAAAAAAGCATTTTACGATTTTTCATTGAAGACCGGATTGAAGCCGTTTGGTCTTGAAGGCTGGGAAGTCAAAGCAATCCGCGCGCGCGGTAC
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GTTATTAAACAGTCGGAATCAATAAGTTAATCGGAAAAACCGAACGTCAGGTTACACCATGCTGCGCGTGGATTTCATTTTACCGCGGAAAAATCAAGATGGAATCGGTTTGGCA
AAAGGTAAGAAACAGCAGTAAACGACAAAGTATGAAGAAAGCGGACTGGAAGCGGAGAAACAGCGGTTGATTAAAGCATACCGC

SEQ ID 5846

MFMAIANKKAHDFHFIEDRIAGLVLEGWEVKAIARAARVQLKESYIYMKDAFYLVGCHITALTASTHIKPDVPRKLLKQSEINKLIKTERAGYTTIVPLDLHPSRGKIKMEIGLA
KGGKQHDKROSMKEADWREKQRLIKHTR

SEQ ID 5847

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ACCGATTTGTGCGAGCGAATGGATTGCTGTGCTGTCGCGGACACGCTGCTGTGCAACGACGCGGCTGATGCAATTTGGCGGCTGCTTTGGGCAAGGAGTAGTGGCGGTTTACGGTCTT
CCAGCCGACGATACGCGGCTTTGAGCGACAGGCGAAAAATCGTCAGCTGCACTTGAAGTGTTCGCGCTTTTCAAACGTGAATGCCGTTTGGGCAATACCGACTGCTTCAACAGGCT
GTATCCCGAGAGATTGTGCGAGCGGTTGAAGAGCGGTA

SEQ ID 5848

MSIKILIIISPWIGDCVMTQPLFRLLKLHPGCTIDVFPKWSMAVFERMPEVNEILENPFHGALELKRWRVRELGRRGYDRVIVLPGLSKSAVIALATGIGKRTGYVGSRYFLIND
IRRLDKERLPLMWDRTYALAHQSDEDFDGHSGFPEFSIDERRREISVETPGLNLKPLVAFCPGAEPGPAKRWPARHFAELGKHYSAGWQVWFLFGSQDKNEIAEENCLSDGMVNLCK
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SEQ ID 5849

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GCCGCTATTGCCACGCTTTGGGCGAGATGTTGGCGGTGTTGCGCGTTAAGGAGTATGTCGCTGCGGATTTGTGCGACAGAATTTGGAACAGGAATTTGCCGCGTCAAAAAAGCCT
TGC CGCGAGCGTTTGTGTTTTCGGAAGACGCGCGGATGCAATTTTTCGCTCAGGAATTTGCACTTATCTTCAAGGCTCATCTGAAAACTTTTGCACGCTTTTGGAGCAGATTGGCACCGA
GTTTCAAAAGCAGGATGGGACGCGCTTTCGCGATTCCTTACGCGCAACCGCGCTACAAAGAGCAGCGCAGCGTTTGGGCAACCCCAAGCGCTCCGCGCGTTCGCGCGCGCAAC

GGGCAGAACAGGTGTCTGTATGATTCCTTCCACCCGCTCATCGGCAGCAGCGCAAACTGACCGGCTACGCGGGGGGTTGAACCGCAACAGTTTTTACTGGCTTTGGAACGCGCGC
AAGTTCAGACGGCATGTGTTT

SEQ ID 5850

LPQDPQFRRSLFYRRAGHAEIGDFAVKFMIGIRSKRMITLPSLNNLPSKWEIRHCLSTRVFCGVMYPNLTCEAGQFERDFWONIGCAPEEYVIRRAIRLLELYRPSLNEIVC
AALATPLGEMLAIVFGVKGCLLEFVGQKYLEQEIAAVQKALRGFPVREDGRMQLRQELDLVFKHGLKTFATPLBQIGTFQKQAWDALLAIPIGTFRSYKEQARLGNPKAVRAVAAN
GQNKVSMVIPCCHRVIGSDGKLGTAGGLNRKQPLLALERGEVQYALF

SEQ ID 5851

ATGAATCCACTTATTCATCAAGCAAAGGAATCATCTATGCAAAACCGCATCTCTCCGCCGTACTGCTGGCTTTTTCAACCCGCTGCCCTTTGCCGGGGGCGCATTCACGCTGCAATTTCGACA
ACCCGTCGCAAGACGGCGGCTTACGCAAAACAGCTTTTACGCGCTTACGCGCTTCCGGCGGCAATGCTTCCGCCGCGCTGTCTGTG

SEQ ID 5852

MNPLIHQAKESMQTRILSAVLLAFSTAAFGAGFTLQFDNPSEDGGFTQNLISAPYFGCSGGNASPALSM

SEQ ID 5853

TTGAGGGTCTGGTTGCGCAATGCCTAAATATACATATTTCCAAAGCATCAGGGAAGGAATGTTTCAACACACAGGACGACACATAAAGCGTGCCCTATGAAAATTTTCAGACGGCGCT
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AGGAATCATCTATGCAAAACCGCATCTCTCCGCCGTACTGCTGGCTTTTTCAACCGCTGCTTTTCCGGGGGCGCATTCAGCTGCAATTCGACAACCGCTCGAAGACGGCGGCTTAC
GCAAAACAGCTTTTACGCGGCTTACGCGCTTCCGGCTGTTCCGGCGGCAATGCTTCCGCCGCGCTGTCTGTGTTAAACCCGCGCGGAGGACAAAAGTTTCTGCTGACCGCTTACGA

SEQ ID 5854

LRVWLRQCLNIQYFSIRERNVSTHRTTHKASPYEFQTAFKGSSETTIFAPAHSGTSSNRFQTLPLP/LAYNESTYSSSKGIIVANPHPLRRTAGFPNRLCLRGRIHAIRQFVRRRIH
AKPAPERALRLR/LFORQCFARAVVVKPARRDKFRPDRLR

SEQ ID 5855

ATGAACCGTCTGTAATTTTGGGCGAGCGCGCTCCGCTCTCTTTGGCTTCCCGCGCTCTTTCCGCGGTGCGCACGACACCGCGACTACCACCATCATCAGGATATGACGCTGCCCGG
CATCCGCTACACCGCGCTCCGCAAACTGCCGCACACTGTCTGGATGCCGACAGTTTGGCTGACCCACTGCTGTCTGCTCTCCTCAGGCGGACACGCTATGTCCGACTGTCCGCT
TGCGGTGCCGAGATGCTTTCGCTTATGCGCGCGGCTGACGACCTTGCCGACAAAATTCCTCTGACACGCGACGCGGCAAAAGTGTGCTCGAAGCGTGCAACAGTGTGCCAAAGCC
TGTAAGAACACTCCGCCACCATTGCGGAATGCAAAAGCTGTTACGAGTCTGCTCGACTGATCAAGAATGCGAAAACTCCGCGCC

SEQ ID 5856

MNRRQPLGSAAYSLASAFARAHGADYHHHDMQPAASAYTAVRQTAACHLDAGQVCL/THCLSL/LQGDTSMSDCAVAVRQMLALCGAVHDLAAQNSPL/TRDAAKVCL/EAQKQAKA
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SEQ ID 5857

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TTTGTGTGGCTTTACGTCGCGTTATPACCACTATCCGACTGGCGAGCTGTATTTGCCGCACTGCGCGAGGTTGAAGGAAACGCGCGGTTGAAGGAAACGCGCGGTTGAAGGAAACGCGCGGTTGTTAT
GCTTTGAAGCAAGCGCGGAGGCGCAACGCGCGCGCGCTCGGTTCAACAAAAAGCGGCTTTTGGGGAACGCGCTGCTGCTGCGCGGAAATGACGATGGCGCGGTTGAAGCAAGGCAAAAG
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AACCAAGACCTGACCGCGTTCGCAACGCTACGACGCGCTGCAAGAAACCTTGGCGGCTTCTGCGCAAGCGAGCGCTGCTCCGCGTTCATAGGACAGTACGCGCGCAAAAACGACT
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GAACACCTGTCTTCCGCGCGTCAAAGCGCAGGACTACGCGGTGTTTTCGCGAAGCAAGTGAACGAACGCGCAAAATGTTCCGCAATGCGCGCTTTCGCTTTTCAGACGCGCGTCCGTGCC
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CGAACGCGAAGTGTGCGCAAGTTTCTCGAATCAACATCCGCAAGATTTGACCGCGCGGTGAGTTTGTGGTGCAGGTGTGACGAGAACCGCGAGCGGCAAAATCCGATGCTGCGT
GATGTCGATCCGAGGAGCT

SEQ ID 5858

LPACMIYHRIAVNVPLSDGLLTYSHSEPLPPGTRVLVFFRNKTVVGMWETDIAPMDAARILSVQTVFVEEKPLSQSWRDLLAFTSRYYHYPTQAVPALPQGLKETRAVEMPQPLFY
ALNEAGRAQTPPPARFNKAALWDALLSGEMTMAALKQANAQAALIEDWAEQGWIEETPEAKFVLPRYRQASHSEFVLNTGQKASDEIQTALGRFSPLLYGITGSGKTEVYFDAHAK
VLAQGRQVLFLLPEINLTPQLLKRVENRFADVPTAVLHSRMAAGRRTPQDYLRLM/QAKLVIQTRLAFTPLPDVGLIVVDEEHDGSPKQDNELRYHARDLAVWRAKGGCGPVVLGSATPS
LESWHKAQSGAYRLQLTERAHASQLPQVDILNIGRLKLDNGFSPQALQLLKQNFAGGMSLVYLNRRGFAPALPCGDCGHTFGCPNCSAKMVLHQRARQLRCHHCDHREPIPFKCPDQ
NQDLTAVHGHTQRVEETLRAFPLKAAVVRVDRDSTAHKNWADLYRRIANDEIDILVGTQMLAKGHDFARLNLVIVINADGSLYSADFRAPERLFAELMQVSGRAGRADKPKRVLIQTQLP
EHPVFAAKQADYAVFAENELNERQMFAMPFFGFQTAVRADAPRVADAMEFLNAKETLAPLLPESVSRFGAAPMLHVR/LAERERAQVLESTSRQDLHRAVSLAVVQLQNRDQKIRHSV
DVDPQEA

SEQ ID 5859

TTGCGTACCGTCCGTGCTCGCTCGGAAGCGGAGCGCGCGGCATATCGCGCGACGCGGCGAGGTGAGCGTCCGCTGTTCGACCGTGAATTTTCGCTTCCGCCAAGCTGTTTGCTTAGTGGA
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SEQ ID 5860

LRTVGGPLGSGAGGISAHGAGQRCSTVNFASPKLFAVLEKPTSTGVDSAVMFGSLATFSVSVNS

SEQ ID 5861

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SEQ ID 5862

VRRYAAGSASERTTDTGTQPNSSLKRALKRDQS

SEQ ID 5863

GTGTTTCTGCTTCCGGAGGACACGCGCGCGCTAGCCCGCGCGCGCAAGTCCGTGCGGGTTTCAGCGCGCTTTGGCGGCGCTGCTCATTTGTCGGTAAATGCTGCGGCGAGCGG
CGGACATCGCGGGAATGTGCGGACCAACCGAGTGCATCCGTCAGACCGATCGCGCGCTCTTATCGTAAACGGTCAGGACGAAACTTTTGTCCCTGCGGCGGGTTTTACACGACA

GCGCGGCGAAGCATTCGCCGCCGACAGCCGAAGCCGTAAGCGCGCTCAAAAGCTGGTTTTCGGTGAAGCCCGCTCTTCGGACGGGTGTGCAATTCAGCGTGAATGCGCCCCCGG
AAAGCAGCGGT

SEQ ID 5864

VPPAFGRTRAARAEVRAGLQRAFGPRLASLGNACQAAIDGNGVDHPVHPVQTDRRVPIVNGQDETFPCQGRVLPQRGRSIAARTAEAVRAQKLVIREAVFGRVVELQRBAPG
KGS

SEQ ID 5865

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GTTGGCTATGACTGCCCGTCCGTTTACGCGCGCTTCAAAGAGCTGTTGCTGCTACCGTTCGGTGGTCCGCTCGGAAGCGGAGCGCGCATATCGCGCAGCGGCGAGTTCAGCG
TCGGTGTTCGACCG

SEQ ID 5866

LBNITVPSNYFHTRRERLALGGIVQHHTALYRSVAVYEPTVVIVRRGCKKLRLWAGRELRIAAEAVLGGQTLVDVINIPDSGLYQAQWIAFBEQETVERFAAQYGTQAQVDAVKLPHPG
RMGAAYDAAVLADDEVPHNAEALCGVLAWLQHDGIGFVYGGVNLMRQIRKLITADMAADWSSAMLAQRINCSAALRRRLARQDTNFRLLTLDVRRMRALTLQVTVNSVAQIAGA
VGDCPSRFSARFKLPGCVSVVRSEAPAAAYRTGQVSVGVRP

SEQ ID 5867

ATGCCCGCTTATACACCAATCCAACCGGAGGTGCTCTGAAAATCAGCTTCAGGACATTTTCAGACGACCTGATTTCCAAAGTGAACAAATGACCGAAACCAATCCCTAGAACTCGCCA
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CATCTGCTGTTGCGACGCGGCACGAAAGCTCCCGTCTGTTTTCAGGCGATACCGAGCTTGTGCGCAGAGTCTCTGTGAAAATGGGATTTCGCCCGCTTCGAACCGACCGAGCGGAC
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TTGTTAGAGCTGACGAGAAATTTGGGATGAAGCAACGAATATTTCCCGCCGACGAGCTTCAAATTTCCAAATATCAACGGCGGACAGGCGCGACCAAGCTCATTCGGGCGAGCTGA
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SEQ ID 5868

MPVLYTNPTRRSENQLQDISDDLISKVNMTETQSLAKALISRPSTPDRDCQKLLAERLHKIGFAAEELHFGDTKNIWLRRGTAPVVCFAHGTVDVPTGVEKWDSPFPEPTERD
GRLYGRGAADMTSIACPFVACERFVAEHPDHQGSIALLLTSDDEGDALDGTTKVVDVLRKARGELIDYCIIVGEPTAVDKLGDHMKNGRRGSLSGSLTVKGRQGHLYPHLAVNPIHTFPAPA
LLELTQEIWEDEGNEYFPPTSFQISNNGTGATNVPGLNVKPNFRSTESTETGLKQRVHAILDKHGVQYDLQWCSGQPFLLTHAGKLTDVARTAIETCGVEAELSTTGTSDGRFIK
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SEQ ID 5869

ATGCTGAGCCCAAAAGCTGCGATTGTTCAATATCCCGTTTTTCCAGTTTGCACGCTCAAAAAATACCAGCCGAGAGCATTCGCGAAATCAAAGCCGACTACAAGAAAACTGCGAGA
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AACCGCTGGCTGGATGATTTCGATACGAAAAATACCGCGCATTCGATATGTCGACGCGCGGAAAGCGAATATGACGATTACCGCACCGTGCACAAACGAAATCCGACCGAAGGT
TGCAAAACGACGAAGACTTTTCTGCTGCGCAACACATTCGAGCGCGCATTTGGCGAAGCAGGATGTAGCAAAATGGATAGCCGAAACGCTGGAAGATTACTGCCGCTTACGAAGC
CTGTCACGCGCAA

SEQ ID 5870

MLTPKSCDLFNIPIPPQFAQLKKYQPSIPQIKADYKENWQIQQLIQQVAADLSEPPAPPHIERWCNMGVRAHFFAYFYKYAKNSAAILSLILNRRRLSVSLDWHYKADVSPIALPEY
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SEQ ID 5871

ATGAATCCGTTTGAACCCAAAGCGTTACCTTTGCGGAACCGATTGAATGCTGTATGCTGCCACGGCAAGATGCGCGCTTTTTCGGTCAAGTTGCTATGTGTGCGGCTATATCGCGG
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CGCGCGCAGCCCGTGAAGCGGTGAGCAGGCTGTTCGCCAACATATCGGCTGTACGACACAATTCGGCGGCTGTTTCGCCGAAATTTGCGCAAACTCGAAGCAGACACGCTTATATCCCC
GATCGGAAGCGTTCAAACGCTTTCGCGAGGATATGATGTGCATCTGCGGATTTGAAGAGCCTTTGTTGACATGGGCAAAACGTTTATCCCCGAGAGAAGCTGACCGAAATCGGCAAAA
TCATGGCGCGCGCGCTGCAAA

SEQ ID 5872

MNPFETQSVTFAEPIEMLYACHGKVRFPQGIAMLSGYIAENGQNLVLQTRIQISRYFNVAAPLHHEDEENFFLLLYAPQAREGVDELLRQHIGLYDNWAAVSAEFAKLEADNAYIP
DAEAFKRFVEGYDVLHIAIEPLFDMGKTFIPEKLTETGKIMARRCK

SEQ ID 5873

TTGAGACGATTGTTTCAGACGCGATTATTTGCAACCGCGCGCGCCCATGATTTTCCGATTTTCGGTACGCTTCTCTTCGGGATAAACGTTTTCGCCATGTCGAACAAAGGCTCTTCAATC
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CCGGAGATTTCGGGATGTTTGAACCAAGCTGATTGACGCGCTTTCGCGCATATAGCCGCAACATAGCAATCTGACCGCAAAACGCGCGCACTTTCGCGTGGCAGCATACAGC
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GTCTCTT

SEQ ID 5874

LRLRFQALFAPARRHDFADFGQLLPGDKRFAHVBQRLFNQMHYISLHKAERFRIGDISVVCFEFGKFGGNSRPVVVQPDMLAQQLVHAFTGLRRVLQQOREKVPFVLMVQRRGNVEI
PGDLADGLQNLIAAVFGDIARQHSNLTAKTAHFAVAGIQHFNRPKGNGALPKRIHVFLVNGDSSSHFIKQPAQSRLSVF

SEQ ID 5875

TTGAACCGCAACCGGAAAGGAGATATGAAGAGCAGCAGCAGACCATTTTGAACACACCGCCATCCCGAGGACATCGCGCTAATTAAGACGCAACGCGCTTGGCGAAAAAC
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CGCTGCCCGGAAGACGAAGTTTCGTTCTGATGGGCTGTTTTCAGGCTTTGCAAAACAGGTACCGCGCTGCACGAAAAAATATGCGCTGAAATATTTGGCAGCGCGCAACG

TTTAATCGGCAGATTCTGCAAGGTATCGAAGAGCGGAGCCCTTGACGGCAANTATACCGGTCTGACCTGAGCAFTTGTGCGGATTACGCGCGCCGCTGGGATATTTTCAGGCGGCAA
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CAATTTCTGCTCTGCGCAGATGGCGTATGCGAGACTGTATTTCCACGACATCTGTGCGCCGATPTTCAGCAAAACCGCCCTTAGATGCGCGCGTCTGTTCCAAAACCGCAACGCGCG
TTCGACGCACTTCCGAGCACTGCCTATCGGACAGCAAGGAAC

SEQ ID 5876

LNAEPKADMKSSQTLILEHTAI PRHIAVIMDNGRWAKRFLPRIMGHKRLDALENMVKHAKLVQVYLVTFVAFSTENWRRPDEVSFLMGLFLQALQKQVRLHNNRLKILGSRER
FNRQILQGIIEEALTAANNITGLTSLIAADYGGRWDLQAANKLIAEGVSEITDTLAKHLMGDAPEPDLFIRTGETRISNFWLWQAYALYPTDLWPFDETDALDAVASFPKRRER
PGRTSBLPIGQQRN

SEQ ID 5877

TTGATTAACTTGGTTTTCATATCAAAGATGATTGAGCGTGTGGAAAAGTGGCATGTATCAAACCTCTGTTGCGCCTGCATTGCGCGAGGCTCAATTTATCGTCTGAAAATAGCTTCCG
GCTGT

SEQ ID 5878

LINLVFISKIERVGVKVALYQTSVAPALRRGSTYRLKIASGC

SEQ ID 5879

TTCACCTTGAATTTCGTAATAACCGAATATTTATTTATCGATTGGAGATTACCATGAAAGCTTATCTGGCTCTGAFTTCTGCGCGCTTATCGGTTTGGCTGCCCTCTCAAGAACTG
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GCGCGCAAGAGTCTTCCCTGCACTTTGGATCTGCGCAATGCGCTGACGCGCACTACAAATTTGCTGCACTTCCCGGTCACGGTGCTTTGATGAACGCGCAAGTGAATTTGGTGCAT

SEQ ID 5880

LHFDKRTYFFIDWRTMKAYLALISAANVIGLAACSQEPAPAAEATPAGEAPASEAPAAEAPADAAPAAAGNCAATVESNDNMQFNFKDIQVSKACEFTTTLKHTGTQPKASGHN
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SEQ ID 5881

GTGACCCGGAAGGTGCGAGCAATTTGTAGTCCGCTCAGCGAATTTGGCAGGATCCAAAGTCAGGGAAGACTCTTCCGCGCGCGCGATCAGTTGGTGTGGGCAACACCGCGCATCG
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GCAGAAATCAGAGCCAGATAAGCTTTCATGTTAAATTCCTCAATCGATAAAATAATATTTCGCTTTTACGGAATCAAGTGCACACCGCCATTAACAAACCT

SEQ ID 5882

VTRGAGKFFVAVSQFGRIQSGRLFAAADQFVGNNARIVRFDIVIGISTYAVFYKAVHVSFGNHKVVTHAGFGLRTHMPQSDGELFTCFADLDVFGVELHIVGFPDSCTVAGSRGFG
SICRSSFGRRFGSCPTGRSCLGSRRGRPLRAGSQTDNGGRNQSI SFHGSPIDKIIPGPTIKVQPLTKP

SEQ ID 5883

GTGTTGCACAAACAGATGTTTCGGGGCGCATTTTGTACAACTTCATTTGAAATCAAAGCTGTTTGCAAGTTTACAATCGTTTACCCAAAAAGGCAATCTTACCCGAACCTATT
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GGATGCGGCTCTTCCAACTTTGCGCGCGCGCAATCGAACTCTCCAAACGACGCTTACTCAAATGAGGATTTGGTTTTCGCGGTTTTCGCGTTTGGAAACGAGCTGACCGAAAC
GACCGTATCGAAGCATCAAGCCCTGCCAGCTGCGGCAATACCGACGGGCAATCATCTTCAAACGCGATGCGCGCATATTGTTTGCGCCAAAGACAAAGCTGCGCTCTTCGATACATG
CGTC

SEQ ID 5884

VLEKQMRFGILLQTSFEIKACLQVYNRLPKKRAILPRTYFFNIRAAVPRRANINGYLQHPCRPPYAFYFTSSSSASANSGRSSNFAAESKLSNAALLKCRVLVFGGFSGFSTSLTET
DRIEASSPASCNGTDGAILPKRDAAILFAAKRTSLPSSIHAV

SEQ ID 5885

ATGAATTTGGAACAGTTGGCGAGGCGGACGCGCTCTTTCCGACTTTTGAACAGCGCGGACAGTGCGCGGTTGGATGCTGCGGTGAAAAAAGCTGCTGCCCAACTGCACCCCC
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GAACGCGATCCCGAATGGCGGAGGCACTGGAGGAGCTGGTCAGGAAGTACGGGGCA

SEQ ID 5886

MNLBQLGRDAILSGILLQAGQWRRLDAVKKLLPANLHPHPTACTIEDGRLVLLAANMAASRLKMIAPSVLPQLAGLDASIRSVSVRLVPRPEKPPKTNLHLKAALESFDSAAKLE
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SEQ ID 5887

ATGCTGACAAACATTCGCAAGAAATCTTCGCGAGCGCAACGACGCTTCTGAAACAAATACCGTAAATCCGTTGCCAGAAATCAACGCGCTCGAAGAACAGATGCAAGCCCTAAGCGATG
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SEQ ID 5888

MLTNIAKKIFGSRNDRLLKQYRKSVARINALEBNQALSDADLQAKTAEFKQRLADGQTLGILPEFAVCREASRRVLGRHFDVQLIGMVLHDKIAENRTGEGKTLVATLAVYLNAL
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NQTLASITPPQNYFRILYTKLSGHTGTADTEAFEPQSTYINLETVIIPINRFPVQRKDLNDQIPRAEKKFPAVVKDIECHKRGQPVLVGTTSEISLVSRLILQAGLPHNVILNAKEHREAL
IVAQAGKVGALTVATNMAGRGTDIVLGNLKHQTDALRADETLSDEEKQAQIAALENGWQAEHDKVMEAGGLHTIIGTERHESRRIDNQLRGRSGRQDGPSSRFYLSFEDPLILRLFALDRA
AAILNRLAPERGVATIBHNLTRQIEGAQRKVBGRNFMRRQVLEYDDVANEQRKVITYSQRNEILTSKIDIGLDMQIRSDAVSGPRGYLYAARQHGRMTGHPDTGKPPGCRITQASGRHPTILA
EGGQCD

SEQ ID 5889

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SEQ ID 5890

MPSADLVDTYMPDSMEQNDIPTLENLAAEFRLQEDIQSWLKADNAIDGQDIKERLIERIENYAAKTELVGKQAMADFERNVMLQAIQNWREHLAAMDYLROGIHLRSYAQKNPQKQ
YKREAFMFDQLWNGIKFHIALSLTSVQIEQNPVAVEEQPVNGIQSIHSESPDIKELLGQSQTDVLTFAFPDGTDFSPLEARGQIVHRNDPCFCGSGLYKQCHKKLA

SEQ ID 5891

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SEQ ID 5892

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MIVPKVRGNDNPEVRAERKKQOTLEETAAADFPYAOQLKFNPAKAYLDKRLSAEVIAYHGLGYAPDQWQPLAQVFPQYPNTALVDTGMVINDGRIHDFRHRIMFPIRNPQGV
GFGGRVLDDSKPKYLNSTPPLFDKGNLYGLYBGAARVKEAERILVVEGYMDVVALAQFVGVGVAALGTATTAEHVILMRQADSIYCFDGSAGRAKAMRALENALPOLKDDKSLHF
LFLPEHDPDSYIRAYGKAQFEDALLNQSKPLSEYFWEHLSDGILHATQEGKAELVTSPLLVQITAPALAYLLKQRLSELVGDIDPNLAQLLQEPKPRHVQKNYKLPPIVSKQPVMP
TLVQRQIRSLILNPDWAIYIDLPLYALDGDFAELANLAETIKNHPSVPATQVLEHMRGSPYETINIRFRSALQSEMEGGGEGEDCENFOIGIKKILNELKYSQIETLKQSLQSLNE
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SEQ ID 5893

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SEQ ID 5894

MLKQRVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALTALWEYARMAGLKCTETNHLYAATLVGVVAYAGWMLNENLVVYVLAFLWLAVMPLWLRFKWRLNGWQVYAVGWLMLPFWFA
LVSLRPHPDALPLLAVMGLVWVADVCAFYSGKALGKHKIAPAISPKGSWEAGTGAAGVAVYMTAVRSAGMLAFDTGWFDTVLGLVLTVVSVCGDLLESWLKRAAGIKDSNNLLPGHG
VFDRTDSLIAVISVYAAIMSVLN

SEQ ID 5895

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SEQ ID 5896

MTKLIKILPPTVPLPLACGQTPVSNANAESAVKASAGKSVAAALKARLEKTYSAQDLKVLVSSETPVKGIYEVVSVGRQIITYTDAEGGYMFGELINIDFRKNLTTEERAADLNKIDFA
SLPLDKAIKEVRNGKLVAVFSDPCFPCKRIHEFEKMTDVTVYSFMPPIAGLHPDAARKAQLWCQPDRAKAWTDWRRKGFVPGSICDNPVAETTSILGBOFGFNGTPTLVFPNGRT
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SEQ ID 5909

ATGAAAAAGGCTTGGAAACCATGTTCCAAAGCCTTTTCAAAATGCGCTCTGAAGCCTGTGCGGCGAGCTTCAGACGGCATCTTTGTTCAAACTCAATCTGCGCCATGCAATCTATCGGAT

SEQ ID 5910

MKKAWNHVPSLFGMPSEACRGSPRRHLCSNLNPAFPHLSD

SEQ ID 5911

TTGCCGACCATGGCCGTTGCGTCAAAATGTCAGCTTGGATATGTCCAATCTACGCTGTACGATGGGATTACCCCTATATATTGCGTCCCTAAGAAGGGGCGCAATATATAAGGTGTGGC
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SEQ ID 5912

LPTMAVASNVSLDMSNPVLRMGLPLYIASLRRGAIYKWFVEDALRAVPADSFEPETAQKLKLFKAGANTILFYEDQNVVKGLEBQFPAYAAFPVWADQANAMVQYAVWTTLAAGVAG
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SEQ ID 5913

TTGAGCCTTGTGCGTGGAAAAACGCCCGCTCTATTGGCGGCTCTTGTGTCAAACTGCCGTGCTGGGCAAAAGCGAAAAATCCAAAGGCTTGGTAACCGATGCTGCTGAAACGCAAAA
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SEQ ID 5914

LSLVGRKRRRLFGGSCCKLPWCARKATSKGLVTDVCLKIRNFVEISSENEAGYEIYVKEKSVLNLQNKRAYEALGIESEAKNRRTPKPVTLPRGCVKTSISSEPSAP

SEQ ID 5915

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TGGTGGAAAAACGCCCGCTCTATTGGCGGCTCTTGTGTCAAACTGCCGTGCTGGGCAAAAGCGAAAAATCCAAAGGCTTGGTAACCGATGCTGCTGAAACGCAAAATCCG

SEQ ID 5916

VFTPSDDEQESAKIFNVLEIQIGKRPLOEIAPELSPNTRFYILGLAPNAARLSVRFWLDTTFFQLAENLAHWQDLALEPCANKTPPSIWRLLLTAVLKGSENIQRLGNRLCPEQNP

SEQ ID 5917

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TTTGGGGGATAAAACCGCTTACCGCTTGGCGTGGAAAGCAATAAACAACAAGCCGAAGCAAAAGAAACCGTTTACGCGCTCTGAAAAACCTTTGAAGCCTTCAAGCAATACCATCTC
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SEQ ID 5918

MILASLVRYRYRLATETDETGNPKVPSYGFSEKIGWILVLDKEGRLKTVVFNLTADKKPQPKLMSVPRPEKRTSGIKPNFLWDRKATAYALGVEANKNAEAKKPTTPEKTFEAPKQYHL
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SEQ ID 5919

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SEQ ID 5920

LGMMLHDIDFDHGNTPHFRTPQMKDGLIDVPPFYAEVKA

SEQ ID 5921

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SEQ ID 5922

LYGSRRLPCAQTADGAQKTAAYKQDPKAVTHYLTRPAGFSDCQRVCDETFDORRLFRPYARSLKQMAKARIRVNRERRRYRKARQTAIMAGCCTLLILITATRRIFSARK

SEQ ID 5923

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SEQ ID 5924

MLSPRRRTAAHQSSRLSFACGKNAACCRDQNYRAASSPNRGLPRFTTPTAAVHPYPRFHLFQAAGIGABQAAVESCFIRTNALAVGKSGRPQIMRYFGRVLSFVSGGLFLRAIR
ICLGAWQTAAAVQSKCLAISCRQASCRPTTRAGFCLSDLAAPFPVT

SEQ ID 5925

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TCAAGAAACAGCTTTACCTGCGGATTGCGCTTAAACAAACAGCAGCGC

SEQ ID 5926

MAYSADLRNKLNHSLTKIRTRRRAGSTNGTEPIRPAHLHLEBSFPLSRGGATPYRLLIRYITDIAKTPAKPOQLTCQETRTGCFALKNKQAA

SEQ ID 5927

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SEQ ID 5928

HPSEASDGIYKVLINTPQVLTILGSTGIGESTLDVSRHPEKPRVFPALAGHKQVEKLAACQDTFRPEYAVVADAEHAARLEALLKRDGTATQVLHGAQALVDVASADEVSGVHCATV
GAAGLPSALAAAKGKTIYLANKETLVVSGALFMETARANGAAVLVDSEHNAIPQVLPDYDRLNEHGIDSIILFASGGPFIATDLSFTDSTTPEQAVKHFNWNRGRKISVDSATNANK
GLELIEAHWLFNCPDKLEVVIHPQSVIHSVMVRYRDSVLAQLGNPDMRTPILAYCLGLPERIDSGVKLDFGALSALTQKPDFGRFPCLKPAYETINAGGAAPCVLNAANETAVAAPLDD
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SEQ ID 5929

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SEQ ID 5930

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SEQ ID 5931

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SEQ ID 5932

MTDFADRASEREAEFLVEALAKHQPPSENTAGFSHCEDCGDPIPEAKRKAVRGCTRCVVCHEYIQLKTK

SEQ ID 5933

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SEQ ID 5934

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SEQ ID 5935

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SEQ ID 5936

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SEQ ID 5937

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CGCCCTGAGCGAATTTGGAACCAACCGCAACACCTTACAGGAG

SEQ ID 5938

NIETVRAKRLLLAVLLAWACGYRYAADKVEABQTAALIAAYRHSSMVAEYALQLKKAQDERQRWYDFSQKQSTDLAAALSELDKTRNTLQE

SEQ ID 5939

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SEQ ID 5940

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SEQ ID 5941

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SEQ ID 5942

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SEQ ID 5943

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AAAGCAATT

SEQ ID 5944

MSDIDDFKSYLESHQAAPSAWGRFVAKETQNLNVLSPVPVANFLKLEAKPGVKEISSALAKIGRKNYTPQTMFDLVGVRFVALLAEHIQIVCEIJESSQWNAKSKDFADEIQNP
KAI

SEQ ID 5945

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SEQ ID 5946

LKXIITHRIYKPNENRERVEPKISTHLIDLPIIARITLRLTKALGNKSHGIEZSVVNTAENSFPQIAAAIQLEKEAEFIEDSAQFAHMLTDAQLNTPNPGSILLVLKGRVGTGKPFIC
VIAEPDQDGFRTKEEDDPTIEFLERLLTDSARLFKIGFLVAETVRPLEQISGNYRAFLYDHLMTQTETRPASYYFQVFLGMSIAASSRKLTQDFFEWTRNFIDNSDLSDAKLDARE
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SEQ ID 5947

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TGCTGAAGAAAAAGAACTGCTTCCCTGTTCCTGACGCTCGCAGCGCGCAGCCGCAAGAGCTTCTGACTACCCCGCTTTAAGCTGTGGTAGAGAAAAAGCCAACTGCGCTTGGT
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SEQ ID 5948

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KVSNG

SEQ ID 5949

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SEQ ID 5950

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SEQ ID 5951

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CGCGCTTTGAGATAGGGAATAGGCTTGAATTT

SEQ ID 5952

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SEQ ID 5953

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TTAC

SEQ ID 5954

VFLAMDAHPVIGISNKLSDGLGLTFSQVSRDIDDLVASGLVILKENGNYATGKTLQIAERFRKQERLNARLQELNRIY

SEQ ID 5955

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SEQ ID 5956

MATELGHITGVGTANELAIHSMVMDKFSGGEAYNETVWIERGRFADAKRWKGLSRDAR

SEQ ID 5957

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SEQ ID 5958

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SEQ ID 5959

ATGAGCCGTCAAATCCCTGCAACAGGCTGCCAAAGCCGCGTTCGGTTTATTCGTTAAATAAAACCTGCCCGTTGGCAAAGATGAAATCGTCCAAATCGTCGAACAGCCGTTTGCACA
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SEQ ID 5960

MSRQSLQQAESRRSVYSLNKNLPVGKDEIVQIVEHAVLHTPPSPNSQSARVVVLPGEEDHDEILL

SEQ ID 5961

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SEQ ID 5962

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SEQ ID 5963

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SEQ ID 5964

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SEQ ID 5965

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SEQ ID 5966

LEVGIRSOISRLRDMFEOMAAHGEAHGFDHRAKMVGTLNQIILDCEQLRESYALPTEAPADNVPEWLGGETGEGDESGND

SEQ ID 5967

ATGAAACAAGCGACGCTTAAGCTGATGACGTTGGGCAAAATCCAAACTGCTCGAGCTGCTGGTCGAAGACGACGACACTTTGTGTGAGACTTGCAGGCGGTGAGGTCAACGGCAACACTTTGACGATGTGACCGTATGACTATTAAAGAGCTGCGCGTGCCTTGC CGGAAAGCCGTGAAACGGCGGAAGCGAAAGATAAGGTGATTGCCGATAAAAAATAAAGGTGCGATGAGCTGGCGGAAAGACTGTGCGAAAGCAGACGGGTGTCAAAGAGCCTTAAACTCTCGGATGTGGGCATCGAGCTGACAGATGCACGCTTGGCAGCTTGACAGCTTGGAAAGTCGGTATCCGCTCGGAAATCAGCCGATTCGCGGATATGTTTCGAGCAGATGGCGGGCGACGGCGAGGCGCATGGATTTGACCAACCGCGCGAAGATGGTCGGCAGCTCAATCAAATATTATTGTGACTGCGAGCAACTGCGCGAAGCTATGCCCCTACCGACCGGAAGCACC GG CAGACAATGTGCGGAAATGGTTGGCGGTGAGGCGGAGGAGCGAGATGAATCCGCAATGATTGAGCGCTTTAAAGCACTGCGAAATCAGGC GGAAGCAATGGGCGCGGCGCGCAGCTCTGCAATATCTTAAGCAGAGCGGCGAGATTTGGGCAATCGGATTCGCCCATCGCTATACCGCAAGCTGAGGCGCGTCAAGCTCAAGCGCAGCGCCAAACGGCGCAGATGTGCGCGAAGACAGGCTTTAAACCGGAAGCCCAAAATGTATTTCGCGGTTTGGCGGAGGCGATGAGGCGCAACGGCAAGCGGTGTGATGCCGGTTCGCGCAGGCGGTGAAATGCTGCGGCCCAACGGGAAATCTGAGCGCGCGCGGATTGACGGGAAACCGGGGAAGTCATCCCCCTTTCTGAAACACCATTAACCGGGCTTTACGGGAATACAAGCTGCTATCCGACAGCTTTTGACAGCCGCCCTCAGCCGCATGAAATCGGAACACCGGAACCAATGTGTGCAAAATCGACCCGAGTTTGTGCGTTTGTATTGCTTGC CGCGCTCAGGCGCAAGGATACGGGCTGCGGGTGATGAAGGAAGAGAGATTTTATAAAACAGCCGAAAAACGTCGTCGTAATCGAAACGACCGCGTTTGGCGGTACACGGGGACAGACCATGCTTCGCGCAGATTTTCGGTGTATTACTTTCGCGCGCAAAACGAGCGCAACCTCTGTGATTTTTCATCTACATGATGCAGGCGCAAAAAAGACATCGGCAAAAGACCGCTTCGCGAGCGTACCGCGCATGGTCACTGCTTGAACCGGCGCGCAATACTTTCGCGCGGTTTAAAAATTTGTGCAAGCCCTTGGATGTGCGTAATCAACAGCGGGCAATCCGCTGCCAAGGCGCAAGTGAATAAAGACCAACGATCTTCGTTGAAACGGCATTTGAGAGCGGTTGCGCTTACCGAGGTACACGACATGCACGCTCAATGCTTTATTCGGAACGCTGGAATGCGTTACTACACAGGTACCGCAAAACCGGACCGCCACGGCATGACCGCTATCAGGCGGTGGAACAATAACAAACCGAGCAGCTCATCTGCCCGCGCTGCCGAATATTGCCGAGAGCTTGCCTCAGCGCGCGCAAGAGGCGAAAGTCTCGCGGGATTGTGGAATCCGCTTTGGCGGACGGGTATATAGCTTAAAGGCATCAAGGGGATTTTGGTCGGTAAGAAAGTTTGGTCGGTAAGAAAGTTTGTGCGTAAGAAATCTTTGGGAGGCAACCGGGCGCGGCTCGCCACTTATGACCGGAGGGTTAACGAGGTTTGGGTATCCGTACCCGAAGTAGTTTTTGACAGAGATGGGCTTCAAGGCTGATGCCCGCGCTATCGGGCGGAATACAAAGCCCCGCGCATACAGACGCGCAACGGCATCGCAAGAGGCTGACAAAGCTGGCGATGGGTGCGGAAACGCTGGAGGCGGCGAGCGCCAAACGCAAAAGGCAAGGCAGTCCCGTTTCGCGCGCAAAATCGACCGGTACAAACATCAAGAAGATACGCTTGC CGCAGCAATACGCTCTTTATGCCAAACAGGGGCAACAGATGGATTACAACAAGATGGAGGTGCGCGAGCAGGTATTGAGCAAGGTGCAAAATCGCAACCGCTTTAAACCCCGCGCTCGAGGACAGCGCGCATGGAACACGGCAGTGTGGTCTATCTTCAACACTACCCGGAAGGTGTGACCGAGGCGAGGCTGGAAGAGGCTTTGAACCGCACCCGGACAAGATGCGCTGTGAAACTTTGAAAAACCGGT

SEQ ID 5968

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 ADCAISSRRWTRARRMDLTARWARSXIKLFWTASNCAMKPYRKHQRQYTCRMGWAVKREKAMNPAMTERLKAIVENQOQAMGGRGARSAYILKQQAQEGISLSTLYRKLAEVSVKPTR
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 IVETAPESGLEFTEVHDIDQLNALSERWMRYNYMGTQKHSRHGMYTQJAWNNKIQEQLLPPPAEYCYRELAVSAPKRAKVSADLEITRPGGVRVYSVGKIGKILVGKVLVGGKVLVGNKNPWEA
 NGARVATYDABEGNEVDSVFPVPPVDMGFKDAADVIGEYKAPADTQQRHRLMDKLMAGETLEAAAAKRRGKGVFPFGKIDTPYKHQEDTLAASNTLPHKPGQGGMDYNKMEVABQVLS
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SEQ ID 5969

TTGCCGACGCGGTTCGCTGCCGCTGCGGTTCGCCGCTCGCTCCCGAGGCATCGGACAAGCAGGGTGGTTTTTATAGTGGATTAAATTTAAACCGGTACGGCGTTGCCCTGCGCTTGGCGSTA
CFATTAGTACTGTCGCGGCTTCGCGCGCGCTTGCC

SEQ ID 5970

LPTRFACRVGLPVRPEASDKOGGFYSGLNLNRYGVASPCRTICTVCGFAALS

SEQ ID 5971

ATGGCTCTGGGACGGACGGGCAAACCGACACGGGACGCAAAACCGCGTCGGCAAAAAATGCCGCTCTGAAAAAATTCAGACGGCATCTTCAGACACATTACCTGCAAAACGGCAACACATTCCAAAT
CAGACACCGTCTAGGCAATCAATACGAACGGCTGTCTTACATACCTTACCAGCTTTCACCAACCGGTATCGATT

SEQ ID 5972

MPRDGRNRHGTOTASAKMPSEKIOTASSDTLPANGNTFOSRPIROSIRTA VYILTSTFHOPVSI

SEQ ID 5973

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SEQ ID 5974

MSGALENDDGLWYFDKDL PDVFKAKFKTDRKNIKEIG

SEQ ID 5975

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SEQ ID 5976

LIGAIRRKSVFFPALGSLHAYKIKAEIVGRYHSCYVSANILLRTFTTVRFKESDGLMNAKTAALKNGVTDNPTTGLFANKKAARRALSSWAETVGLCPASAGILPDGYAEDRCPVYVS
GRCDKACGRSDQVLAFAHKLFLVDWGMHEVKEITFTDPLTGEKSFCEWAAHWMKMTGFGISIKIYRMCLRRSLKRTGKILKSVKSI PVGESW

SEQ ID 5977

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SEQ ID 5978

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LKFPGLKISGNASVSHISGPLETIADIAGQSAELGLQSYLEFLALVLSISLVLNLLFPVPLVDGHLVFTTVIEWIRKPLGERVQNI GLRPLGLALMLMMAAFAFNDRILIG

SEQ ID 5979

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SEQ ID 5980

MAKMKMAVAVAIAAAVWGWSYLKEPQAAIYITVRRGDISRTVSATGEISPSNLVSVGAQASQIKKLYKVLQQQVKRGDLAEINSTTQTNFIDMEKSKLEYQAKLVSAQIALGS
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TILSEPTPIKAKLDSVDPGLTMSGGYNSSTDTASNAVYYARSFVFNPDGLATGMTQNTVEIDGVKNVLLIPSLTVKNRGGKAFVRVLGADGKAVERIEITGMKDSMNTTEVKSGLK
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SEQ ID 5981

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SEQ ID 5982

LLPEFKENKMI VSRVPLLEKAPLRFGMPVAVVDLESTGGNLYEDRVTEVALVFKGQGRAERYEWLVNPKPIPKFVAELTGISDGMVADAPVFAIAGGLFVSLKGCVLVAHNSRFDYTF
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SEQ ID 5983

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SEQ ID 5984

LPRLAVFLVSGASSHCPDLNLHYIERTPHPVYGRFAWKFEYDSITSEILMKVWGKDMVTNCRGNKPNRGIISGIWNLARPGIEKPLPP

SEQ ID 5985

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TCGGACAAAATATAGTGGAT

SEQ ID 5986

MKNQFNCPRITITQIWTYTLNIAVNNKKAEGALEYAVISVPICQNIVD

SEQ ID 5987

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SEQ ID 5988

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VMGAGLPLDLPEMTEGYHKDVALLPILSESRGINIVLKRMMKGILPDAIVVEHFAHAAGHLGASTVEGVNDKAFDFKRVIRETFEVPKNLGLEGEKIPLLIAGGMANPEKVKTALKNWA
SAVQIGTAFATVEEGDAHLNFKRLTASAETEKVVEFMSVAGLPARGIRTKPLDSYIRREGKLQANAKDPRRCTQGLNCLTSCGLRDGLSKAGQCIDIQLAAAFRGEVDKGLFIRGKDQL
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SEQ ID 5989

ATGCCGTCCGAAGGGCTTTTCAGACGGCGTTTTCAGGTTGTGTTCGGAACAGTGTGAAAAAAGCGAGAGAAATAAAACGTTTTTATA

SEQ ID 5990

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SEQ ID 5991

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SEQ ID 5992

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SEQ ID 5993

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SEQ ID 5994

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SEQ ID 5995

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SEQ ID 5996

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SEQ ID 5997

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SEQ ID 5998

VSQNPIKPKYKHWVFWLWAGPIFVVIASVAMFFVAQGHATDLVTDYYKDGKHIDIQLHDEAVRRHIGVQVLI SPDMAAKVFGGEFDKQPLNLLMHPTRKADDQTVALKPVGS
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SEQ ID 5999

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SEQ ID 6000

LYNSGNIWFKEKRIFSKLETOCLKTRKMTSEKQNGGNGQNTINQSKSECRMTTENQAGSPASGIGTSEOTKAAPKVKTFDPRASVIOIHPEGERIHPKAEGRFAKLRIAAVLATQFVY
VIPFWNWSGRQAVVFNPERHFFIPGLSLGVGLIYLALLMICAFLPWMTTIAGRLMCGYSQPTVYTEIMLWIDNLVEGDRNKRLALEKSPNFPNFKIRIKATKYLLIPLVCANWTGTF
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AACIDACDEIMDKMYPSGLIRYTTESALEHEYAEKDIKKRLLRPVAGYAVLAVVAAFLVGLSTRKMEVDILKDRGVMVRENAKQWLENAYSLRIINSEKEQLITASVKGFDIAL
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SEQ ID 6001

TTGTACAATTTATGCGCGTCCGATGATTGGGCGAATACATTTCCCATCCGATCAAAACGCGCTGATTTTACCGCACCGCCGCAACAAATTAATACTCTTAAAAACAAAGAC

SEQ ID 6002

LYNFMRRFDVLGEYISHFHQNALILPHRPNKIKILLKMD

SEQ ID 6003

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SEQ ID 6004

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SEQ ID 6005

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SEQ ID 6006

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SEQ ID 6007

GTGATTTCGCAAAATATTATAATGGAGATTGGCGGAATGAGGAAGCATCAAGGCGGGAGGGCAAAAAATGCCGTCTGAAAAGCATTTCAGACGGCATT

SEQ ID 6008

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SEQ ID 6009

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SEQ ID 6010

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SEQ ID 6011

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SEQ ID 6012

SEQ ID 6012
VWKSCINKSSIYLKGNIIYTLPPKMTNIRKGAFMSDCNRIQFVLLSVLRIVTAYILFLHGTSKIFAFPIEMGSGSPGGILLLAGILETVGGILLVLGLFARPAAPVLSQGMNAVAYFMAHA
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SEQ ID 6013

SEQ ID NO: 6013

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SEQ ID 6014

SEQ ID 6014

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SEQ ID 6015

SEQ ID 6015

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SEQ ID 6016

MEHQRLPLGLFALALLAAMTWTGLPIAVRQVLKVPDAPTLVWVRFTVAAAVLFLVLLALGGRLPKRRDFSHEHSFRLLLGVTGISANFVLIAQGLHYISPTTTQVLWQISPTTHIVGVGLVFK
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SEQ ID 6017

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SEQ ID 6018

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SEQ ID 6019

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SEQ ID 6020

MSLNKLVILIGRGDPEVRYPMNGEAVCNFSVATSETWDRNGQVQRTVEHNNITMYRKLAEIAGQYLKKGGLVYLEGRIQSRKYQGKDGIERAYDIVANEMKHLGGRNENSSGAPYDEG
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SEQ ID 6021

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SEQ ID 6022

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 AQMALFALPFAFAMTRILGLEKIQHWKYLPTSTITGLVVMVPLIIVGETFRNKLQKVPVLGIVCIAAAQLGLLSGMSIWLITAYLVVYFIGFNVLEASLPSEVSKIASDLEKGTAMGVYNTIQ
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SEQ ID 6023

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SEQ ID 6024

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SEQ ID 6025

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SEQ ID 6026

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SEQ ID 6027

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SEQ ID 6028

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SEQ ID 6029

TTGTGGAAGACCGCTTATGTGGTCGAACAAAGCTTCGGTACGCTGCACCGTAAGTTCCGCTATGCGCGGGCAGCCTATTTCCGACTGATTAAAGTACTGCGCAAGCCACCTGAAGGCGA
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SEQ ID 6030

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SEQ ID 6031

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SEQ ID 6032

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CRQRE

SEQ ID 6033

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SEQ ID 6034

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SEQ ID 6035

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SEQ ID 6036

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IPSITL

SEQ ID 6037

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ACGGAAGTACGCAAGACGCCATCAAGAAAGCGACAGCATCCGCGCGCTGGGCTCGCGCTATCGCGGTTTCGCTTTGACATCACGCCCAAGCTGACCTGGACACCGGCTACCGCTA
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SEQ ID 6038

VQADLAYAYEHITRDYDAAGANQKKISTVSDYFKNIRTHSIHPRVSVGYDFGWRIAADYARYRKWNLNKYSVDIKELENKNQNKRLDKTENQENGSPHAVSSLGLSAVYDFKLNDKPK
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SEQ ID 6039

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CTTAATCAAAGCCAGCCCGGACCATTCACCTTCAGGCGCTCCCGATACGCGCAACCAAGCGGAAACCTGCACCGTTACGCTCAACGACGCGGCTACCATTTGCCGCTTCGGGTACA
AACCAATCTGCCCGGCTTCGAC

SEQ ID 6040

MKNVQKGTLLLEMLIAVAILGILFLIAYPSYKTYIRRLSEVKSTLLMNAQNLERYRQKGTPEKYDSTKLQNKYFKITLILKASPDHFTLQAAPDTATNBETCTVTLNDGGTIAASGT
NQSCPFD

SEQ ID 6041

TTGTTATCCGCGCATATTGTTGTGAAACACCGCCCGGAACCGGATATAATCCGCCCTCAACATCAGTGAAAACTTTTTTTTAAACCGGT

SEQ ID 6042

LFRHIVLKHRRPEFDIIRPSTSVKIFFLAG

SEQ ID 6043

ATGGCGGATGAACAAACCGGTACGGGTGCCCCGCCCGGCTCAAAGGGAACGGTTCCTTAAGCGGTCAAGCACGGGCGAACCAGGTTCCGTACCATCCGTACTGCTCGGCGCCGCC
GCCTGTGCTGAATTTTGTATATCCGCTA

SEQ ID 6044

MADEQKPVVRVAPRLKNGSLRRPSTGRGVSPLPAARLVLIVNPL

SEQ ID 6045

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SEQ ID 6046

LRVGLVSRINAGGHHPLVGGISRGVHYWKNDFSEQLSLRSLFGRQNRSVTRSPGTVPVQNLIGSSRYNFAAGFNADFRRILGERWRLTLNAGNWKHYQEDRTAARYGSHMPLAGAT
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VEKDFK

SEQ ID 6047

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TACCGGTTTGTTCATCCGCTATTTGT

SEQ ID 6048

LRLFEILPHAHENLRIFACVKTPIAADPQIABIELRRKALPRDFVVRQVCLIFVVFAREAVHNCFGCIKSPAGIAQVCPQQAVERFDRADTQTLADGSLFRLFRHVVRVPTAVRQ
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SEQ ID 6049

ATGCCGTCCGAACGTTTTCAGACGGCATTTTGTGCTGCGGAACATACCGTCGGCAACATCCGTGAGCAGAATCAAAAACAGCGCATCATTTATTGTCAACGCTGCGCGCTCAGAG

SEQ ID 6050

MPSERPSDGI PCRKHTVGNIREQNKQPHILLSTPAPSE

SEQ ID 6051

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SEQ ID 6052

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SEQ ID 6053

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AAAGTTGAAGCGTC

SEQ ID 6054

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TGYHKSAYILENADMPGFSRKEQTILAQLVIGHRGDMKMGIGIIGNEMLWAVLSLRALALFCRSRQDLSFPKMLQRLTDTSCGFTILRIDSKWLRHPLIADALEYESVQWQKINHPF
KVEAV

SEQ ID 6055

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SEQ ID 6056

MFSEALQTAFRGNIRRSFTMIRL/TRAPAAALIGLCTTGAHADTFQKIGFINTERIYLESQARNIQTLDGEFSARQDELQKLRGLDLERQLAGGKLKDAKQAEEKWRGLVEAFRK
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SEQ ID 6057

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SEQ ID 6058

SEQ ID 6058
LKRSAIMKQAVVNVKNVAGDVEVVVERVRLPEYGEALVEVEYCGVCHFDLHVAAGDYGEKPGRVLGHGIGLVKEVADGVKNLKVGDVRSIAMLFGSCGSEYCNTRGRETLCRSVLNAGY
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SEQ ID 6059

SEQ ID 6059

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SEQ ID 6060

SEQ ID 6060
M²TLPSLKVFRQVVQSGGPTRAADALGISTAMASKHVSHLENTVQAKLLHNSRNLSLTAGEEYYRQCSYALDTLDDAAQKAAGGTEKPGGLRVIMPLWTFAGSQICNWLAEYRERYPEV
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WAE²FHVLPGGPIVELLPGVAVPTDRI²NAVYADRAFLSAKRVSEIDFLNEKIASRGGCRNAV

SEQ ID 6061

SEQ ID 6061
CMTTCGGAATCTGAACAGGATCAAAGCGCGAGCACCCAAAAAAATCAAAGCGGAACAACCCAAACCGCAACGCGGAAACCCAAAGCCGAAACTGCATCCATGCCCTCTGAACCGTCCAAACAGGCAACCGGTAGAGAAACCGATAGAGAAACCTGTGCGAAAAACCGGTGTGAAAAACCTGTGAAGCAAAGATTGCGCGCGCCGGAAGCAAAGCGGAAAAACCGGCCGCTCGACCCGAGCCCAACCAACCGGAGTGTGCGAAACTCCGCGTTTCGCGGACAGACAGCCCAACCGCGAACTGTACCCGCTCGCAATACTGCGCCGATCGGAAACCGCTGCGCGAATCCGCCGCCCCCAAGAAAGCGCGGCTCTGTGCAATCGACACCGCGACCGAGCAACCGGTAACACCGTTTCCGAACCTGTTCGCGAAACGAGCTGAAGATTGCGCCCGAACCCTGTGCCGAACCTGTGCAACAGGTTTCTGCCGAAGAAGA

SEQ ID 6062

SEQ ID 6062
HSESEQDQSGSTQKQNSGTTQTANGETQSRNCIHAV*TVQTGNGRETDRETCRKTG*KT*SKSCRARSKSGKTKGRSTRTQTQTSVRNSGFGDRTPTRTCTCKYCRIGNRCRIRPPKKPPLL
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SEQ ID 6063

SEQ ID 6063

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SEQ ID 6064

SEQ ID 6064
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IAENFAGKR

SEQ ID 6065

SEQ ID 6065
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CATCATTCGCGCAATCAA

SEQ ID 6066

SEQ ID 6066
LGCRQAASRHFCQGNKLPGGVFHFVCRFLSRVGSFVQSVFSRFAYRPFPGCRVFGFSYSLGTCLCISRSIFDLAFRFFDGRSGRLGGRSRSVFNIGIANGLRGFPNLLPGFLRLTSCQGR
HHCNO

SEQ ID 6067

SEQ ID 6067
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SEQ ID 6068

SEQ ID 6068
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SEQ ID 6069

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GGTTCCCGGT

SEQ ID 6070

LRQSIIFSC LILLELLIKVLLKNRTV F HQSADFAHRPERK RFPV

SEQ ID 6071

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SEQ ID 6072

LDFS NLAEKVRAAGKLKRRGCVLOFSEFS

SEQ ID 6073

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SEQ ID 6074

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SEQ ID 6075

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SEQ ID 6076

CCTTGAAHDTFKKIGFINFERIYLESKQARNIQKTLDGESFARQDELQKLOREGLDLRLQLAGGKDKAKKAQAEKWRGLVEAFKKQQAQFEEDYNLRRNBEFASLQQNANRVTVKIAKQ
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SEQ ID 6077

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SEQ ID 6078

VYRHVKSVVMMIAAAFFFHIDHHTAGDFAFAHLENGGCFIQSTQLDFRHNQTFRAELGGFFQIFARADQRADHFDVAVQNQTRDQGIIHRFRRQPDGNHTSARADAITHGRVECGSRYGGYDYS
 VCAAGFFLNFHFGSVLFGGVDNQIRAGFFGKCLVVVDVGDNVRAEYFFRVLDTQVAQAARAVNRNPLTRTNAGNFNGFISGHAGTSNAGSLRRIQTFRDFRVIQTHDAVGRHTAVGGVA
 RVQYGTAGGFAAGLAVPARAAALBQPGDADAVDPQIFHTVGNFFNQTDALVSQHAARFPAVVACRNQVQGMHAALPDPDQCLAVPQRANLAFYFHILARYIFTHNCLFIEDCAPPGQK
 KPVNGMLSDIRVSIRFRILRVKVVVEKYMLYYNSWGGAALDGGMRMRQVSSLKKRKGPKVPMKSEAVSGRHYFGAGFGGGLVEAGALVCTGSGNGTAVVERNGAGFAFVGRIRIGSGL
 KGEVVGAGFD

SEQ ID 6079

ATGAGCAAAACAGAGTTCTGACGGCGTAACACCACGGCACCCCGCATCTGGGCAACTACGTCGGCGCCATCCGCCCGCCCGTCCGCGCGGCGCAAAACCCCGATACCGAATCCTTCC
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CTACCGCCAAAGCGACATTCGCGAAGTGATGGAGTTGAAGTGGATTCTGACCTGCATCACCGCCAAGGGTTTGATGAACCGCGCCACGCGCTACAAGCCGCGCTTCAAGCCAATGCGGAA
AACGGGACGGAAGACCCGATTTTCGCTGTGGAATGGGTTTGTTCAAGTTATCCGATTCTGATGACTGCCGACATTTTGATGTTCAAGCCCAACGAAGTCCCCCTCGGGCGCGACCAATCC
AACACGTCGAAATGGCGCGGACATTCGCGGCCCTTCAACACCGTTTCCAAGAACTCTTCAACCTCGCCGAAGTGAATAACGAGAAACGTCGAATCTTGTGCGGTTTGACGGGACG
CAAAATGTCCAAATCCTACGGCAATACCATTCGCTTTGGGAAAAAGCAAAAAAACCCAAAAATCGGTCAAAAAATCATTACCAACATGAAGAGCGGGCGAGCCGAAACAGCCCGAC
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TCAACCGCGAATTTGGCAAGCTCGCGGAACGCTACAAGCAATTTGACCTCTAATCTTCGCAATTCGAAGAGATTTTTCAGGCAGGCGCGCAAAAAGCGCGCAAGAAGCGCGGAATTTGT
GGATAAGGATACGCGCATGGCTCGGCATCCGCCCTTGAAAC

SEQ ID 6080

MSKKRLVIGVTTTGTGPHLNGYVGAIRPAVRAAQNPDTESFLFLADYHGIKCHEQEMIHQSTQAAVATWLACGLDPERTTFYRQSDIPEVMEIWNWITCITAKGLANRAHAYKAAVQANAE
NGQEDPDPGVEMGLFSYPIILMTADIIMFNAFNEVPVGRDQIQHVEMARDIAGRFNHRPQELFTLPEVKIDENVELLVGLDGRKMSKSYGNTIPLWZNDKKTKQSVNKIITNNKEPGEKQPD
ESPLFETYKAFSPPTSETAEFTOMLADGLAWGEAKKLSAAKINAEALIRERYNALTSNPQSIKETLOAGAKKARKKARELLDKVRDAVGIRPLK

SEQ ID 6081

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SEQ ID 6082

MPSEMPSETWQAEVFTALGLFQRADADRIAYFIQQFARFFARFLRACIQNLFDLRRIRGQCVVAFAPFCQFVDFPRRRKPFRLAPSQAVGKHLRKFRRRRRGGFIDFKQRAVFLFLRIA
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GFVGVGAVHQTFLGGDAGNPVQLHFGNVALAVEGGALGVESACKPSGGNGLGLVNLHLVAFDDAVVIGEEBFGIGVLRADGGADGADVQMRGAGGGYAGQNSFFAHRKNVLTAA
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SEQ ID 6083

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AAGGTAGAAGCGGACGCGCAGACTGAAATTTGCC

SEQ ID 6084

MRVDKLTAKPQALAEQSLALAADSSYLEAGFVLKALLDDQNSGAAALLAHAGVNPQVKRQLQHLNLSLPKVSQCGEILPSRELQAVLNLMKAAATKRGDAYTASELFLLALVQND
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AALAGAKYRGEFERLKGVLNDLAKDNGNLTIFIDRIHTLVGAGKTGDAGNMLKPALARGELHCIGATTLEDEYRQYIEKDALEERRPQKVLVGEPSVEDTIALRLGLQERYEIHGI
DITDPATVAAAEISDRYITDRFLPDKAIDLIDEAASRVKMEKETKPEAMKIDRLIQLRMEKAHVEKEDDAKRLLEIDEIDGLQKEYALDDEIWKAEKASIDGANAIEKIDIEVKI
KIBQAKRQDLALASKIMYEDLEHLEKQRAAERADTSTKPAKLLRNNGVAERIAEVVSRMTGI PVSKMMEGERDKLLKMEVILHRRVVGQNEAVRAVSDAIRRSRSLADPNKRYGPF
LFLGPTGVGKTELCKALAGLFDSEDLIRIIMSEYMEKHAVARLIGAPPYGVYEGGYLTQVRRKPYSVILLDEVEKAHPDVPNILLQVLDGRLTDSGRTVDFKNTVIVMTSNIGS
QHIQMQGTQDYEAUVKVMEDVKEHFRPEMINRIDEVVFVHGLDQANIRSLAKIQKLEKRLERQNLRLTVSDAALDIIAKAGFPDIYGARPLKRAIQSEIENPLAKALLAGNYAPESI
KVEADGDRLKFA

SEQ ID 6085

ATGGATAAATTTCCCAAGTCTGCAAGCTCGACCACTGCTGCTACGACATACGCGGGCCGGTTTCAAAAAAGCCCTTCAGTTGGAAGAGGAGGGCAACAAATCCTCAAGCTCAATATCG
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AG

SEQ ID 6086

MDKFPKSAKLHVCYDIRGPHVKALQLEEEGNKILKLNIGNPAPFGPEAPDEILDVIRNLTSPQGYCDKGLYSARKAIVHYQNKGLRDTIVNDVYINGVSELIAMSHQALLNDGDE
ILIIPADYPLWTAATLAGGTVRHYLCDEENGWPNLADMEAKITSKTKAIVINPNPAGVYSKEILLLEIAELARKHGLIIPADEIYDKLLYDGAHVHYHIALAPDLLTVPFNGLSKAY
RVAGFRQGMVNLGPKHAKGYIEGLDMLSSMRICANTPMQHAIQTAGGYQSINEFILPGGRILLEQRNARWELVNIQIPGVSCVKPMGAMVMPKIDTEMYRIRDMKPVYDILLVREKVL
VQGTGFNMWIKPDHFRIVFLPVVHQIIBAMGRILARFLQFYHQ

SEQ ID 6087

TTGGGCAATGGGTGGGAATGACTCTTTTTCACGCAAAATTTAAAGCATCAGGCGGGGTTTTCAGGCTTTTACCTGCCCTCTTTCGCGCGTTCGCTGACGCTTTTGGCGGCTATATCC
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TTCTTTCGCGCGGTTACTTTAATATTGACA

SEQ ID 6088

LGNGWECTLHFAKFKASGRGFQAFYFLSLRSLTLLEPISQLSVSTSSITTTVVSGFLPSTRASNSITPPISSAFCAAVGASLPPTLLILT

SEQ ID 6089

ATGCTTTATGTCATATTAAGTAACCGCGCGCAAGGAAGCACCAGCTGCCGCGCAAAAGCGGAACTGATCGCGCGGTAATCGAATTCGTCGACGCGTCTGGGTAAATCCCGAAA
CAACGTTGTCTGATGACGAAGTGGATACCGTAACCTGGGATATAGCGCGCAAAAGCGCTCAGCGAAGCGCGCAAGAGGGCAGG

SEQ ID 6090

MPYVNIKVTGKEAPTAQKAEILGGVIELLARVLGNPETTVVVVIDEVDNDWDIGKSVSERRKEGR

SEQ ID 6104

VPKTGLHNLNPNRPFSPILPSKQKCRLKWFTQASVQVTSIPAAQLHRFFNTADTHIRRGQTQIDITLLRQVFNIAERAAQDDDFFLNFKVLPIIALQVHLEIGNDHAAAVQCNIGH
DQYAVLMDQDNWGPGRSRVACFPHDFRADFPVGFVGSQVLVFCQARGEYVHIQSQKFGVGNFFAVTGFVGDEAPFLFLPKQRFHFAQVPTVDSNVNSRYGDNFRAGLNRVLAVGVVAHIAETLN
GVGCAPHFLPAQFPOSIDGGEVHVAHTGSLCTRQRAEELNRPAGKYARRGMFHHVFIGIHHPRNFAVGVHIGGGNDIFFRSAGQSLRHKRGRCVFPVPPRNBNADPR

SEQ ID 6105

SEQ ID 6105
GTGCGTTCCTCCATCCCGGTGTGAATCTGGACGAAGTCAAGGCACCTGTGCGATTGGGATGACCATCAAAATGCTGCGTTGCAGGCATTCCTTACGGCGGGCGCAAGGCGGCGTACCTTGGATC
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TTATGTCGTGGATGGTGGATGCCTA

SEQ ID 6106

EQ ID 6106
VRSHPGVNLDVKALSIWMTIKCCVAGIPYGGGKGGVTLDPROYSEAELERIARAYAEAIAPLIGKKNRYSRPRCEHQRONYVVDGGCL

SEQ ID 6107

SEQ ID 6107
ATGTCTGATGCCGTTGCAAAAGAAACCTCAATCCGTTTGAANAATCGCGCGAAACAGGTCAAAAACCGCTGCGACCGCTGAAAACCGATCCGCGCGTTTATGAAATCTCGAAGAGTCGGA
CCCGCGTGTGGAAGTCAAACCTCGACGACGGCAGGTCGCAAAACCTTTACCGGTACCCTGCGCGTGCCTCCCATCCCGGTGTAATCTGGACGAAAGTCAAGGCATCTGTCGATTTGGATGA
CCATCAAAATGCTGCGTTGCAGGCATTCTCTACGCGCGCGGCAAGGCGCGCTTACCTTGGATTCGCGCGATTATTTCCGAGCGCGAACTGGAACGCATCGCCCGCGCTTATGCGCGAAGCGAT
TGCCCCGCTGATCGGCGAAAAAATCGATATTTCCGCCCGCGATG

SEQ ID 6108

SEQ ID 6108
MSDAVAKETFLNPFETARKQVKTACDRLKTDPAVVEILKSPTRVLEVKLDDGTVKTFIFGYRSRAPPSRCESGRSQGTVDLDDHQMLRCRHSLSRRRQRRTLGSARLFAGGTGTGTHRPRLCRSD
CPADRRKKSIIPPPM

SEQ ID 6109

SEQ ID 6109
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AGCGGGCGCAAGGAAACGAATTTTCTCTCTCCCGGCATAGACGAAGCCCGTTTCAACGCCAAGTCACTCCCGGCGACCAACTCGTCTTTGAAGTCGAACCTCTGACCAAGCCGGCGC
GGCATCGGCAAAATTCACGCGCTTGCCAAAGTGGACGGACAAGTCGCGCTCGAAGCCGTGATTATGTGCGCCAAACGCTGGTT

SEQ ID 6110

SEQ ID 6110
MDVQLPIEAKDIQKLIPHYRPFQLQDRITAFEPMKTLTAIKNVTINEPQFGHFDPDLFVMPGVLIIEAMQACGTLLAILSEGGGRKENEFFFGAGIDEARPKRQVIPGDQLVFKVELLTSRR
GIGKFNVAKVDDGQVAVEAVIMCAKRVV

SEQ ID 6111

[illegible]

SEQ ID 6112

SEQ ID 6112

VIDAVRVLGEASAKQLRGESMODVIFNGAATRRPAPRASVELVFDNSDHSLQGAWQCYAEVSIKRQLTRQGESTYPIINNQTVRRRDITDPLFTGTGVGARGVAVIEQGMISRIIEARPEEL
RAYIEAAGVSKYKERRKETEGRLKDTREHLQRLGDLQNELARQVEKLEKQAEATERYKSLTAQLNQDQLDLYAQWQSLAAADKATAQHQSLOAQODEATAQVQALNNEVHALQTABQS
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HITPAEWOHALSVILAERLHARSVPNSFPVPPAPLPQGAAMLSDGLSGGIKSLPVOALLNQIQAPPPQTALHHMLDGLVCAPDLSYALAHQNDLGTQIWLTPBEGHQVDKVSVLLYAK
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VQTLTQLPQLQAAQTALLQQEALNAKRYHQLITERAADLVLEALAKESAKVLNNSISGSLTRQIEALGAVNLAAQLLEAREARDGYTRSQSEVQAAALILEEAIAQIIDDKTARF
KETFDVANGVKQYTPPTPLPGGGEATLKMIGDILLTAGVVSIMARPPGKKNSTIHLSSGGEKALTMSLVFALFSLNPAPFCLLDEVDAPLDAMTSPFCKLVKMSVQEQFTLYISHNRLTWE
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SEQ ID 6113

SEQ ID 6113
ATGATTTTTATTTTTCAGCCGCACAGCATCCGCTCTGAAAAAGCAGCGCGCATCCGAAAGCAATGTCCAATTAAATAAGATATAGTCATCATTTTATTTTAAAAAATTTAATTGGAA
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SEQ ID 6114

SEQ ID 6114
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SEQ ID 6115

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SEQ ID 6116

MNAIEHVQAVFDLGLTCDSPDLAAAAEAMLEQLGKPLPAKVVSYSVGDGIGKLVHRVLTNDREADESELWEKGFVSVMKYRDLHSVTFPRYPETAGLALLKSLIGLPLVITTK
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SEQ ID 6117

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GGCCTATAGTGAAGAAACCCGCGCACTGCTTCCGACCGCTCAAGCGAAAGCAAGCCCGCATAGCGGTGTTCGTAAGAAATTTCAAACTTCCGCGCCACCTCAAGAAACAAACA
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SEQ ID 6118

MKPQKSLRARAMDILSRQEVSRIGLKRKLAPHAEELEENLVNEFAERNWQSDLYAEAYIRSKSRKHSGLRLKQALAQGIDERTSRNLLPDRSSEKQAAALVLRKKFKHPAANLKEKQ
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SEQ ID 6119

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CACTCGTGTCTTCTGCTGTTTTCGCTTTTGGCTTTCC

SEQ ID 6120

MSBQPEKHHSPIEDERKNPYYRMGBAVAGFMLAVWAGVLALVFFLVFRPHLS

SEQ ID 6121

ATGACACACAACGCCCACTGCCTTCCACGAACTCATTATGTCGCAACTGATGATCGCGACACCGCCAATTTTCAGCGGCAACGTACACGGCGGGAACCTCTGCTCTGCTCGACACAGG
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CTACACGGGACGCACTCGATGGAATCGGCATCGGTGTCGAAGCACAAACATCCGACCGCGGAATCCGCCATACCAACAGCTGCTACTTACAGTGGTTGCGGTCAAGACGCGCAAA
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SEQ ID 6122

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SEQ ID 6123

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SEQ ID 6124

MLVLSFRHRPSPAAGHVSGLLEADFSAPFFGFFVAALAVGQDFQRDGDGFVFDNRHREVAAVGMADFAGADVLCFTDADPHRGASRVVDSGVKGNQIADVDGFFKQDFVNRKGNAI
IAAVTAGAGIGNLVBEQFAAVYVAARIGSVRHHQFCHNEPVGRQLALLCHGVPLRLKGVLRKWRNFRWEGSGIQAOKSYGGTVCRNGPPHPSSEAFRRHPVQBSQKRKTKWTSASTPA
QTASHNPATARPTR

SEQ ID 6125

TGGAAGCCGAGAGTTTGATGTGGGTGAGCGCATTAATGTCGAAAAATAAAAAAGAGCGTATTTTAAACGAAATCCCGCCGACCAACCCCATCTTTCGCGGCAAAACCTTACCGCA
TCCCGCCCGGTGCGGAGGATTTTGCATATCCCGGCATCCGATTAATAACTTTTCGCTTTCCACACCTTTCC

SEQ ID 6126

LKPESLMVRRIMVGNKREAYFNGNPAAPPHILPAKPYRIPPRCGRILHIPAIRIKIPAPFTLS

SEQ ID 6127

ATGCCGTGTAACCCGCCCTCCCGCTTTATGCGGACACGCGCGCGCGCACACGCTCGTCTGTTCCGCCAAACCTCCGCAATCCGCGACAACCGCCGCTTATGCGCGCGCTTCCGCAAG
GTTCCGCCGTTATCGCATTTTGGATTGACGATGCGGAACAGACAACCCGCGCGCGCGCTTCTACCGCAATCCCGCGCGCACTCGCCCAAGGGCTGCGCAAGCGCGGCATCCCGCT
CTACACGGCGGATCGCTGCGCGGCTTGTCCGCTCGCGCTCCCGCTCAATATCCGCGCGCTCATCGCGACGAATCCCATACTTTTCCGCAACAACTCGCGCAACCGCTTTGGCAC
GAATTGACAAACACGGCATCGCTTAACCTTCGTCAACGACGCTTCCGTTTTCGCGCAAAACCGACCTGACACAGACAACGGTACGGCACACCGATTCAACCGCTACCGCAAGTAT
GGCTCGACCGCTTTTCCAGCAGCCCCCGCGGTTTCGGACCTATTTCGGGCATACCGCAACCTTCCCGGAAACCTGCGCGCGCGCGCTTTCGCGCGCTTTCAGACGGCATCTTCT
GCCGCAAAACGGCGGCAACCGCGCTTGGCGGAGTGGCGGCTTCTCGAACAGCGCGCTTCTACTCGGTTTAAAGGATTTCCCTTCGCGCAAAACAACTTCGCTGATGGCGCG
TATTTGAGTGTGCGCTGCATCTCGCGCGCTGCTCGCGCGGAAAGCTTCGACGCGCTGTAACGCGTGGGCGGACAACATCATCGCGCGGATTTTCTTCAACTTGCCTTGCAGC
ACGCGGATGACGACCTTCAGACGGCAATCCGAACACACCTGCGCTGACGCTTTGGCAGCAGGCGCGGACCGCATTCGATTTATCGATGCGCGGATGCGCTGTTTGCACAAAACCGG
CAGCTTCCACCCCGCTGAGACGCTTGAAGCGGATTTTCTGCCACGTTTAAACCTTCCCGCGCGGAGGCGAGATATGTTTCCCGCGGAGCTGACCGATTTTCATGCGCGCAATC
AACCAAGGCAACTGGCGCTTGGCGCTTACGGCACACCTGCGCGCATTTGCCCGCGCTCATACCGTACCGACCGGACCGGTACTTTATCAACGGCACATTCGCGAATCGCCACC
TGTCCGCGACACCGCTTCCGCGCTTTCGCTGTCGATACCAACGGCTATCCCGCGCGCGCTTCCGCGCGCTA

SEQ ID 6128

MPSETALFLYADTRAHLVWFRQNLRIIDNALCAAVAGSPVIGIWIIDAETDNPRAAFYRQSAEALQGLARRGIPLYTAASPAGLVRLAVRLNIRAVIADESHFTADKLADNALRH
ELDKHGIALTVPNDRSVFGKTDLPDNGTAHTDFNRVREWLDRFSKQPPAGSDFLAAYRQPPENLPAPPAALSDGIFLPQNGGETAANRWRRFLQEAASYSLVKDPSPRKVTSIMGA
YLSVGCISPRILLARESLERRINAMADNIIRDFFLQALQHADDDPSDGNPEHTLRLFLMQQGTGPIPIIDAAMRLHRTGSLHPLRLSADPFCHVILNLPREGEIWFARQLTDFDAI
NQGWRLLAASRHTCPDIAAASRYRDPDGTPIKRHIPELAHLSADTVHTPWRFAASVDTHGYPARPVAGV

SEQ ID 6129

AGGAATACGACAGACATGACGCTACAACTCCCATCGAAGCCAAAGACATCCAAAACTCATCCCCACCGCTACCGCTTTCTCCAGCTCGACCGCATTACCGCTTCGAGCGGATGAAAA
CCCTGACCGCATCAAAAAAGTAACCAATAAGCAACCCCAATTCAGGCGATTTCCCGACCTGCCGTTATGCCCGCGGTACTCATCATCAAGCGATGGCGCAGCGCTGCCGACGCT

GGCGATT TTGAGCGAAGGCGGGCGCAAGGAAAAAGAAATTTTCTTCTTCGCGCGCATAGACGAAGCCGTTTCAAACGCCAAGTCATCCCGGCGACCAACTCGTCTTTGAAGTGAACCTC
CTGACCAGCCGGCGCGCATCGGCAAAATTCACGCCGTTGCCAAAGTGGACGACAAAGTCGCGCTCGAAGCGTGTAATTATGTCGCCAAACCGTGTTTGAGCGTTTCGGAAGAAAGTCTGT
CTGAAGGTTCTGACGACCTAATAAAAAAGAAACCCACCGGTTTAGGTTTATTCAAACCCAGGACAC

SEQ ID 6130

SEQ ID 6130
RNTTDMDVQLPIEAKDIQKLIPHRYPFLQDKRITAFEPMKLTITAIKNVTINSEPOFGHQHFDLPVMPGVLITEMAQACQCTLAILSEGGKEKENEFFFPAGIDEARFKRQVIPGDQLVFEVEL
LTSRRGIGKFPNAVAKVDGQVAVEAVILMCAKRWV*AFGRKSSESRPRPNKKKTHRPFRIQTQGH

SEQ ID 6131

SEQ ID 6131
TTGCAACGGATGAAATCAAGCAAATACCCAAACACAGTCAAACAAATTTATACGCCCGCTCCCTTCGGAATGATTTGAAAAACACAGCCGCCAAAAACAAAATGCCGTCGGAACCTTTC
AGACGGCATTTTAAACC

SEQ ID 6132

LOTDEIKQIPKHSQTNLYAPSLRNDLKTQPPKQKCRKTFQTAFLT

SEQ ID 6133

SEQ ID 6133
ATGCCGCTCTGAAAGGCTTCAGACGGCATTTTTGTTTGGCGGCTGTGTTTTCAAATCATTCGAAGGGACGGGGCGTATAAAATTTGTTTGACTGTGTTTGGGTATTTGCT

SEQ ID 6134

MPSERSSDGIFVLA AVFSNHSEGTGRINLFDCVWVFA

SEQ ID 6135

SEQ ID 6135
TTGACGCCACCTCGAAATGAAGCTGCGTCTCGGAAGCATCGGTATTACCCATCAAAGCAACCTGCTGACCGCGTTTGACCTGCTGACCTTCGCGCAGCAGCAATTTTGGTTGTGCCCGTAC
GCGGTCAGGAAAGAGGAATTGTGCTGGATGATGACCAAGTTTCGCGTATCCCCTCAAACC

SEQ ID 6136

LTHLEMKLRSGSIGITHOSNLLTAFDLITFADQQFLVVPVRGQERGI V LDDQVSVSPQT

SEQ ID 6137

SEQ ID 6137

TTGGCATACCGCATGACCGTTTTTCAAATACCGCTGGGTTTTTGGCGCTTGAGAAGAAGCGGCATTTTTATTATGATATACCGCATTCAGGCTATATATCGGAACATGAAGGTTATCTTATGT
TGCAACAAACGACACATTTTGGCAGCTTTGACCGCGCTGGCGCTCTGTTGGGCGGTTGGCCACCCAAACAGCGCTGCTCTGTCTATTCGAGGCAATTCAGGTATGCAGACCGTATCTGTCTGC
CGGAGTTTACAATTCCTTATGGCGCAACGCGGTACAATGCCGCTCCTGCCGCCAACGATGCGCCGTATGTGCCGCCGTTGCAAACTGCGCCGGTTTATTCGCCCTCTGCTCTATGTTCCGCCG
TCTGCACCTGCCGTTTGGGTACATATGTTCTCTTACGCCACCGCTGCACATCAACGGCGGCGACGATACATTATGTGCGGTGGCGACACGGGTGACAACATTTCCAACACGCTACCATATCT
CTCAAGACGATTTCCGTGCGTGAACGGCAATGACCGCAATACGTTGACATCTGGTCAGATTGTTAAAGTCAAAACCGGCAGGATATGCCGCCACCGAAACCGCAGCCGTAGAAAGCAGGCG
CGCCGTACCGCGCTGCCGGCGCAAAACCCCTGTGAACCCCGCCGCCAACCCGCCCTTACGTCCGCCGCCGCAACCTGCCGCCGCCGTGCGGAAAAATAAGCGGTTCCCGCCCCCGCCCGCC
CCGCAATCTCTGCCGCTTCGCTTCCGGCAGCGGTTGGCTGGCGGCATTGTTTGGCAGGCTCCGACCGGTAAAGTGCGGTTAGCGGTTGCGGATTTCCGCGCGCGCAACAGGGGTGTCGATATTG
CCGGCAATGCCCGCAACACCGCTTTTGGCGCGGCTGACGGCAAGTGCGTTATGCGCGCTCAGGTTTGAAGGGATACGGAACCTTGGTCATCATCCAGCACAAATTCCTCTTCTGACCGC
GTACGGGCACAAACAAAATGCTGGTCGGCGAAGGTCAGCAGGTCAAAACGGCGGTGAGCAGGTTGCTTTGATGGGTAATACCGATGCTTCAGAAACGAGCTTCATTTCCAGGTGCGTCAA
AACGGCAACACCGGTTAAACCCGAACGCTATATCGCGCTTC

SEQ ID 6138

SEQ ID 6138
LAYGLTVFQIPSGFALEKNAHFYYDIPHSGYISEHEGYLMKQKTTLLAACTAVAALLGGCATQQPAPVIAGNSQMGTVSSAPVYNYPGATPYNAAPAAANDAPVYPVQTAAPVYSPPAYVPP
SAPAVSGTYVPSYAPVDINAHTHTIVRGDTVYNI SKRYHISQDDFRANWGHTDNTLSIGQIVKVKPAGYAAPKTAAVESRPAPVAAAQTPVKPAAQPPVQSAQPAPAAEAENKAVPAPAPA
PQSPAASPSGSTRSGVGIWQRPQTQGVKVVADFGGNGKGVDIAGNAGQPVLAADGKVVYAGSGLRGYGNLWIIQHNSSFLTAYGHNQKLLVGEQQVVRGQQVALMGNTDASRTQLHFVVRQ
NGKPVNPNNSYIAF

SEQ ID 6139

SEQ ID 61398

GTGTTTCCACAGTATCAACCGTGGCGCAAAATATGGGCGACGATACGCTTTATTTCGGGGACGGTTGCGCGCGCGACCGAAGCCTATCTGATGGGTATGCCTGCTGTGGCGGTTTTCCTTTAAAG
ATGCTTCCGGACGCTATTGGGCAACCCGAGAAAAGGCACCTGCGGACATTGTTGGGCGCATTTTTTAAAAAACCGCCGCTCGCGCGCCCGCTGTGGGAAGTGTCAACATCCCTCGTGTGCGCAAC
GGAAGATGTTCAGGGGAATCAAGATTACCCGTTTGGGCGAGCGGCATCATGAGCAGAACATCGTCCGCTCCCGCAATCCGCGCGGGCAACAGATTTATTGGATAGGGCCGGTTCGGCGAAGTT
TCCGATCCGGGAAGAGGGGACGGATTTTGGTGAATCGCGCGCAGGTTTATTACCGTAACCGCCCTGCAGAAATCGATTGACCGCCTATCCGGACATGGCGGAGACGGCGGCGGTTTGTGCATA
CGGAC

SEQ ID 6140

VFSGINRGANMGDDTLYSGTVAAATEAYLNGMPAVAFSLNDASGRYWATAEKALWTLAHFFKKPPSPAPVLNVNIVPAVAPEDVRGIKTRLGRRHHEQNIVPSRNPGRGEQIYWIGFVGEV
SDREEGTFDGEAGGAGFITVPLQIDLTPYDPAETAAPWHTD

SEQ ID 6141

SEQ ID 6141
ATGAACGCTTTTGATTCCCAACGACGACGGCTATCTGCGAGAAGGCATTGCCATTCTGCGCGGGTTGCGTCGGAATTTGCCAATGTCAGGGTGGTGCGCGCCGAGCCGGGAACAGGAGCGG
GGTCAGCAATTCGN

SEQ ID 6142

MNVLI SNDDGYLAEGIA ILARVA SEFANVRVVAPEPGTGAGSAIR

SEQ ID 6143

SEQ ID 6143

TTGCAATTCTTCATATAATCAGCCGGCAACGGTATGGAAATCGGTATCTCTCTCTGCTGCGCGAGGTTGAGTTGGGATGCCAGCTCCACATATTCCAACGGCCCTCCACCGTTCAGGCTT
TCATTCGGGATTTCTCTGAACGGCGGGTTCTCTCTCGCGCTCGAATTTCTCGGGGAATCGCCTCGCATGGCTTTCCAACAGGCTTTTCATCTGTACCATACCCAACACCGCGCCGAACCTGT
CCACCACCAAGCGTAAATCCGCGCTGCTTTGGCGGAAGAGTTCGAGCGCGCCCAAGGCGGTCTGTCCGTGGGACAGGAGCGGCTGGCGCATGCGCTCTGAATGTGCAGAACCCGCTGT
TTTCAGCAGTGTGGGACAGCAGTCTTTTGTGTGATGTAGCCCAACGGTTCGTCCACGCGCGCTTTCCGACAACGAGCAGGCGGCTGTAAAGCGCTGTTTTCGAGTTGGGCATCTGTCT
TOGCGGCTTTGGGAAATGTCACGCGTTCGATGTTCGCGCGGTGGAATCATACCCCCATAATCGGCGGTTTCGCAAGCGTCACAGCGTTCGCGATCATCGGATTTTTCGTTATCTTCAAAAT
GCGCGTCATCCAGGATTTCGCGCCCGCATCAGCAAGCAGCTTTTCGCGTATGCCCATCATACCCAAAACGTTTTCGCGGTGCGCTTGCGCCACGAGCTGCCGATGTAGTCTGTTTTCG
GCTGTTTCGCTTGCAGAAATCTGGTTAAACAGTTCGAT

SEQ ID 6144

SEQ ID 6144
IQFFHNQPGNGMEIGIFILLRQVELGCGQLHIFQRAFHRQAFIGILNNGGFFFALEFFGELACDGFQOVFHRHHTQHRAELVHQSVIRAALAEKEFERAQQGSRVAGQDERLAQCLRLNVETAC
PQQLGQOVFPVDVAQRVHARLSDNQEAARVRVLQLGLLFFAALGNVPQFDVAAWNRRHPHNRAFGKRQHAAYHRFPVFPKMRVINGHFAARISKHAPAYAHFTQNVFGGALAPRAADVVFPA
AVAILRNLVKQVD

SEQ ID 6145

SEQ ID 6145

TTCTGGTTTGAACCTT GAGGAACACGAAAATCATGGATTTCAGTTGGTTGGCAGAACCGCATCTCGGATAGTGTTT GCCACGCTTTTGGTGTGGAAGTCGTTATGGGGATAGACAACCTTG
TCTTTTGGGGGATTTTGGCAAAACAGGTCACGCCCGCAGCGCGCAGCGCGCAGGATTACCGGGCTGGGGCTGGCAGTCGTATCCGATCATATGCTGCTTTTATGCGCATATCTG
CAGCTTGACCGAACCGCTGTTCCAAATCGCGCGCTCGCCGTTTCCGGCAGGACATGATTATGCTCGCGCGCGGTTATTTCTCGCTTAAACAAGGCATACCGAATCGACGAAAGGCTC
GAAGGGCATACCGGTTTGGCGTTGCCGACGACAAAATAACGCGCGT TTTGGGGCGTGTTCGGCGAAATCTGATATCGATGATGACGCGCTGTTTTCATCATGTCGTCATCATCCGCG
CATCGTCATGTCGTCGCGGATGCGCGCGCGGTCGTGTCGCAATGGCTGTCATGATTTCGCCAGCAAACTCTTGACCGAATTTGTGGACAGGCATCCACCGTCGTGATGCT

CTGCCCTGGTGTTTTGTGTGATGATCGGTTTCAGCGTGTATGCGGAAGCCTTCCATTTCACATTCCCAAAGGCTACCTCTACGCCGCCATCGGGCTTCGATTTTAATCGAACTGTTTAAC
CAGATTTCCGAACGCAACAGCGCGAAAAAGCACTACATCGGCAGCTCGTGGCGCAAGCGCACCGCGGAAAAACGTTTGGGTATGATGGGCATACGCGAAGCGTGCTTGTCTGATGCGGGCG
GCGAATCCGTGTGATGACGCGCATTTTGAAGAAAAAGAAAAATCGATGATACGCAGCGTGTCTGACGCTTGGCGAAGCOCGCCGTTATGGGGGTGATGATTCACGCGCGCGCATCGAAGCGCT
GGACATTTCCCAAAGCCGCGGAAGAACAGTATGCCCACTGCAAAAACAGCGCTTACAGCGCGCTGCTCGTTGTGCGAAGAGCGGGCGTGGACGAACCGTGGGGCTACATCAACAAAAAGAC
CTGCTGTCCCAACTGCTGGAAACAGGCGGCTTCGACATTCAGACGGCATTGCGCCAGCGCTCGTCTGCCCGACGGCACGACCGCTTGGGCGCGCTCGAACTCTTCCGCCAAAGCAGCG
CGGATTACGCTTTGGTGGTGGACGAGTTCGGCGCGGTGTGGGTATGTGTGACGATGAAGAAGCTGTGTGAAGCACTCGCAGGCGAGTTCGCCGAAGAATTCAGCGCGGAAGAAGAACCGCG
CGTTCAGGAGGAATCCCGATGAAGAAGCCTGACGCTGGAAGCGCGTTGGAATATGTGGAGCTGGCATCCCACTCAAACCTGCCGACGAGGAGGAAGATACCGATTTCCATACCGTTGCCCGG
CTGATTATGGAAGAAATTCGAACCATCCCGGATGTCGGCGGATTTTCGCGGATTTTCACGGCTGGCGGTTTGAAGTGTGCGAAAAAGAAAGGCGAGCGCATCGAGCGGGTCAAAATCACCAAAAT
TGCCCCAAGAA

SEQ ID 6146

LRJLNRANTKIMDFSWLAEPHTWIGPATLLLEVVJGIIDNLVFWVAILANKVQPARDRARITGLGLAVVIRIIMLAFMAHITITIEPLFQIIGGLAVSKDHIMLAGGIFLYKATTELHERI
BENHRPAVADQKQHAFPGWQVAILLIDAVFSDSVITAVAMVDHIVVAMGAVVAVAMVIMSASKLITFVDRHPTVHMLCLGFLIMIGFSLIARAFPHIPKGYLYAAIGPSILIELFW
QISQRNSRKNDYIGISSWRKRTARNVLGMMGIESVLADAGESVDDAHFEENEKSMIRSVLTLAERPIMGVMI PRDIERLDISQSRBQYALQNTFYSRLLVVGKAGVDEPIGYINKKD
LSQLETLGGLDITQALRQPLVLDPGTALIGALELFRQSSADVALVDEFGAVLGMVTKMDLLEALAGEPFEEREREPEPAVQENPDESLTFVEGALYVELASQNLPPQOEDTDPHTVAG
LIMEELQTIPTDVGDFADFGWRPFEVEKEGORIERVKTIKLPZE

SEQ ID 6147

TTGAAACGTCFAATTAAAAATAAAGAATCAGGGTTAGCGTGAATTATAAGGAATGCTGTAGTATTTTTCTGATTTTCAGAATGGAAACGGTATAAAAATCCGGTTAGGAAAGACAAAGCAG
CTGAATTGTATTTATTTGAATTTATCTTTATCAAGAGAACTTTTTTCATGTTGTTTCTATATTTGAGATCGTTTTAAGAAACAAAATTGATATTTGCTTTCCGGCAGGAGTTTAAAGACAGAA
CCGGTTATATGATAGCATACAAACCAAGGAATCCTGCATGAAATATCAAGTTGCTTTTTAAGAAATGGTACGAAAGAAATCTGCCGAATTAATCAAGGTTGCAFTATCTAAAATACAA
AATAATAGCGGAGGAAAGTTTGACCAACAACCAATTGGTTGCAGGACTAGGATTCGGTTTTTGGCGGTATCTGTTTTGCGGGAGGGAAAGATGCTCAATTTGATGCTGCAGGAAAGTATTGA
TGAAAGTTTTTCCAAAAAGCCCAATCTACACCAAGTGTCGCAATATAACCAAAAATGGATTTTTTCGAGAAGCTTTCCAATATTAACAAATTTCCGTAATCGTTTGGCACAATCAGAACCGGAT
TGTGTTTATGTTTAAAGGTGCAATAAAGATACCCGGCTAGCTAGAAATATTCACCAATCTATTTTGAATGCTTAAATACATGGATGAGATACCTGCTTCAGTATTTAGCCATTTTACG
CATCAAGTGATTTGCGGCTGCGGATGAAATGCACAACTG

SEQ ID 6148

LKRQFKNKESRVSVNYKECCSIFSDFRMERYKNAYRKDKAAELLYLNLNLSRELPHVVSIFETVLNKLIDCFRQEFKDRNRLYDSIQPTNPALKYQGCFLNGTKESAELIKVALSKIQ
NMSGGKFDHNQVLWAGLGFGFWRYLFAGGKDAQFDAAGKVLMKVFPKPKSTPSVQYNQKWIFRELSNINFRNRLAHHEPICFSFGAIKDTGYARNIHQSIFELLNMDVDVPASVFSHFS
DOVIAVCDREIDL

SEQ ID 6149

TTGCGT T TCCACACT TTCTGT GACAATA TACGGAGG AGGATT TCCATGA AAAACAAA AACGTCA AAGCAAG CAAGCAAG CAAAGCAAG CAAGCAAG CAAGCAAG CAAGCAAG CAAGCAAG CAA
GCAAGCA AGCAAG CAAGCAAG CAAAA

SEQ ID 6150

LRFPHPFDKYTEEDSMKTKTVKQASKQASKQASKQASKQASKQASKQAK

SEQ ID 6151

TTGAACAATTTCAAAATAAGCCCATGCGTTCGGAACATCTTTCAGAGGGCATGGGTTTTGGCAATTGCCCGATAAGCTGTATAACTGTTTAAATTATTTCGACCGAAGGTACACGCACA
TGAAGAAGCCCCGAGCAGAGCAGTAAGCCCGCCCGCGTTTTTTGTGCGTACTGTCTGTTCAGGCAGCT

SEQ ID 6152

LKHFKISPCRFNILSDGMAFCHCPDKLLNCLNYFDRRYTHMKDPEQSSKPARRFLCVLSVQAA.

SEQ ID 6153

ATGATGGAAGAAACGAAAAACATTCCCGAGATGGCGTTTGGCTTGAAAGTGC GGCGCTGGCACCTCTTAATCAGCCTATTGGTGTG CAGGGCTGGCGGCTTGC TGGTTTTTAAGGTTTGGT
ATCCTTATCCTTATGCGGAGCTGACGGGCGGTCTGTCGCTTATCAGCTGGTGGTGGCGGTGCAATATCGTATGCGGCGCGCTGCTGACTTTAATTTTGGCAAGCCGGAAGAAAAAGACAAA
GGCACGCATGGTTCGATTTTCCATGGTTCGCAATCATCCAGCTGGCGGCTTGGCGGTACGGTTTGCACAGCGTTTCGCTGGCGCGTCCCGTGGTGAAGCGCTTTGAACAGGACCGCATGACC
ATTGTTACGGCGGCGGAAGTCGTGGTCGAAGATTGCAAAAAGCCCCGGAAGGGCTGCAAGGCTGTGTCGTGGTTTGGCGCATTCGCGCGCATTCGCAATTGAAAGAACTTGAGGATGCGGATGAGA
AGAAACAAGACGCTGGATTTTGTCCCTGAAAGGATTCAGCGCGAGTATGCGCTCCGACCGGTGGCTGCCGTATTCCGCAAGGAAGCAGAAAAATCCGCAACATCTGAAACCGCTGAAAGT
CTGGCGGATGCGAGAAAAACGAGGCTGCGCAATCTCTGAAGCGAGCGTCTCCGCAAGGGGAGGAGCTGTATTACCTGCCGTTTACAGCAGCAGCAGAAAGAGTGGATAGTCATT
ACCGATAAAGAGGAGGAGGAGGAGGCTTACGCGCCGATGAGACGGCTTCATCATCCCT

SEQ ID 6154

MHENGKTFPRWRFALKSAGWHLLISLVLVAGLAALLVFKVWYPYPYABLTGGLSLYQLVVAIVDVGPLLTLILASPKKTKARMVDFSMVGIIQLAALAYGLHSVSLARPVVEAFEQDRFT
 IVTAAEVVVEDLHKAPEGLQSLSWFGIRRIALKEPEDADEKNKTLIDLSLKGIEPSMRPDRMLPYSUKPAEKIRKHLKPLKVLADARKTTVADILKQAGLAEGEELYVLPFTSSRQKENVIV
 TDKGNTKGYAPIDGFIIP

SEQ ID 6155

ATGCCGTCCTGAATGGCAGGGTTTCAGACGGGTGTCGCATTTTAAGCAGTCTCTATCTGTTGTACAATGCGCCCTGTTTTTACGGTTATTTT

SEQ ID 6156

MPSEHOGFRRCRILSSLYLLYNAPCFYGYF

SEQ ID 6157

TTGAAAGCGGGTTATCCCGTATACCGGAGGACACGAAATGAACGAATATTCCCAATTAATCAAGCATCCCGATATTTCCCTTTCCCGCGATTTCAGAGCGCATCGGGTCGGCAATCCGGCGA
CGGGCGAAATTTTGGCGTATGTCGCGAACACCGGTTTCGGAACAGCTGAAAAACCTGATTTCAAAGGCGCGCGCAGCGCAAAAATATTATGGCGCGCGAAACCCGCTTTGGAACGCGCGCACAT
ATFTGCTGGCTTGGTATTTTATTAGTTAAAGAAAACAAAGGAAGCATGGCGCGCTCTATGACGATGGGACGAGGCAAAATCGATTCTGACCGAGGCGCGCGGCGAAATCGATTCTCGGCTTCTGTT
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CGGCATTAATACGGGCTTAATCAGTAATGAAGCGGCAACGGTTTCGGCGGGGTGAACACGCAAGCGGTTTGGGACGTGAAGGCAGCAAAATACGGTTCGCGAAGTAATCTAGAATTGAAATATTG
TGCAATGATCGCGGG

SEQ ID 6158

LKAVIPYTGHEMNEYSQILKHPDISLSPISDGIWGNPATGEILAYVRNTGSDKLKNIQAAAAQKLNAAKTALERADILMRWYFLVKENKEALRLMTMEQKSLTEARGEIDYAAAF
VRWFABERRIDGDLTVSVKASQKLVVLKQPVGVTAATTPWNPFSAMILARKAAPALAVGCAMIVKPSLTPLSAYALAVLAYEAGVPQDLLEPVVSGRASEISHEFATNPTRKLSFTGSTE
VGAKIFAGSAADIKKLSLELGGNAPFIVDDADLDRAVEGALASKFRNSGQTCVCTNRVYVQSGIYDVFCRLSEKAAALKLGDGLDEGVNQGFLIEEKAVEKVEQHIADALSKGAVCLTG
GKRSLAGSTFFPEPVLVSGVTAQMAVARESTFGPLCFVPRFETAEVIRAAANFTEYGLAAYLFTSDTARQWRVGEVLEYGWVGINTGLISNEAAPFGVKRSGLREGSKYGADEYLEKLYL
CIDAG

SEQ ID 6159

TTGCTTCTATATATGTATACCTATCAAGGGCTGCATTACTTTCTTTCTAAAGATTACTATCGCATAAAAGTATTTTCTTAAACGACAGGGATGCCCGCTGCCATATTCAAACACC
GCCCGGATGTTCGGCTGCCGATCGGATGCTTCAGACGGCATCGGAAGGTTTGCAGTTTGGGAATATGAAGATGATAATGTCCGCGAGATTGACGGCATT

SEQ ID 6160

LLIYCTLSKGCITFLSKDYIRIKSIFLKRQGCARALFKHRPDVALPDRMLQTASEGFVLEEDNVREIDGI

SEQ ID 6161

TTGTACGAAAGTGTGGGAAACGCAAGATTTTAAACGATGGCGGGATGTGCAAAATCTGCCGACCGGGCGGGATGCCGTAAGGTTTTCGCGGCAAGATATGGGGTGGTCCGGG
GGATTTCCGTTAAATACGCTTCTTTTATTTTTCGACCATATGCGGCTGAOCCACATCAAACTCTCCGCTTCAATCTTTTACCGACCGGACACGATTATGTTCCGGGGCAGC
TTGTCCGGTTATCGGGCGCAACGGCTGCGCAAGTCGAATGTGAT

SEQ ID 6162

LSGKCGKRRDFNTDRDVQNPAPGRDAVRFCRQDMGCGGISVKIRFFFIIPSDHYAPDPHQTLRLQIFRPHDSCSGAACRGYRAERLRQVECD

SEQ ID 6163

TTGGCGCTGCGCTGGTTCGCGCGGTTTTCGCGCTGCGGATTATTTTCGTTCTGCTTCGGGTTATCTCTGCGGACGCGCTCAATGCCAATCT

SEQ ID 6164

LAVGWRFRFSGVADYFSFRSGFISAAAQQL

SEQ ID 6165

ATGTTTCAAGTTTGGGTTTAAACGGCAATAGACCACTATATCCCCCATATCTCGCCATTGGATACCGACAATGAACTTTAGGCACGAGGCTCTTCAAGCGTTGGCAACAGCAGGACTT
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TAAAAACATGATGAGCGGGGATATTTGGCTGCACAACGGCTGCCGAAATCAGCCGAGCGCCATGTCAAGCCGGAAGCGTGGGATGCCATTGATGCAGAGATGTAAATTTTATCATTT
GATAACAGCCCTGAAGAAATCGGAGCAGGTTTAAAGTTGCGATTGAGCCGCTGCCGACAGGATAAAACCGAAGCAACGAAATAATCCGCCAGCGCCGAAACCGCGGAAACAGCGCG
ACGGCCAAACAAACCGGCATAAAACCGCGCGAAATCCGAGCGCGGTTCAACAGGCTGCCCGGTTTAAACGGCGCGGAGGAAATTCGACCGAATTCGCGTAGGCATCGGTAA
AGCGGAAAGGCTTCGCCGCTTTCTGTGCTCACTCGGTTCCGTTTCCGAACAAACCGGTTTCGGCGGATATAGCGTTTCGCCGATGCGGCAACGTTCGGAAGAGGAGGACGCGACGCTGCC
GTCCAGCCCAACCGGATTTTTCGCCCGCTCCAAATTCGGGACGCGCACAGACAAACCGTTCTCGCA

SEQ ID 6166

MFRFGVNGRNPPIPHILPLDNETLGTTLVQALANSRTFYDSSDQDFDTEKFRQRYEDWVANLCNMLGYKTRRALFKNNMSGDIWLHNGCLKISPSRHKVPEANDAIDADDVLSL
DNSPEETGAGLKLALSRCDKPRTKRKILRHARKPEPADGQNKTKIKRPNKPDGSGNRLPRLTGAAGSFDRILAVGIGKAEGFAFLVPLGVSVEQTVFGGIAFAGCGNVGREDGTPA
VQPRDFAAVQIADAHQTVLA

SEQ ID 6167

ATGCCGCTGTCTCAAAACCAAGCGGCGGACGATTTTCGAGCGTTTTCATCGAGAACGGTTTGTCTGTGCGCGCTCCGCAATTTGGACGCGGCAAAATCGGTTTCGCGCTGGACGCGCA
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CGATGCTTACGCGCAATTCGCTGCAAACTTCTGCCGCGCGCT

SEQ ID 6168

MPPVQWQAGPDDFRAFSCENGLSVZVRNLDGGLALRLDGRRAVLSSDVAASGERYTAHGLFNGTWHQKGGEAFFGFTDAYGNSVETSCRAR

SEQ ID 6169

TTGAACAGCGGCATATACCGCGCTCCGCCCATCATACGCTTCGGCACGGCACAGGCCCAAGACAAAACCGATACGCTCAGCGCGAAAACCTGATATTCATAAAAGCTCCCCAA
TAAAAAGAAATATGTTTCAACACACAGGACGACAT

SEQ ID 6170

LNRRHIPASAAIIRFRHGTGRQRQNRVQGRKPDHKSPIKRYVSTHRTTH

SEQ ID 6171

TTGATTTATCGTGTTCCTTTTCGGTTGAACCTCAGCCCTTTGGGCGGTAAATCAGACTTTATTTGGGAGGGGCGCAACCCCTTCGAATCAGGACGCGACATAGGGCGGTCTT

SEQ ID 6172

LIYRVSFVPEQPFQAVKSDFIWEGRNPPRIHTAHLVL

SEQ ID 6173

GTGACGGAATGTACGCGCACAAACGTTAAACGCCGANTAGGATTTTAAACGAAATAGCACACTGATATCGGTTTACTTGGAAATTTGAAAAATTTACATTCCTCCGGGCGGGCAGGC
AGGTTTCAGACGGCATCTGTCAGGCAAAAGCGGTGTTCGAAGACGGGTAAAGAAGGGCGCGCAATCCGGAATTAT

SEQ ID 6174

VDECTRTNVKRPNRILTIQISTLI SVPTWNLKFTFLRAGQVQTASSGKRRCKTKGEGARNPDY

SEQ ID 6175

ATGAAATCACTCAAAACCTTCTCATTTGGGGCATAGTGGTACTGGTTCGGCTTAGCATCTTTACCACTCTGGCCCTCAGCGAGGCGAACAGGTCAGCGCGGTATGGATGTTTACCGCG
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TGCCTGTTTATGGGATTTTACAGCGCCATATCGGTCGCGCAAAATCGGCGAGATTTCCATCGTCCGCTTATTTTGTCTGATGTTGGCGGTAATTTACGCGCGAAGATGTTGGCGAAAGC
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ACACCGCGCGCAAGTAATTAACCAAGCTGAACCTTCCCTGTCGATGCGCAACCCCTGTTGCACACCGCTAAGGAAGTGGGCGAAACACCTCTTGTCCCGCACAGGCGGTTCGCGCTAC
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GATTAGATGAACCGGACCGTTATGTCGGGTGGCACTCGTTCCTGCCGTGGCGTACTGCTTGAACCTGCTACGCCGCTGCAAAAACCTGTTCCACAACGACCCGCGCGCAGCTTC
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ACCGGAGGAACAAAGTGAAGCA

SEQ ID 6176

MKSLKTLFWIVLVGLASPTTLALSRLGQVSAVMVTAASVYCIAYFYSLYIANRVMRLDPNRLTPAERHNDGLDYVPTHKGVLPFGHFAAAGAGPLVGPVLAAGNYLPGTLMII
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SIHWFDLGILQITWAIMYGPVAVLPVWLLTPROYLSFLKIGTIAALALGIVINPALQMPAVTHFDGSGPVFSGTLFPFLFTIACGAVSGFHALISSGTPPKLENETHVRHIG
YGMLESFVAHALAAAASLDPGVYFAMNSPAALIGTDANTAAEVITTKLNFVDAATLLHTAKEVGENTILSRGTGAPTLAVGMHIMSRILPEAMMAFWYHFAALLFEALFILTAVIDA
GTRVARFMIQDLGSIFYPFGNFDISIPANLIATFFAVALNGYFLYTGVTDPLOGINSINLPLFGIANQLAGVALIMCAVVLIMKRDYVWVALVPAVGVLVTCYAGLQKLFHNDPRASF
LAHAGKYSITLAKNEVLAPAKDIGEMAQIIFNDKINAGLTFLFSVVVTAAYGLRTALKARKVGNPTAKEIPAVYRDGKQPREQSEA

SEQ ID 6177

GTGAAGCATAAGCTCGCGTCTTGGTGGAAAAACATCAAGCTGACGGCAAACTTGTATGCGAGCGTGCOCGATTATGAAAACTACGTTGCACAACAACGTAAACATAATCCCAACGCCCCG
TGATGAACAGCTCAATTTCAGACATATGCGCAACGCCGCTGCGGCGCAAAACGCGGACGCTGCTGT

SEQ ID 6178

VKHLASWMTIKL/PANLMAGVPDYENYVAQQRKHPNAPVMMKLPQDYCRKRCGANGERRC

SEQ ID 6179

ATGACCCCTCATCCACCCGACCGCGCTCATCGACCCCAAAGCCGAACCTGACCTCCGCGCTCAAAGTCGGCGGTACACCGTCAATCGGCCCCAACGTCGAATCGGTGCGAATACAGAAATCG
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GCGGTATTTCAAGACTTCTTCGCAACATCGACCGCGCATCATCGC

SEQ ID 6180

MTLIHPTAVIDPKAELDSGVKVGAYTVIGPNVRIGANTEIGPHAVINGHTTIGENNRIPQFASLGEIPQDKYRDEPKLIIGNGNTIREFTTFLNGTGTGIGETRIDNDWTHAYCHLH
DCVVGNNHTIPANNASLAGHVTVGDYVVLGGYTLVFPQCRIGDYAMTAAAGVHVDVPPFMASGYRAEPAGLNSEGMRNGPTABQISAVKDVYRDLVHRGIPFEAKADILRAETQAL
AVFPQFFAQSTRGIR

SEQ ID 6181

TTGGGGTGTAGGCAAAAGCTCAGGGGTAATACCAAACTTAGCAACCTCAATCGGCACATCTGCCGAAGCAATGCAACCGGGGCGATTGGCTTTAGGGGGAAGTTCTGAAGCATCGAAAA
AATTTAGTATAGCAGAAAGCTATCTGGCATCTAGTGATGGCTATGGTGCAATAGCATTTGTTCTGCCCGCAAGATAAGCAATTTGGAAGGCAATAAATCATATTGTGGGAACGA
TAATAAAGGCTTTATGTCGATGACAGCGCAATGTAAACAGATAACCGTAAGGACTGAGTCGGAAGAAATATTTCTCTAAGATACGCTCAAACTTACGGTGGGTGGCACTAGGGTTT
AGATCTTCTTACATATCTTTTGGCAGTTCATTTGGAGCGTTTCTACAGCCACAGCTATTGAAAGCTTGGCACTGGCAGTCGCGACAGCAGCAATCAACGGGCTACCGCAGTGTACTTTTG
GCACTACAGCAGCGCTTTGGCAGAAAGATTTGGCATTAGGTATGAACTCGGCAATGCTTATGTTCTGTGCTTTAGTGCAGATCTGTGGCGAATGAAGAAATACCGTATC
AGTGAGTTCGATACATTGAAACGAAATCGTTAATGTGCGCGATGGCAGCAAGATTTA

SEQ ID 6182

LGLRQKLRGII PNLSIGTSABANAPGALALGSSSEASKFSLAEGYLASSDGYGAIAIGSAKIKQLEKGTINHIVGNDKGLYVDADGNVITVTRTESEKDIILSRGTGTYGVALGP
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SEQ ID 6183

ATGCGGCTGAAGCCCGTTTCCCGCTCAGACGCCATTTGTACGGATGACCAATATCTCCGTTTTTTTACTTTCAATAATCAGATATGCCCGAACCCGCTCGCAACAGATACCGTA
CCGCATCCGCGCAATGT

SEQ ID 6184

HPSEARFPLQTPFTCDPISSVFLLSIIIRYARTTVRQRYRTASACQ

SEQ ID 6185

ATGAGAAAAAGCCGCTTAAGCCGATATAAACAATAAATCAATGAACTGTTTGTGCGAGCGTAACGCAAGAACAGCAACAGAGCTGACAGCATTTGTTATACGGAATGTTATCGTC
GCTATGATGATTGGATGCGAGCGAATTTAGCCATTTCCGTATCAATCACAGCACATTTTCCGCAAGCAGCAAAACCATATTAATGGAATGGGAATTTTGGAAACGGGCAAAACGCTCA
TTACGCAAGTTTGACGCGATTTCCAAAGAGCATTTTGAGCGTATTAAAGAGGTGCGAACGCGCTTTT

SEQ ID 6186

MKSLRLRYQNKILFVAGVTARTATEPDSIVTDCYRRYDVLDAFESHFRINHSTHFAERQNHINGIGNFWNRKRHLRKFDPKHFEPYLKECERFP

SEQ ID 6187

ATGCGGCGACGGCTGCTGATACCTATTCTTTTTCAGTTTTTATTTTATCCGCTGCGGGACACTGACAGTATTTCCATCGCATGGCGGAGGCAACGCTTCGCGGTGCAACAGAACTTG
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CGTATTCGGAAGCATAGCAACAGAACCGAAATGCCTATACAAATGCCGAACACTGAAAGCCCAACAACTGGAATATTTCGAGTAGACAGAACCAATAAAAAATGCTCATCAAA
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SEQ ID 6188

MRARLLIPLFVPIFSACGTLTGI PSHGGKRFVPEQELVAASARAANKMDLQALHGRKVALYIATMGDQSGSLTGGRYSIDALIRGEYINSPAVRTDYTPRYETTAETTSGLLGL
TTSLSLTINAPALSRTQSDGSGSSSLGLNIGMGDYRNETLATNPEDTAFSLHVLQVTFPLRGIDVVSANADTDVF INIDVFGTIRNRTEHMLYNAETLKAQTKLEYFAVDRTNKLLIK
PKTNAFEAAKYENYAVDGA

SEQ ID 6189

TTGATTACACATGCCATAACCGCTTGTGCGCAAGGAAACAAATGAATTTGCCATTCAAAAATTCATGATGCTGTTTGCAGCGGCAATATCGTTGCTGCAAAATCCCAT

SEQ ID 6190

LHRTAITACCGKQNEFAYSKIHDVCSGNIVAANPH

SEQ ID 6191

ATGGATATGACGGGCTCAAGCGCGGCTTATCCGCCGCCGAGGGGCAAGGATATATACAGCTACCATATCAAGGAACCTCAACCAAAACAAAGA

SEQ ID 6192

MDRTGLKAAVIRPPEGQGIYTATISKELQPKQR

SEQ ID 6193

TTGCTGCAAAATCCCATTTAGTCATGCGAACGGTTTGGATGCCGCTTGGCGGATGATATGCAGGCAAAACACTACGAACCGGGTGGCAAAATACCATCTGTTTGGTAATGCTCGGGCAGTG
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CGCAAGCCCCTTTTTCAGACGCTGGCTAAAGAAAATGCCGGTGGCGCTTCCGGTTTTCTCAGCGTGGGATGAAGCAGGAAATCATATGGGAAAACGACCCCGATAAAATTTGGCG
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SEQ ID 6194

LLQIPISHANGIDARLDDMQAKHYEPGGKYHLFNGARGSVKNRVCVQTFDATAVGPILPITHERTGFEVGIYETHPSGHGHEVHSPFDNHSKSTSDPSGVDGGFTVYQLHRTGSEI
HPEDGYDGPQGGYPPGGARDIYSYHIKGTSTKTKINTVPQAPFSDRLWKENAGASGFLSRADEAGKLIWENDPKNWRANRMDIRGIVQAVNFFLTGFGQLGVGATDSAVSPVY
AAARKTLQGIHNLNLSPQAALAAALQDSAPAVKDSINSARQWADAHNPITATAQALAVTEAATFVWGGKVELNPAKMDWVKNFTGKYPAAHMQTVDDGEMAGGNKPLESKNVTNN
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SEQ ID 6195

ATGGAAATTTTGAATATATCAGAGAAGCAGATGGAATAATCATAGATTATTTGTCCTTAACCAACAACTTCTGAAAAATAGTAGA

SEQ ID 6196

MEILNISEKMEKLIIDYLSLNNFLKNSR

SEQ ID 6197

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CAGTTTTCGCCGAGCGGACCGGGCTTTTCGGCGCGGGGTTTGGGAAATTCGGCGGCAAAACCGCAACCTCGCGTTGCCGCAAAAACCGCGGCATCTTCGAAAGTTTTCGCAATTCGGG
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SEQ ID 6198

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SEQ ID 6199

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SEQ ID 6200

MLTDLEKNAIRDHYQNIKNLPGFRPRASQREMIYAANAFSRTLTREBEGBPBKREGESIAVIEGTPGVGKSLAYLLAGGIMAQTRGKRLIVSSATVALQELVDRDLPLFVEKSGLEIF
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LADISMGGVILPAPENSPYCIDAEHLPLKALSRFAARHSNIAVWLEKLPLQTKIAL/TKAEANLADAAASLLDSLHEWQPHLEEPSLSMGLSENDRTNSEPTWLMEDGKIP
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LQSLGPNLILRQTLGLWLPETTTALKSPFFDEKQGLYIPSTYASPKDPEAHTAAVIEWLPKLI/SPTEAIGTLVLFSSRKQMDVALHLPDYLPLLLVQGLPKAVLLQKHQAIEEG
KASIIIFGLDSFAEGLDLPGTACVQVILAKLPFAMPIDNFIETQNRWIEQRGNPFIETVPEAGIKLQAVGRILIRTEQDYGRTTILNRIKTRQYQQLLAGLPFFKRIG

SEQ ID 6201

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TTATTTATCTCAAAATAAATTAGAGATGATACGTGCTTTTGTTTTGAATTTATC

SEQ ID 6202

MLNKEIFEYSRQGESLIGIGIREALPVPTAIDILNLP/INERILVLGGDIYIKKNYFYQTYDNWYEGSNLFSINKAMHYLSQIKLENAYVSFVLFKI

SEQ ID 6203

ATGCAGACTGTAGATGGGAGATGGCAGGAGAAACAGCCAGTTGTAAATCTATTAGACCACTACGCGAGATGAATACGTCAGGATTCGCAAGAACAGGTTTACAGCTACTGGTT
CAGATGCGGCTCAATATGAACATGGAAAGTCTGATGCGGTGAAAAATAGATATTCGTCCAAATGGAGAGGTTATAAGAACCCAAAGAGTCCCGCAACCGATGGTGACAGGAAAAA
TCCGCAACGACAAGATTATGAAGGCAATCCATTGCCAAATAATCATCATCTTCGGATTTTGTCAAA

SEQ ID 6204

MQTVVDEMGAGNKFVVKSIPTTRDELQALQEQGFRRTGSDAAQYETWKGPDGVKIDIRPNGEVIRTPRVPRFDGVQGYKYPQDYEGNPLPNNHHSYFVK

SEQ ID 6205

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SEQ ID 6206

MVYRENIRNDKIMKAIHQIIILIDILSNEKKYFSQCKPL

SEQ ID 6207

TTGAATTTTAAATAGATACAAATAATTTCTGTAGATTATGAGGATAAGGAAGATAGCTTGTTTCCCTTGTTTATACCCGAAATAGAGCTATATAAATACCAATTTTATAGTGAAATATTTA
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SEQ ID 6208

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SEQ ID 6209

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SEQ ID 6210

VSLIQDSAPAVKDGINSARQWADARPHITATAQTALAVAEAGTVHGGKVELNPTKND

SEQ ID 6211

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TGAGATACATTACATTGAAAAATACAGAACCAGGTGAGAAAAAGAGATTCAAGTTAAAGGAT

SEQ ID 6212

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SEQ ID 6213

ATGTTTTAGATGATGTAATGTTTTTATAGATGATTTAAATACCAATCCAATCACTGACGAATGGTATATGTCCAATTTTGGCGATAAACAATTTAAATTTTGGAAAGTTACGAAGCCT
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TACAAATACACAGAAACAGAAAAATTTGATAATTTATATAAACAAGAAATTTAGTCAGGATATTTTAAATGAAATCTTTAGA

SEQ ID 6214

MFLDDVNVFLDULWNPITDEWMSNFADKHILKILESYEAFDILKQFVDMIESEHDEKSEYELMELRLQKYQADTNEKFTYNTQKQKIVELYKQELSDILNELFR

SEQ ID 6215

ATGAGAAAAAGCGCTCTAAGCCGGTATAAACAATAAATCAATGAACTGTTTTCGCGAGCGTAACGCAAGAACAGCAACAGAGCCTGACAGCATTGTTTATACCGATTGTTATCGTC
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TTTACGCAAGTTTGACGGCATTTCCAAAGAGCATTTTGAAGCGGATTTTAAAGAGTGCGAACGGCGTTTAAACAACAGTGAGATAAAGTTCTTGTTCACATT

SEQ ID 6216

MRKSLRYKQKLIELFVAGVTARTATEPDSIVTTCYRRYDVLDAGEFSHFRINHSTHFAERQNHINGIGNFWNRAKRLHFKPDGIPKEHFEPYLKBCERRFPNNSIKVLVPF

SEQ ID 6217

ATGGCGTTAGCTGTGCAACAACACTTTCTGCTGCTTAGCGCGGCGGAGGCGGCACTTCTGCTCCGACTTTAATGACAGCGGCGACCGGTATCGGCAGCAACAGCAGGCAACGATAG
CGGAATCAGCAGCAGTATCTTACGCCGGTATAAACAAGCAATGTGCAAGAAGCAGAGCATGCTCTGTGCGCGGTGCGGATGACGTTCGCGGTACAGCAGGAGTCCCAAAATCAAGGCC
CCGAATCTGCATACCGGAGACTTTTCAAACCCAAATGACCAATATTAAAGATATGATCAACCTCAAACCTGCAATTTGAAGCAGGCTATACAGGACCGGGGTAGAGGTAGGTATCGTCAT
ACAGCGGAATCCGTGCGCAGCATATCTTTCCGGAAGTATGCGAGAAAGAACCGGCTATAACGAAAAATTACAAAAACAATTTACAAAACTATACCGCGTATATGCGGAAGGAAGCG
CC

SEQ ID 6218

MALAVATTLASACLGCGGGTSAPDFNAGGTGIGSNSRATLAESAASVYAGIKNEMCKDRSMLCAGRDDVAVTDRDAKIKAPRICIPEFTQTQMTNINIKMINLPAIEAGTYGRGVEVIVD
TGESVGSISFPPELYGRKEHYNNYKMKLQKLYGVYAEBSA

SEQ ID 6219

ATGCGGAAGGAAGCGCCTGAAGACAGAGGCGTAAGACATTGAAGCTTCTTTTGACAATGAGGCCCTTATAGAGACTGAAGCAAAAGCCGACGATATCCGCATGTAAAGAAATCGGAC
ACATCGATGTGCTCTCCATATTATTTGGCGGGCGTTCGTTGAGCGGCAGACCTGCGAGCGGTATTGCGCCGATGCGAGCTACACATAATGAATACGATGATGGAACCAAGAACGAGAA
A

SEQ ID 6220

MRKEAPEDRGGKIDIASLDNEALISTEAKPTDIRHVKEIGHIDVSHIIGGRSVDGRPAGGIAPDATLHIMNTHDGTKNEK

SEQ ID 6221

ATGAACCTTCAACCGGTGTCTCAACCAAGTCTTAAGCAGCGTTCAAAAAAAGGCAACACATTTCTCCGCGAGCCCGCTCAATTCATTGCGCGGAGGCGCGCTGGTTGCCGTGTGCCCTCCA
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ACAAAGCGATTTCACCTCGCCGGAAGAACTGAAGAAACATACAGCCGACCGTATTGCTGATCATGATAGCCCGCGCGCTTCAGACGGCATGATAGCAAGCCGAACCGCGGACTATC
GAACAGGAAAGCGGCACAGACCCCGAACTGCGCGATGGCTGCGCCGCAATACCGCTGCGCCGAAGCATCGGGGACATCGCCCGCGCTCGGCAACGATGAGGCGCTTGGCGCGGAGAG
CCTATCTGGCGCAAGGTTGGTCTGTGCCGATTGTTGCGCGGAAGAAACCGTCTTCTCGCCCGCTGTGCGAGGCTTTGAAACTGGATGACAATCTGGTGGAGAGTTTGGAAAGGCAACT
AGGGATT

SEQ ID 6222

MNFRLLNQVLSIVQKGNFTSGSPLNSFGGALVAGVASHLLNGKNRKTITKIGSTAAALGLYLAIRGYQMWNQNKGRATVTQSDQFPAGKTEETYSTFVLRTHIAAASDGHIDEAERTTI
EQESGTDFTFAWLAAYEYRLPASIGDIAAVGNDEALAAATYLAARLVCAADLSRKEVFLARLSQALKLDDNLVESLERQLGI

SEQ ID 6223

ATGTCGACGCAATCCGCAATGCAATGGGTCAAGCTGGGCGAACGTCGGCGTCCGATCGTCAATAACAGTTTGGAAACAACATCGAGGGCGAGGCACTGCCGACCAATTCACAAATAGCCAAAT
CGAGGAGCAGTACCGCAACAGCTTGTCTGACTATTCGCGCGGTGATAAAACAGATGAGGATATCCGCTGATGCAACAGAGCGAT

SEQ ID 6224

MSAAILRNANVKLGRVIRVNNISFGTTSRAGTADHFQIANSEBQYRQTLILDYSGGDKTDEGIRLMQSD

SEQ ID 6225

TTGTGTCTCATTCGCTGTGAAAGATGAAAGAGATGTTTTTATTACGGATGTGTAGGACAGGTTGCCCTAATCGCTCTGTGTCATCAGGCGGATACCCCTCATCTGTTTATCACCGCG
GAATAGTCGAGCAACGTTTGGCGGTACTGCTCTCGAAATGGCTATTGGAATGGTCCGAGTGCCTGCCCTCGATGTTGTTCCAAACTGTTATTGACGATGCGCAGCCACGCTTCG

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ACGGAACGCGCCCGCAATATATGAGGAGACACATCATGTGTCCGATTTCTTTTACATGGCGGATATCCGTCCGCTTTCAGTCTCTATAAGGGCTCATTTGTCCAAGAGCTTCAA
TGTCTTTACCGCTCTGTCTTACGCGCTTCTTCCGCATATACCGCTA

SEQ ID 6226

LCVIAKRDKEIDVITFDVVGVQVALLHQAADTLICFITAGIVEQRLAVLLLRIGLYEMVGSACPRCCSKTVIDDHAHTFAQLDPCIDAGCRHYFSFLVPSVFIIMCSVASGATPPAGLPS
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SEQ ID 6227

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SEQ ID 6228

LSIWQIPTNPAQTKPYTSKGLQLGDKGTLYTRLGKLLKVDGTAITDGLIYMSARGKAGYLNSTGRHVPFLSAAKIGQDYFFKNIKTGGLLASLDSVEKTAGSEGDTPSYVRRGNAA
RTASAAAHSAFAGLKHAVEQGGSNLENLMVELDAESSATPBTVEVADRTIMPGRILRRITFTTAAVQHANTADGVRIFNLSLAATVYADSAHAADMQRRLLKAVSDGLDHNGTGLRV
IAQTQDDGGTWEQGGVEGKMRSTQTTIGLAATGENTTAAATLIGRSTWSSENSANAKTDSISLPAIRHVDIGYLLKGLFSYGRYKNSISRSTGADEYAEBSVNGTLMQLGALGVNVP
FAATGDLTVEGGLRDLKQDAPAEKGSALWGSNSLTETGLVGLAGLKLSQLSDKAVLSATAGVERDLNDRUYAVTGGFTGAAAAATGKTGARNMPHTREVAGLVDFEFGNGWGLIARY
SYTGSKQYGNHSGQIGVGYRF

SEQ ID 6229

TTGCGGCTGTTCTTATGAAAGAAACCCCTATTCCAAATGCGCTCTTATTGTTTCAAGACTTCTTCCAAAGATTTCGGCATCAATCAGACGTATACGCGATTAAACAAANTCAGGACAA
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CATATTGTGT

SEQ ID 6230

LRLFLMKRKYNSCLLLLQDFDQRFQINQYISGLTKIRTRRAADGTNGTEPIRPVLGRLEFPFLSRGGATRTGFCSSAILC

SEQ ID 6231

ATGGCGGATGAACAAAAACCGGTACGGGTGCCCCCGCCCGGCTCAAAGGGAACGGTTCCCTAAGACGCCCAAGCACCGGGCGGATCGGTTCCGTACCATTTGTACCGCTCTCGGCGCGCC
GCTTGTCTGATTTTGTGTAATCCGCTATACGT

SEQ ID 6232

MADEQKPVVAPRLKGNLSLRPSTGRIGSVFPVPSAARLVLIFVFNPLIV

SEQ ID 6233

TTGTTATCCGCATATTGTGTGAAACACCGCCCGGAACCGGATATAATCCGCCCTTCAACATCAGTGAATCTTTTTTTTAAACGGT

SEQ ID 6234

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SEQ ID 6235

TTGCTTCACTTGCCTCGCTGCGGAGAGAGAGAGAGGTTTTTTTGGCGGCTGGATTCAATTTTCGGCTCCTTATTCGGTTTAAACCGGTAAAAAAGATTTCCTGATGTTGAAGG
CGGATTATATCGGTTCCGCGCGGTGTTCAACACATATGCGGA

SEQ ID 6236

LPSLAACAAEKRFFAGWIHFRLLIRPNRLKRFSLMLKGLYRVPGVSTQYGG

SEQ ID 6237

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SEQ ID 6238

VQADLAYAERITHDYPEPTGKKDKISTVSDYFRNIRTHSIHPRVSVGYDFGGMRIADYARYRWNNKYSVMVKKVNNKGEKINVTQYLKAENQNGTFHAVSSILGLSAVYDFKLN
KFKPYIGARVAYGHRHSIDSTFKTTEFLTAAGQDGGAPTYYNNGSTQDAHQESDSIRRVGLVIAGVGFDTFNLTLDAGYRYHNNWRLNTRFKTHASLGNRYTF

SEQ ID 6239

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SEQ ID 6240

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SEQ ID 6241

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SEQ ID 6242

MSWRIITRPAAGYKCRKRALAEFGFRVKNV

SEQ ID 6243

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CCACGACAGTTTCGGCGGCCCGAA

SEQ ID 6256

SEQ ID 6256
VRHIASPKPAEABVIRKTAIVFFFLVLSQTCFRYHNTLTQASRLRLKTTTTTVPVPRQDTFNMKQTQISLAATATALFLSACGNGGAPQAOPKGEISENRATAAFKSMMPDFSRLMGVWKGEERYDVE
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SEQ ID 6257

SEQ ID 6257
TTGTATAGTGGTTTAAATTTAAATCAGGACAAGGCGACGAAGCCGCAGACAGTACAAGAAGTACGGCAAGGCGAGGCAACGCTGTACCGGTTTAAATTTAAACCACTA

SEQ ID 6258

LYSGLNINQDKATKPQTVQEVROGEATLYRFFKFKPL

SEQ ID 6259

SEQ ID 6259

TTGATGCAAGCTGTCCGATACAGGCCCTGAAATTGACGGATTGCGGGCCGTGCGCGTGCTATCCGCTATTATTTCACACCTGAATAACCGCTGGCTGCCCGAGGATTCTCTGGGGGTGGACA
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SEQ ID 6260

SEQ ID 6260
LMQAVRYRPEIDGLRAVAVLSVIFPHLNNRWLPGGFLGVDIFFVISGFLITNII LSEIQNGSFSFRDFFYTRRIKRIYAPAFIAAVSLASVIA SQIPLYEDFNQMRKTI ELSTVPLSNITYLGF
RLGYFDLSAENDPVLHIWISLAVEBQQYILLYPLLIFCYKTKSLRLVLRNISII LPLIITASSFLPAGFYTDILNQPNITYLSTLRFPPELLVGSLLAVYGTQNGRRQTENGKRQLLSLILCF
GALLVCLFVIDKHDPFIPGITLILLPCILLTALLIRSMYGYTLPTRI LSASPIFVGKISYSYLXYHWIPIAFAHYITGDKQLGSLPAVSAAVALTAGFSLISYYLITBQPLKRKKMFFPKKAFFC
LYLAPSLMLVGYNLYSRGILKQEHRLPLPQTPVAAENNPETVPLTLGDSHAGHLRGFLDYVGGREGWKAKI LSLDSECLVWVDEKIDENPLCKRYRDEVEKAEAVTADQPYDLRMGGQVPP
RFEAQSLPIPGFKARFRETQVKRIIAVKPVYVFANWTISIRSPLRBEKILKRFALNQYLPRIRAMGDIGKSNQAVFDLVKDI DNPNVHWDAQKYL PNTVTEIHGRYLYGDQDHLTFPGSYNGR
EFHKHERLLKHSRGGLAQ

SEQ ID 6261

SEQ ID 6261
TTGCGCAATATTAAAATCAATTTTACGAAATGTGCGCGCCGCACATCAGGCACAACGCCGCGCGCGCCAAACGCGGAAAGCCATTTCCTCCCGCGCCGCGTTA
TTTCCCTTTCTTTCCCGCGCGCGCTTCAACACGCCAAGATCGAACAAAGCGCGAACAAAGCGCCAAAATATGCCA

SEQ ID 6262

SEQ ID 6262
LPNIKINFTEVVPFHIRHNAADAAAKRGKAI SPFLSRRRVISPFLSRRRVQTRQDRTKREQSRQNP

SEQ ID 6263

SEQ ID 6263

TTGCGCGGGGAATGTGCGCGGCTATTATGGCATATTTTGGCGCGCTTTGTTCGCGCTTTGTTCGATCTTGCCTGTGTTGAACGCGCGCGCGGGGAAAGGAAAGGGGAAATAACGCGCGCGCG
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GTCAATCAAAA

SEQ ID 6264

SEQ ID 6264
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 PKVKRIYTLASLEKVSIAAFLSTYPDAEIKTFDGTNNLIRESSYLGGEFVAVNGAIKRNFAHMGVDSIAKTRNASDEHYTIFGLKNLMDGGKRMFTYLLPLDASGLKAGDEGTGTVRI
 LGSFDKEMKEIKSEAKAKNFNIQYVAHPHQTYGLSGVTALNSPYVIEDYILREIKRNPHTREYIYTFFGAALTMKDFPNVHVYALKPASLPEDYNLKPVYALPQADIPILAFDDKNQSH
 GKSK

SEQ ID 6265

SEQ ID 6285
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SEQ ID 6266

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AVFWLDENRPHDKSLAKVKAYLAELDTNGLYTRVLAPEEBAKPSIGRLKNGEDTISVTGNVRLDYLDLFPILLELGTSAKMLSIVPLMNGGMPFETGAGGSAFKHVQQLFRENHRLNDSL
GEFLALAVSFELAQKTGNAKAQLVADTLDAATREKLINLNDKSPKRGELDNRSHPYITLYWAQELAAQDKDAELKAAFPALAAALTADEAKIVEELSAVQKGAVIDIGGYAANPEKAAQ
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SEQ ID 6267

ATGAAACCTGTTCACCAATCTCTGACCGCATCTCTTTTGGCAACCGCCCTTCCCGCATCGCACACGGTATGCATAAGAGCAAAACCCCTGGCTATGGACGAGCTGCCCGGATTTGCCAAC
AATATTTCAACCGCGCGCAAACTGTTACAAACAAAGCCGGAACAAAGCAGATTTCCGACGCAACAAACAAATTCCTATTCACAGCCCTACCTGCGCGCGATTTGGGACAGCTTAAGCA
AATGTGCCAAATCGCTATGGAATCGTTTGCAGAAAAAACCCGCAATCTGAATTCGGAATAAAGCCGATCAGCAA

SEQ ID 6268

MKTVPFILTGILLATAPASAHGMHKSPLAMDELPPICQYVFKRAFTCYNKAQKADFARNFKFLPQALPAADLQKQKMCQIAMDSPAENFQSELRIKPHQQ

SEQ ID 6269

TTGTTCAGGTTGTGTCAATTAATCTATATAAAATCATCGGTTTACGATGATTTTCCGTAAAGCCCTGCAACAAACCCCAATCGGCAGACGCTTTTATCAATGTTTATGTTATTAATTTAT
ATGTCATTTTGGGATGGGAGCTTGC

SEQ ID 6270

LFRLQLLYKNHRFTMIFRNALQQTAFGRFLSMFYGINLYGHFDGLP

SEQ ID 6271

TTGACACAACCTGAACAAAAAGAACCCCTGAATCAGGGCGGTTTGTCTTTCGGCGGAAACGGCGGGATTCGACTAAATTTTATTTTATGATTTAAATACATTTATTTCTTATAAA
ATTTAATTTTACCAATAAAACAGCCATATACAAATCTTGGAGTAATCTGCAATTAATAGAGGATGCAGGGCTATG

SEQ ID 6272

LTQPEQKRTALNQGPFALRRKRDSTKPYFDLNTFISYKNLIYHNKSHIQKSWSNYCIITLLBGRVM

SEQ ID 6273

TTGTCTTTAAACCAATGGGAAAACTAATTTTATTTGCACCTTATTTGCACCTTTTATATAAATAAATTCAAATATTTATTTATATATTAATTAATAATTTATACATGACCCCTGC
ATCCTTCTAATAGTGAATGCAG

SEQ ID 6274

LFNPLGKTNFICTLFAFPFIMIIQIFNLINLIKYYMTLHPSNSVMQ

SEQ ID 6275

ATGCGACCTCCTTATTCATTTCGACCTGCATTTGAGCGAAAAACACCCCGAAGTACCGAACTGCTGCTGCGTTTTCAGTTCTGCGCGCGCGCGGAGCGCGCGCGGTTTATATTT
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SEQ ID 6276

MRPSYISDLHLSEKHEPTELLRLFLRSAAAGQARAVYILGDLDFWVGDEVELATSVAREIRKLSDKGVAVPVRGNRDLFLIGRDFCRQAGMTLLPDYSVLDLFGSNTLICHGDTLC
TDDKAYLRFRIIVHCRRLQLFLMLPLKWRTRLAALKIRRVSKMEKQVKPADIEDVNAFTARQVRAFNAERLIHGHTHREHHEHNGFTRIIVLGMHNDYASILRVGDGAVFPPEEC

SEQ ID 6277

GGACAAGCGACGAAGCCGACAGTACAAGAAGTACGGCAAGCGAGGCAACGCTGTACCGGTTTAAATTTAAACCACTATAGATTTTCAAGTATGGCAGTGGCAGCATTTGATGATT
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SEQ ID 6278

GQDEADSTRSTARRGNAVPI*ITTTIDFRMAVGSIDDFCRPHPH

SEQ ID 6279

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SEQ ID 6280

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VAVSEFTHFACTSEDIINMLSHALMLQEAETVILPKLAETIGKLTAMADHLAAVPMNSRTHGQPATPTTLGKETANVYRLQRQFKILQAQEFLLKINGAVGNYNHMAAYPDVWETHC
RNPVEISLGLTFNPPYTIQIEPHDYMAEFQTLRSRINTILIDPSRDVWGYISLGYFKQKVAGEVGSSTMPHKVNPIDFENSEGNLGMANAVLGFLEKLPVSRWQRLDSTVLRNMGVGV
GYAVLGFAAHLRGLNKLFPNPAALADLDVTWELLAEPIQTVMRRYGVANPYEKLKDLTRGKGITPEVLKGFISLEIPAEAKAKLLELTPALTVGKAEALAKRI

SEQ ID 6281

TTGATTTTGTGGGGGAATGGTTGACTTTGAACGTGTCCACGTTTATAATTCAATTCATCGCGCATCGGGTCCGATACGGGAAAAGCCCCACCGAAGCGGGGCTGTACAGGGAG

SEQ ID 6282

LILLGEMLTLNVSTFIQIFIGASGADTGKAPPKRGLYRE

SEQ ID 6283

TTGGCGGCTTCTTTATGCCGTCCGAAAGCCCTTCAGACGGCATTTTCTTTGATTTTGTGGGGGAATGGTTGACTTTGAACGTGTCCACGTTTATAATTCAATTCATCGCGCATCGGGT
CCCGATACGGGAAAAGCCCCACCGAAGCGGGGCTGTACAGGGAGTAGGAAA

SEQ ID 6284

LAASLCRPKALQTAFPPDFVGGMVDPFVRVHVNSIHRRIKRYGKSPTEAGLVQGVGK

SEQ ID 6285

ATGAGCTTCATTTTCCTACTCCCTGTCAAGCCCGCTTCGGTGGGGCTTTCCCGTATCGGACCCCGATGCGCGATGAATTGAATATATAACGTGGACACGTTCAAAGTCAACCATTC
CCCAACAAATCAAGAAAAATGCCGTCTGAAGGGCTTTCCGACGGCATAAAGAACGCCCAAGTTTGGCGCTTGGCGCGGTGGGGCTATTTAAGAACTCTTTTCGGATTGTCTCTT

SEQ ID 6286

MSFIFLLPVQAPLRWGSFRIGRCADFLNYKRGHVQSPPFQONQRKMPSEGLSDGKIKPPSLRLGGRAILRLTLFGFVL

SEQ ID 6287

TTGCCATATGGTTAATAAAAACTGGCAGAAAACCGAAAGCGTTACGAGCAAAAACGAGTCATAAAAAGTCTCGTTTAATGCGGAAACAGAAAAAGAGCTTTTGAATATGCCAAAAATC
TCGATTTTCCCAATGGGTAAATCAATCATATAAAGAAAAATCAAAAAG

SEQ ID 6288

LPVWNEKLAENRKRYEQKRVIKKVSFNAETEKELLEYAQNLDPSQWVKSIIKEKIK

SEQ ID 6289

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GATTTTGGGCATATTCAAAAAGCTCTTTTCTGTCTTCGCAATTAACGAGACTTTTAAATGACTCGTTTTCGCTCG

SEQ ID 6290

LVRFSINGCAVVRILNVDPFKVNYFLIFSPMIDLFWKSRFWAYSKSSPSVSNLNTFLMTRPCS

SEQ ID 6291

ATGAATGCTGTCCAAGTTTAAACTTTCAACAAAACCTCCGTCCGTACTGTGCGGATAACAAAAGCGAGTTGTGGTTTGGCAAAACGATGTTGCGAGATTTAGGCTACACCAACCCCTC
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SEQ ID 6292

MNAVQVLNFPQNSVRTVADNKGELWFLANDVCEILGYTNPRRTVDLHCKSRGVTKRYPTTSGEQEMTYINEPNLYRLIISRKPAABAFEEWVMTVLPAIRKTGGCQVGPKTITADRTG
LRQVAVALVGRKIDYSSAYSMIHQRFNVESIEDLPAGKLEPAVAYVHALTLHTGLTGEVLDAPPKAEKPLPIDGNSLADIAAMVYGTWNTIESGKDISAPLKQLGCRQAVTWVWVHETR
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SEQ ID 6293

TTGGAATTCAGCATGAGTGTCTGAAGAGTTTTCAGGAAACAGATCGCCTATTGGCTGAACGAGAGCCGCAAGGCATCAGATAACGCGGATTTGAAGGCTTTGAGTTGCCCGACCGGAAC
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SEQ ID 6294

LDLMSAERPKRQIAYWLNBSRKASDNADLKAFEPAGREPADYREMLKRYARVKNVRRFRHPPFTLP

SEQ ID 6295

TTGGTTTATTTGGGCTTTGGCGGAGGCTTTTCGGCATCCCGGATCGGAGACTTTTCGACCCGACGCTTCGGAATCGGCAAGGAGGCGTTTCGAGCTGTATTTCCGCCCTGCCGCCGACAGTG
ATTTGCCCGCTATCACGCGTGAGGATCGGCCACCTGAACAGGCATTTTGGATT

SEQ ID 6296

LVVNALAEAFGIPDAETFPDQRESARRRPFELYFGLPADSLRLRITREDAPHLNRHFWI

SEQ ID 6297

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AACGGATACCTGTCGATTTCATACGCATAACCCGCGCAAAACCGCGCGCATAGCATAAAGCGCGCGCCCTTTTCCACATCCGTTACAAACGCATCGTCCGAATGACAGCAGCGCGCC
CGCAGGCAACGCTTCGTGAACCGCATCGTTCAACCATCCGACACCTCTCTGCTCGCTCCAAAATACGCGCTCGGCTTATCATTTGGCAAGCACGCGGAAACGCGCAATCAAAGCCTTCAAA
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SEQ ID 6298

MMYGIDPRLVPPRHIPRQAIIPGKQPAVTVRRRRKRLPVALHRIHQPRILPVAPTGANIRRLRRNLQAHRSVAVGHKTDVDFIRITRRKPARRISIKRPPFFHIRYKRIVRMQQPA
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SEQ ID 6299

ATGTTACGCCCCTACCGAAACCGACTTCCCGGCAACGCGCCCTTGTTCGCGCTCCATAATCCCGGCGCGCGCGCGGAAATGACGGCAATACCGGAATCCGACAGCCCGCGCCAGAC
GCGAGGCAACGCA

SEQ ID 6300

MFSPTETDFPANAPLFAASIIIPGPPPEMTAIPESDSRRARRQANA

SEQ ID 6301

ATGAATTTGAAGCTTTGATTGCGCGTTTCCGCGTTCGCAATGATAAGGCCGAGCCGATATTTTGGAGCGACGAAGAGGTGTCGGGATGTTGAACGATCGGTTACAGGCGTGC
TCCGCGCGCGGCTGCTGCAATTCGGACGATGCGTTGTACCGATGTGAAAAAGGCGCGCCCTTTATGCTTATGCGCGCGCGGTTTCCGCGGTTATCGGTATGAATCGACAGTAT
CCGTTTGTGTCGACGCG

SEQ ID 6302

MNLKALIRFRVLANDKAEYPYFWSDEEVSGNLNDVHEACLRGRLLHSDDAFVTVVEKGRPLAYAAAGGFAAGYAYEIDSIRFVSDG

SEQ ID 6303

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ATCCCCGGCGCGGTTTTCATTCCGCTTACAACTGGCGGAACCTCTCGCG

SEQ ID 6304

MIDTVAPHGTADILDKNLHPTPRRRPDGIVKYSNAAKANPRAAPHSAYNHNPFS

SEQ ID 6305

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AGGCTTTGGAAGAGCGCGCGCTTCGGAATCGAACGGAAGCGCGCGCTTTGACGCGGTGACGATGTGATCTGCAAAATCAACCGGATGGGCAAGGACGAGCTTGAACTGTATCGGAA
GGCGAATTACGCGCAGGTTTGGATAAGCGCAAAATCGCGGAGAAATTTGCGTGAGGCTGTGGTTCGGATGTTTCTGCTAGTTTCGGTATCGTGCA

SEQ ID 6306

LVPEDQVREVSAGAAKLLRHGDVFAAVPGKRVEKADDTALEKAGASELEREAAAFDAVDVILQINRMKGDELELYAKANYQGGLDKRKSANLEBAVVRMVRQFGIVQ

SEQ ID 6307

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GCCAGTTG

SEQ ID 6308

LSSWGGFMARHVRNNGNRFGGVPGYGNLAAEHYCIIVAKQDGAIGADAYGPKDGDVLAALGVLEQGFRLDDAQIIVKTAMSSGITADVGFAYADGADDAHVQDAAYFASGADFASAGRI
RCQSAKLVLPKQALITVTLKGAENKKAADIDILYGEKPGQL

SEQ ID 6309

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AATACCGGCAACACGCGGATGCGCTTTCTTTGGTCTGAGAAGGAGCTTGACACCGGCAACCGTGTGGAACCGCTCGTGGTACGATACGCGGTGTGCGGAAACCGGCTTTGCGGTGG
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SEQ ID 6310

MAQKTNPAYGDQAMMQAAGLPMHMQRNSTLNRLAGKMPAGTAGAETLRKQTTQHPVVRQDLTRGMDEIRFNLVNPVSALPDMGDNATBGRGVGMSLSEAGLRVNOARFPVDDGG
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SEQ ID 6311

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SEQ ID 6312

LRRIEKELEKAEKPGVETADGSDNSLFGDFDEEDVKKGVEKLIQEKLAGYRDMKRQBAKAHYREIYTAHPDADSIVESRELEWLAGONPLVRKAFNDALKDGTAAEVIQAFDMFKAA
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SEQ ID 6313

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SEQ ID 6314

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SEQ ID 6315

GAGTATGCGAGTCCGCGAGCTTATGATTCTGCGCGCGCGCACATCCCATTCGAGACATTTTATGTGACCTCCGCGCTGCTTTTAAATAATTTGCAAAACATTTCCGCGCTTGAACC
GGCTGTCTTCGGTGAAAAACCAAAAGTATTTTCAA

SEQ ID 6316

EWQSAALMISAARHIPRTFHCRLRCP*IIANNFRSLNRPVPGERTKSIPQ

SEQ ID 6317

ATGGAGATGTAAACCGGTCGCCGAGCAGGCAGCTTATGATGCGGAATCGAGGAGGACAGCAAGCATTTGGCGGACGTTTTCGCGCAGTACGATTTTTCGCGAGCGCGCGACGCGCG
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GTCGGAACACGGCTTCAGACGGCA

SEQ ID 6318

MENVNRVPEQARYDAECROADEALAVFPVAVSIFGSARTPDQHDYAFACRLARRLSDSGIAVSGGGPGTMEANKGAFAGKSVSVGLNIALPHEQKPNPYQDIALFSPRFAERKAVFFR
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SEQ ID 6319

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SEQ ID 6320

LPTGRRIAGRNGGPWOTLQSRICIRPRIRGOTPAALGOTLPHILPHILROTLIFRG

SEQ ID 6321

[illegible]

SEQ ID 6322

LARGTEKQPDVSGIPSGDEAGFELDTGVMPDGLARQYADMAKYRAKPSSEAVGIDPDGDGAVSAAAAAADSGAAVPSAVSDMEARSVADDAPSGRSADADRGVPSAYGNVRPGGAPGAA
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 FENVRRHQTVADYTDAGIDMRREAGHADMGRGHYPEGLAESAGAVRAYRAQHPESADVLDRLNRAVGYRRNNWGSVPLLSRSEERLQGVRTALPDGDASAVVGGGRGLTRALPTEDRGLA
 QDVRQDVRQLGTQGGRLTDPADAGANAAALQGLPGSIVASGNAIPARRQNLQVRARABGAAPGLSASENLACTDGGKRAFPVAGKKPDTPTVFLVLPNQVAESAGRVSPKKRMADAADAFTRRL
 AADRRRPEKAGVPLGGGEYRFEHTDRRHIDALAGVPGRPGKGMPEEFADMAGPNSNDGLVSDGRRLTKGREAEFTLRAGGLSEAVSPSEGRDYPRTQPARAKVMARPDAAADGKPAGR
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 YAAQRTGGWAGIENRYGVKVGNGLRKGIAGVLARI GALLRRVLORLAGKAGGAMSDADVFMALDLHGNVEGARDAPWGNGHRAVMFARAEDGAAERKSSESLEKLRAEFTIRISGREVPE

GNNLEYYKRNALFEYKSLRGPIVYNNKDTGREI SLGRSGITEILRH DYKDAEHLQSLAIPQI IENAVYIDTLPNEDLAKNGDIQGYEYVVSGLNVGGADYTVRAAVASVRNGNRYYDHKLTK
IEKGNVLSLLDRVSTTGASESKSPLSGIDDKRLILQIQDKDAGKGIADFTAEVRFSAANTI EAAIGRTGKKSIDL RNALKDRWDASKGIQLQFLGRRIQIEDIYGGVLDGLKEYGRISSEL
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NELGGVYVFLPARGDYLDVVKDAGNCSANVSRAETLSEAELRLDALKADPGAGFKVSPVMKSRDYIRSRDAVSGSGFMRELGEAVGMLDLDLPQARIALDTLPTQLYLSNLSPTSWAKHGHR
KYVPGFSDRARAKQYNMGSGGANYLAKLRYADNMAEQLDLVHQAQFDVGRKYEYEGFQDQRLQVADEMRKRHEAVMNPNSKLAQALTGFGFLMMGMSPASAVVNLSTQTMVAVYVPMARKG
YGAAREILLRASKYQILGRFPKEFNITEDSLNGDEKFLPRAADYGVILDSQARDLAGLVNDDPGLGASAWQKVMKDAWNLFHHAEEKFNQVTVFAAYRLAKRAGADSEAFQAKKATYDG
HFDYAAQNRPRFMGNAAKVVFLFKQYSQNLIALGRNAYLAFKDGKARKTLTGLVSHAMSGILGLFPVSTLLAVASMLGSDDDDPWDAREALRNMLADAFGDKAGEVLAKGFSRLTP
LDVSGRLGLNLQVLPFDIQDGLBGGKWAESLVVSGTGA VVGAGI GAADGVRTESSVPRTANLTLNKS

SEQ ID 6323

ATGAGTGATTGTGGTCAGATACGATCCGTTGGAACACGGGCGGCTTGTGCGGGGTTTGAAGGAGTACCGCGGCTTTACGCAAAGGATGCGCGGGCGGCCGCGACGATACGGCGTTGACGC
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CAAAATCCCAAGCGCGCAGGGAATTTGGCGGAGGCTTGGGAAAGGGCGGGGGTTCGCGCGCGGCCCTGTGCAATGTGTGGGGGAGCTTTAAGAAGGATATGCGCGGAGAAAGGTTTGACCGC
CTCTTGGAGATATTTGGCGGAGATGGCGGGTTCGGGTCTGGAGCAGCGGCCCAATGCGCTTGTCCCTATTGCTACGGCAACCGCGCGCGCATATTGGGCGCTTTGGCGGGCGGTAAACCGG
GCGTGGCGCTTATGCGCGCGACCTTTGGGCAATACGCTGTGAAATACGCGCGCGGATGACGAGCGCGGCGAGGCGCGGGCGTTCGACCTTCGCGGCAAGGATTCGGTGTAGCGGTT
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SEQ ID 6324

MSLDVRYDPLEHGRLVGGLKEYRGFTQKDARAAADDTALTRGFKNSMRSMGWNALTGDKEELGLRKAEDMDYRKIQBGRKSQARRELGEAWKEGGVGGGLSNVWGLKLDWREKGLDG
ALELDVGEAGAVLEQAPNALVPLATATAGGILGALAGGNAAGVAYAGATLGNFLMEYGGQLDRAAEAAGVDPADKDAVMAFIGRGAPGALKNAAVKQAVVGAADMAAMKLGGSILAHGKKA
AGKAALERMGVAAADKAAVAAGKTPEFAALAKESARGGLGGAARHAAAYATESAGEFAGEYLGTGLANGWEDEKGAALFAPSLGHSVAGFAGTKAYAAVTDFLPRPGPTGGCAGGYRG
QQEGGQAGPGRGAGVACGGTGGCGRHRRLRTEARNRAARVSIRRIITISRIRLCGSLRTRVSRRRRGGSALPTAIRTRTRNRWRAGKNSRMFRVSRRTGRNFTIRA

SEQ ID 6325

TTGTTTCGAGAGGGTTTCGATGGGTTTGTGTTGAGCCGCTGCCGGGGATTTTGGGAGATGAAGGAAAAGGAGGAAAAAGAGAAGGCCCGGAAGGGGGCGGAGGAGCGGGAGCGGGCGCGG
 CACAGCGCACCGGTGCCGATGCGGTGCCGGTACCGTTGCGAATTATGAGCCGGCGCGCGCTTATCGGAATGTGATGGAATTTGAGCCGTAAACAATTATGAGGATGGGGCGCGGGGTT
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 GGAGAGAGGGCTTTGACCCGAATGTGTTCAAGACTGTCAGTTATGAGGTTGCGGACCCGGATACGGGCTTGACGCGGACGCGCGAGGGGATTTGTCGATTGCGGACGGGCAAGCTTTGGAT
 GTGAGGTTTTCGGGAGAGCGCGAGAAGCGTTATGCGCGCTTGGGCTTTAAGCCGAACGCTCAGAAAAACGGCCGCGGTAAATCATTTATGAGAATGAGAAGGGTGAGAAGAGGGTTGAGC
 AA

SEQ ID 6326

LFGGFMGLFEPESAGDFWEMKEKEEKEKARKGAERERAAAQHRADAVRRTVANYEAGPARTRNVMDLSRNNIBDGARRLRAGAFERAGADAGLGFSGDKALSPDARAGADFARRDTRP
 TDAGGRTPPPLGFDNVYRGKGVPRDFDAQRPVLSAGFDALSPFEERELYKRAITTPYAGALNGQLTAAQLNARGIVAENKNAAVRELGRERLAAAAEAANREAVLQKGRFDAVKANE
 GALNREMAQRNADRAFDVQQAELGMRKQGFENKREADALELDRKRIADLTRAYGFAKSDGQGRGIARQIDALNGKFERQGEKGFDPNVKTVSYEVADPDTGLTAKREGIVDLRTGKPLD
 VEPAGEREKRYAALGFKPNGOKTAGGKIITYENEKEGKRVBO

SEQ ID 6327

[illegible]

SEQ ID 6328

LNPLPLTLLILINDFTAGRFLTVRLKAORRITLLALSRLKHQRLARPQIDNPLALRQARIRVGNLITDSLEHIRVKALLPLPLKLPVKRINLPRNLPALPVRLAKTISPROIGDALPTL
KLQIRILTLHLKPLPLHPQLGLLHKRPVRIPLRLHVAQRTLVRLNRRIKPLLQHRILTVRILRRSRQPFPAPQFDRRIIFIMFRHNPARIKLRRQITVQGPRIRRSRPLIKPLPLRR
QRIRPGRHQTALVKITHRLAAPITHIPVKSQRRRPSARIRRRARIAPRETRPGPIGGKRLIAARKPQTGIRTFFESTRPAQPFRPTILNITVAQIHIPTITRRPGLITRNGTPHRTGTVRL
CRRPLPLRLPLGLLFFLLFHLHPKIPGRRLKQTHRKPSQEKSKISKNPSPIKRLKLTNKNRNPGPINKQOVTOKKHDPGPPGANKKPLIKAVAFONSGCISGSL

SEQ ID 6329

ATGCGCGGGGCGGGTACGTGTGTAGCAACCGCGTATCCGGCCCTTTTGGCATATATACAAGTCAAAACAAGGCAAAACATCAGGACCGGCAAAAGGCTGCAATCGGCCCTGCCCGTTTCCGGCG
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GGTGTGTTCCGATGTATTGAATGCCATAGGATTTACAGCCGTGGCATTAAAGGAGGACATATCCGGCGAATCTGTTTACAGGAGAAATGGCGCGCGCGGTATGTGCGGCACGGAAGAACGCTT
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TAAAGAGGACTACGGGAATATTGGGAAGGAGGCGCGCATGGTATCGGAGGGGGCGGTTTACGGCATGAAATACAGGACGCTTTTCATTCGGACGCGTTACGCTCGTCCCTTATGAT
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CGGACTGGGGCGCAGTCCGCTTTCTGTCGAAAACGCGACCGGTATCGAAGAGCGCATCAGGGCGGCGGATGCTGTTTCCAAAGTGTACTTCGATAAAGACAAAACAGCGCGCTTTTG
GAATGCTGAAACGGTACGCGCCCAATACATGCGAAAACAGGCGTGGCAATGGGGCGGCTGACGACGAAATATTCGACGCGCGGATATGTTCCGCTACCTGGCGCAGGCGGTTGAT
TAATGGATACAGCAGCAATACGGGATACAGGAAACGCGGTATCGGATTGGAGGCTTTAT

SEQ ID 6344

HTGKTVDLKLPAKLDGLFKPCRYKVMYGGGGKSHGAASALLALGAQRPLRLICAREIQKSMRDSVHRLIKDKVAQILGLHFYEITDFIRGANGTLFVPSGLQSHFVDSIKSFEGIDIV
WVEBHGVSKKSDVLPPTIRKEGSEIWIITLNPOMETDETYRRFIAMPSEDWLCIEINRDNPNPPEALNRERLKAQRSMNKEDYGNIBGRPRMVBGAVRYHEIQDAFHSGRVTLVFPYD
SSLPVHTVWDLGWNDAITGLVQRDLTSVRIIGYIEDTHRTLDWYVALEKLPYRWGDFLPHDGRTRNPQTGKSTHEILPLGLGRKSVFVNQATGIEEGRIRARMLPKVYVFDKDKTARLL
ECLKRYGRQIHAKTGVAMGPLHDEYSHGADMPFRLYAQVLDIMDTGSNTGYTETFPVSDWRLY

SEQ ID 6345

TTGGCGGAAACCTGTCCAAAAGCGCGAGCAGATTGTGCGGAATTTGACGGAAGCCCGGAGGACACATTCACAAAAGCGCGTATGTTCCAAACGTTGCGCGCGGGTTAAAGGTTTGG
TGGAAATCGAGCGTAAATCATACGGTATGGATACCGCGAATCGAAGATTTCGGAATCCGCCAAGACGCGGGCATCCGTATCGAATTGTAGGCGCTGAAGATGACGGGAAAGACGGT

SEQ ID 6346

LAENLSKASBQIVAEVYSGPEDTFTKARNPQTVAAGFKVLVEIERKSYGMDTAEISKI SESARTAGIRIEFVGPEDDGKDG

SEQ ID 6347

TTGGCGGATTCGGAATCTTCGATTTCGCGGTATCCATACCGTATGATTACGCTCGATTTCACCAAAACCTTAAACCCCGCCGCCACCGTTTGGAACATACCGCCCTTTGTGAATGFGT
CTCCCGGCTTCCGTACAAATCCGCGCAATCTGCTCCGCGCTTTTGACAGGTTTCCGCCAAATTCGATGCTCGCTGTACGGCGCAACCGTTTCGCTTCCGCGTCCGTACTTAA
TTAAGGTTGAATCCCA

SEQ ID 6348

LADSEIFDSAVSIPIYDLRSISTKTLNPAATVMNIRAFVNVSSGLPYNSATICSALLDRPSAKFRCLRCTAATRFASASVTVLRLKSA

SEQ ID 6349

ATGCGTGGCTGTACGGCGGCAACCCGTTTCGCTCCGCGTCCGTTACTTATTTAAGGTTGAAATCCGCATAATCCGGCGCATTTGCCGTTTTGTCCGCGGACAGCACCATCGCCCGCGC
TTTGCTGTACCTCGTCATTCAATTCGCGCTCCACGCGCTCTTTGCAACCCGTCGCGCGGAAACATTTGATTTGCGCGCATTTTCGCAATGCTCAAAACCCCGCGC
GGTAATCCAGCTCGACTTTGCGCGCAATCCTCATC

SEQ ID 6350

MPALYGGNPRFRVRYLFKVEIRIIRRIAVFVRQHRPRLCLYLVIQIARPHAPGNPADVLRENIVFAPDFGNAQNPAPVFIQDFAPILI

SEQ ID 6351

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ATGTTTCTTCGCTATGCGCGGTACCGTGTGAGCTTGATTGCTATGCTGCTTCGGATACATTAACCGCTTGATGCGCATTTGCCAACCTGACTGCGCTTTTGTGATGCGGAAAT
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SEQ ID 6352

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EGVLAVKYRVNNSKMGSGGPMYYIEKGLKMKWMAVAFALPGTASPFGIGSSVQNSVAQVTSFGIEPAYTGTITLTVLTVAVVVLGGIKIAKAAFPVPMAMVTVVLGLSLIIVINS
DALMPAVKLIPSDAFSAQAVAGGAICTVIRYGVARGVFSNEAGMGSAPLAAAKTDPVRQALVSMGTGFLDTIVVCSITGIVLVMGLLAGGEFVKPELSGAALITVTFQKMLPGIGW
IVTIGLIFAYSTILGWYCYGEKCAVYVFEKPAALYRVGVSSVMPGTVLSLDLWLASDTFNGLMALPNL/TALLLMKVIVNETRDFKQKITNGELPH

SEQ ID 6353

ATGGCACTTTTCCTCAGCATATTCCTCATCTCTGCTGATTGGCTGATGTTGAAAAAAGCATGCTTCTTACGTCGCACTGCGGATTACCGCAGTCTGATTACGCCATCAAAC
TTTTCCTACTTCGCGGATCGGGAATGCTGCTCAACGCCACCGCGCTTCGCGCTTCGTCAAAAGCTCAACCGGATTACCGTATTTTCGCGCGGATGATTGTTCAACCGTATGATGGAAC
CACGGGCTGCATCGATGTCATCCGCAATGGCTGGGACCATCAGCCGCAACCCGCTAGCGCACTGATGATTATCGGCTGGGCTTTTGCTTTATGATGAAGCGCATTCGCGCTTCGGC
ACGCTTCCGCGGATTCGCGCGGATTCGATGAGCTTGGCTTCAATCCGTTGAAAGTGGCGATTTCCTACTTTGGTGTATGAATTCGCTGCGGATTCGTTTCGCGCGGCTCGGTACCGCA
CTTGGTTCGCTTCGCAACCGCTGAACCTGAGTCCGGAAGACATCTCGCCATCGGCGAGGAGACCGCGGTGATGCACTTCTTCGCAAGTTTCGTCATCCCTGTCATCGTTTGGGCTTCAT
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TACCGTCAGCGACTCCCTGACGATTACCTTCGCAATATTTTCGCAAGATGTCAGCGCGCTTACCAACAGCTGATGCTCCCGCTTGGATTCGCTGCTGACCGTTTGGATTGCT
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CACCGTTCACCTGACCTTCGCTCGGATTCAGCAGCAATCGCCCTTGATACCGGCTGCTCGGACCTGATTTGCGGCTGCTGCTGCGCGCGGATGGCAATATGCTGCTG
CTCAACCACTATTCGCGCTATGATCGGTATGAGCTGAAAAATTCGGAAGTGGCATTTATCAAGAAACCGTTATCCCGATGGCGATTACGCGCTGATTGCGCTGCTGCGCGCAATGA
TTTCTCTCTC

SEQ ID 6354

HALFLSIPPIVLLIIMVKKNSMPSYVALPITAVLIYAIKLFYPGDAGMLLNAASGLVKTL/PTITVIFGAIMFNRMMETPGCIDVIRKMLATISPNVQALMIIGWAPFPMIEGASGFG
TPAATAAPILMSLGFNPLKVALFTLVNNSVPSVPGAVGTPWFGFAPILNLSAEDILAIQRQTVMHFPAGFVPIVIGLGFIVPWEIRKNGFVAIAVPSCTIPIYAALAHVNEEFPSLVAG
AIGLMVSFAANQWGLSKDHAKDPNAEKVPFAQAKALAPLMLIGMLVWTRIKQLGIGKILTSKEEWSFQLPFDLSKITVSDSLTITFGNIFGQDVSAZYQLYVPAHPIPVFLTWIC
ILLYKTKPKDAWITIYAVTFNYTKKPLALMGALIMVQMLVGGDNMSVKIIGKEFAAMAGEHNVVPSYPLGAIGAFPSGNTVSNLTPGPIQQQIALDTGLSVTLILALQSVGGAMGHEVC
LNNLIACVTFLVDKNSGEGAIKKTVIPHAIVGYIAVVAHIFFL

SEQ ID 6355

ATGCCGAGATTGTCAGATGAGGATTGGCGCAAAGTCGAGCTGGATTACCGGCGCGGGGTTTGGAGCATTCGCCAAATCGGGCGCAATACAATGTTTCGGCGCAACAGCTGGCGAGGGTTG
CCAAAGAACCGCTGTGGACGCGGATTGTAATGACGAGGTACAGGCAAAAGCGCGCGGATGGTGTCTGCCGCGCAAAAACGGCAATGCGCCGGAATTATCGCGGATTTCAACCTTAAA

SEQ ID 6356

MPRLSDEDMRKVELDYRRGLSIAIRIGRYNVSAQHVRVAKERVWTRDLNDEVQAKARAMVLSADKNGNAPDYADFNLK

SEQ ID 6357

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GATGGCGGTATTGGAATAGCGGATACGGTATTGCACTCAACCCGACGAGAAATGCGCTGTTGGGGGCTTTGATGTCGGGGTTCGGACAGCAGTTTCCAGTATTGATGCGGCGCGAG
TTTTTCAGTGTTCGGGAATTATCTGGAATGTTCCGCCAAAACGGGAGGTTGGATTIT

SEQ ID 6358

MSGLSIDDKVYQGVVDLHNAEQVVSREALAETTLGLKMEITKFTKLLVEHGKIYRVTRIGFKPAIGFGETRPFVSFVLSGNGVLEIGDVLHLNPEMRSLGALMSGFGQQFSSIQMGRE
FSVLRNLYLECSAKNGRLDF

SEQ ID 6359

TTGGGCATCTATGGAGCATGGTGTITATGGGATTAAACACAAGAGGTTTAAAGAATATTAAAGATATGATGACAATACGGGAAAGTTATATTGGCGGAGCGTCCAAAGAAATATTTC
ATAGCGGTTCGATTAACAATCTTGAATACCGGATTTCGCGCAAGGAGGTTTCTTATACAAAGCGAGGTGGGGTATTGAAGTTAAAAATATTAAAGAAACATATAATGCACATAG
ATTAATTTGGCTTTTGTATTAGGAAACACGCTTCTCAATAGGCCATATCAATAGGGATAAGACAGATAATAGAATATCTAATTTGAGAGATGTTACACATGCTGAAAAATATGAAAAAT
AGAGGGAAGTTTAAAAATAATACTAGCGGCGATCTAGGGGTTTATTTCCATAGCCGCTTAAGAAATGGCAAGCTAGGATTATGGTTAATAGAAAAATAAAATATTAGGTTTATTGTAAC
ATATTGAAGATGACGCGAAAGCGAGAGAGGAGCAGCATCTAAAGATTTTGGCTTTGTAGTG

SEQ ID 6360

LGIYGAWCFMGLTQFVLKELLRYDDNTGKLYWAERPRKYFNSGLHYKSWNTGFSQKEVFLYKRLGLKILKIFKKQYNAHRLIWLFPVYKHAASSIGHINRDKTINRISNLRDVTHAENMK
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SEQ ID 6361

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AAAATTTATGGATGATTGAAATGCCCTAACGGCAATTAATGGGTATATCAACGACAAAATTATCAGTTCCGGAAATGCTGAAATATCAAGAAAGATTATATCTTGGGCATCTATGGAG
CATGGTGTATTATGGGAT

SEQ ID 6362

MNGAREFTLTQPNKKQVMRSIWDSPDGFENGLEITIRPRKSKRSVEQNRLWFLYREISEKVFIDGRRFSQDVWHEFLKRFICGIEPNGQLMISTTKLSVREMSYQEKIISWASME
HGVLMD

SEQ ID 6363

TTGCGCGGGCGGATTTGATTTCAAGGTGCGCTTTTCAAAACACCGTCGCGGCTGTCCAAAACGACCGCATACCTGCTTTTGTGTTTGGGGCGTCAGTGTAATTCGCCCGCGTTCA
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ATCGCGCGCGCGGCGCAACCGCACCGAAACCGCGCCCAACCGCGCTTTTCAATCCCGCCCGTGCCTCGCGCGGAAACGCGCAACACGACCGCTTTCAGGTTGTCTATGCACA
CGCCCGCGATGTTGCGGTGATGCGCGCTTTGCGGCTTTGCGTATGCGCG

SEQ ID 6364

LRGRIVISRLPFSNHPGLSGLQIDRITCFLFWGVSVNSAPFISDGLSRRQPPMLQGGVSCAIANGAYKTLCLRLGLRPCRRLRRGGNRTNPRNRRFSIPPRASRPNGTTRPFQGHCT
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SEQ ID 6365

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CGGATTTGAAAAGCGCGCGTTTGGCGCGGCTTTCGGGTGCGGTTGCGCGCGCGCGATCGACGGCAGGGCGCGAGCCCTAAGCGCGAAGACAAAGAGTTTATATGCGCGTTTCGCA
ATTGCGCACGATACCGCGCTTGAAGCATTTGGGGTGTGTCGCGTGAAGAGCGCTGAA

SEQ ID 6366

MSSAIRKAAGGQCTPNIAGVCNDNPETVVLRCRFPGETHAGLKSGLGAGFGCGCRRGAIDGRGAGLSREDKEFYMRSLRTIRRLALGVVGVKRLK

SEQ ID 6367

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TCTGTTTTCGCGCGCGCTTTTGTGCTTGGGTATCAGCGGCATATACGGCAACCGCGCTTCGACGCGCATCGCGCGCGCGCTTCGCGCATACGGCGGACGGTTTCTTATACGC
CGCGCGCTTCGCGCTCTGACCGCGCTGTCGCGCAATCCGCAATATCGGTTCGCGATACGGGTAAAGCAGGATAAGCGCGCTCAGCGCATTCCTTCGCGGTTCGCTCCACAGGC
CGCGCGCAATATCGGGCAGGCGCGTTCGCGCGCGGATGATTCGTCGAGCTTTCGCGCGCTATCGCGCGGCTCCCGCGCGCGCGCTTTTTCGCGACTGCTTGTTCGCGCAGGT
TTTGCACGATTG

SEQ ID 6368

LAALRIALDIPTLSSDEIPTLVCRIRLPHLQFPHLHRQTAAATYRFAAIFGGNAPHLFVVVIGNALKRVQSNLQGVVQIDHRLVCAAVFVRFGYQPHIYGNRAPGRHRARPLEDTADGFLIR
RRLRAPRDPVAPNPFISVCRYGVRQDKARHAHSPAGCVHRPAPNIGQAACAARNYPCSLAAVIAAPAPAAARFCRTALLRQVLHDL

SEQ ID 6369

ATGACGGCGCAAGGCTGCACGGATACATCCGCGCGCGCACGCGCGCTGCGCGATATTGGGCGCGCGCTGTGGACGCAACCGCGAGGGAAATGCGCG

SEQ ID 6370

MTAARLHGYIRAAHAACPIIGAGLWTPAGECA

SEQ ID 6371

ATGCCGTCCGCGCAAGGAAGGGGGTCTATTATTACAAATCGTCAAAACCTGCGCAACAGGCAAGTCCGCGCAAAAGCGCGCGCGCGGAGCGCGCGATGACGGCGGCAAGGCTG
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CATCGGACAGGAGGTTGGGATGTC

SEQ ID 6372

MPSRARKGGLLQIVQNLPOQSPAKARGGSRDDGKAAIRHPRARRLPDIGRRPVDATGRGMRVTRLILPYPVSANRYWIRWNRVRSAAEAAAYKETVRRIAQAGAMPSEGAIV
YVRLIPKANKDGNKTVILDLNALKVFLDALQGVAYHNDQVRRIAAEYGGEEPTVGGGLAVEGKLEMEQTDAADEBWFICQEGNDV

SEQ ID 6373

TTGAGTTTCCACAGAAAAATCCGAAAAATGAATATTTTACGAGAGTCCGCCAGTTCAAAGTTGCCGTGCTGCTCCAAAAACGACGCTACCTACCAAGTCGATACCCACACGGCA
AACGCCACAAAGTGAAGGCAAAATGCTTTTCCGAGTTTTCAGCGCGATATGGCGCGGTTTTCGAAAAACGCTCAGCGCAGCGCGCGGACATCGACACCGATTATTTGTTGGAGATG
CGCGAAGAGGAGTTTACCGCCGAGCCATCCGCGAAGAAATATACGGCCATGCGCGACCAAAACGAGCTGGCGCGGACTTTGATTGCGCTGTACGCGCGCGCGGTATTTCTACAAA
AAAGCCAAAGGCGTGTCAAAGCGCGCGCGAAGAACTTTGAAACAGAGCGCTTGCGCCATCGAACGCAAAAAACAGCAAGACGCGCAAAATCGAAGCTTTGGCGGGAAGCTTTGAAACGCG
CGAGATGCCGTCTGAAATTCGCGCGGATTTGAGAACCATCTTACACGCGCGCAACAGTCGCTGACCTACAAAGCTTTACCAAGCGCGCGACGCTGAAACCTCCGCTACGA
ACTGGCGAAAAACGCGCGGCTTACGCTCATCCGCAATACCTGCAAGAGCGCTTTGAAATCAAATCTTCCCAAGGAACAGGTTTCCCGACCTCTCCCTTCCGAAATGCCGAC
CTGCCAAGCGCGGCTTACCGCTTTTCCATTGACGACGAATCGACCAAGGAGTGGAGATGCTTGGAGCTGACGATTTGGGCAACGGCACGAGCGCGTCCGATCCCATCGCG
CGCGTCCGCTTCCGCTCCGACAGCGCGGGAATGGAACAAATCATATGACGCGGTGTAGTACGCTTTATTTCCCGCGCGCAAAATCAGATGCTCCCGGAAATCGATTACCGCTT
CAGCTTCGATCGAGCGCATACCGCTTCCGCTCAGCATTTATTTGATGTGGAGCGGAGTTCAAGCTCGCGAGCGGACCTGCAAAATCGAAGCGCTCAACATCGCGCAACCTGCGT
ATCCAAGCATCGAGCGCATTTCAACGCGAAGACCGCTTGGACCAAGCGGGAATGATGTTCCGCCACCATCAAGACCTGATTGTTGCTTATCAATTCGCCACCGCGCTGCAAAAG
CGCGCGCAATACGAAACCGCGCGCGCAATACGATTAACGATTAACGATTTGGATGAAGAAGCAACGCTCTCCGCTCGCGCGGAAACGCGGTTCGCCATCGATACGCTGCTCAG
CGAGATGATGATTCTTTCGCAACAGCACTTGGCGCGCAATGCTAGACGAAACGGGCTGCCCGCTTTTCCGCTCCAAACCGCGAGGCAAGTTCGCGATGACCAACCTCGAGCGCAC
ATCGCATGGCGCTGACGATTAACGCTGTTTACCTCGCGCTGCGCGCGCGCGGACTACATCAACCAAAACACTCTCAGCTGATAGACGACACCGCGAGCGCTCTTCCGAC
AAAGCGATGCCGAATCTTTCGCGCGCTGCGCGATTTGACACCGCTTACGCGCTTACGCGGACTTCAACGCGAGATGGAAGCTTACTGGAGCTCTGTACCTGCAACCAAGCAT
CAGCGAATGACGCGAGGATTTGTAAGAGAGCTCTGCGCATGGAAGTCTGCCACTGACACGCGCGGAGCGGTATTCGTTGACGCGCTGCCAAATCCGAGCATGTTTAA
ATCACCGAATTGGATGCCGAGAAGCAGTTTGTCTCCCTCACTACATCAAGCGAGCGCGCGCGGCGCAAAACGCGAGCAATGCCGTC.

SEQ ID 6374

LSFHRKIRKMINIFYEESGQFKVAVVVQKNDATYQVDTQHGKRTKVKANNVFAEFDGMDAFLNQAQADIDTDLLEWVCGKEEFTAEALAEERYGHAPTKELEAATLIALYAPVIFYK
KAGGVFAAPESTLKQALAAIERKKQDAQIDANABALKRGEMPSEIAADLRTHLHAPDKSLTYKAFTKAADALKTSAYELAKKTGGITSIPQTLQDGFELKYPFGTDPDLSPLEPFD
LPRADVTAFSIDDSTETVVDALSLTDLNGTKRVGIHIAAPSLAVRQGGGMEQIIMQRLSTVYPPGKITMLPENWITAFSLDAGAYPAVSIYFDVDFEFPVGEPTCKIEAVNIAANLR
IQALEPHFAETGLDQAGEMPAHQDLIMFYQFATALQKARGKYPEDRAPQYDYSILDEEGNVSVRRERGSPIIDLVSNNHILANSTWQMLDENGILPLFRVQPAKGVNMTQSEPH
IGHGVQHYGWTSPLRRAADYINQQLSLIDDTAEPLFQSDAELFAALRDPDTAYAAVADPQRMAYNSLVYLQGGISELTATILKEDLVRIEGLPLTRATGTPFDALPKSQALFK
ITELDAEKQFVSLNITKAAAPGKTAGNAV

SEQ ID 6375

TTGTTTGGCGGGCGGGCTGTTCCGGCACCGGGATTCTGCCGACGCGCGCGCGCGGACGAGCGCGGTTTCCGTTCCCGCGCTGCTGCCGCTATGGATGGCGCGGTTTCCGCTAGAGGAAG
AAAATCATTTCCGCGGACGACGCGCAATCAGCGCTAAATCGCCATCGGGATTAACGGTTTTCCTGATATATCGACCTTCGGAATTTTTCACGCTCCAATACGGTACATACGGCGATGATGTTGT
TGAGGACACCATATATGCCCATCGCGCGCGCGGACGAGCTGCAACGCCAGAAATCAGGGTCAGGACAGCGCGGTATCAAGGCGGATTTGCTGCTGAATCGGACCGAAGGTTCAGTTGGACAC
GGTGTGGAGCGCGAGAAAGACGACCGGATGCGCGCCAGATACGCGGAAATAAACCAGTGTTCGCCCGCATTCGCGCAAAATTCCTTACCGATGATTTTCCACATCGAATTTGCGCG
CCGACCGCATCAGCTGAACCAATAATCAGCGCACCCATCAGGCGCAAGCAGCGGTTTTCGTTTGTATGAAGTTACGCGCAATAATCGTCCAGGATCTTTGAATTTGGTTTATACAGCA
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GGTAATTTTGGACAAATCAACCGGCTGGAAGCTGAACCATCTTCTTCTGCTGCTGCTCAAAATGCTTTGATTCGAGCTGTTTGTATGCGGTAACACCGCATCGCGATCAGCATACCC
AAAGGGCGAGTCTTTGGCGACTTGGCGCAACGCGCATTTTTCGCGATTCCGGTCTTTGGCGTGTCTTGTCTCAAGCCCGAGCTTTGGTGGCGCGAATACGGACACCATCAGGCGGA
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CAGGATGAAGCCCAACCGATGACAGGGATGACGAAACCTCGGAAGAGTGCATCAGCGCGCTGCTGCTGCGGATGGCGAGGATGCTCTTTCGCGACTCAGGTTTTCAGCGTTCGCGAAACCGAAC
CAGGTTCGCGCTACCGACGCGCGGCAACGATACCGCGCAGGAATTCATCACCAGTGAAGTGAAGTGCCTTTTCAACGATTTGAAGCCCAAGCTCATCAGATTCGCGCGCGCAATCGCGCGAG
GCGTCCGAGAGCGGATGCGCTTCAATCATAAAGGCAAAAGCCAGCGGATAATCATCAGTTGCGCTACGCGGTTTCGCGCTGATGGTTCGCGAGCATTTGCGGATGATCATGATGATGAGCC
CGTGTGTTTCATCATACGCTTGAACATAATCGCGCGAAATCAGGTAATCGCGTGAAGCTTTTACGAGCGCGGAGCGCGGTGCGGTTGACAGCATTTCCGCTATCGCGAAGTAG
AAAAGTTGATGCGCTAAATCAGCACTCGCGTAAATCGCGAGTGGAGAGGACATATGTTTTTTTCCACATCAGCCAAATCAGCAGGACGATGGGGAATATGCTGAGGAAAGTGT
CCATAACGAATCTTTTATGAGCATTTGCATCATAGGCGCGCTGAGGTTTGAAGACGTTTCAAATCCCGCACACCGCATATTTTGT

SEQ ID 6376

LPFGAGCSGTGILPDAPGAAVSVPRVLPLMMAAPRLEENHCRDDGNHAVNRHRDNGFLDNRTFGIFHVQYGTGDDVVEAHHAHRAADGLQRQWQHGGQAGIKGLDILNRTSGQVGH
GVGAGEERTDRAQIRKINPVFAHCGKFLTDPFHRIVAADQHLNHNQTHQGRPFGLIBGYINRPGIPEFGPIQQDANPNQGHENRPSRDVQLVRRADILSENLABGNRQGVAD
GNFGQIKRQLEABPFFAQNAFDSLPDAGNHQADQHTQRBECQDLGERHFFGIHVFVVAQAPALVGGEGYHGHQADCADGERREFFVDHRCQGRINGAGEDGNGDEAQPADFPR
HDEAGTDDRDDETCVEVHAGLPADGEDVFGTQVQRCETEPGRNTDRAERYRHGHHQSENHRPQRIEQAQHNRRNGNRRAEAGCAFNRHKGSPADNHLQRYGVRAHQFPADDIDA
RGPHFTVZHNRAENHGNRRERFDEAGSGGVEQHSRIAIEVERKFDGVNQHCGNRQCDVGRHTVFFHHQPNQDDGEYAREKCHNESFLGICILRRVWVKDQVQIPIHRYFG

SEQ ID 6377

TTCCGCGGACGCGCATTAACCCCTTCTCCACGGCTTGGTCCGCGCGCGAGGCTTCAGGTGGCGCATTTCTTCGCCATTTTGATTTTCTCTTTGTTTTATGTTTAAATATCCGAAG
CCGTCGAAGTCTGCTTCCGCTTTCGCTGCGCTTCCGCGCAAAACCGCTTCGCGGCTTCCACCAAAAGCCATACCGCCACGTCGCGCGCGCGCGAAGCAGCAGCGCGGTGATGATGC
T

SEQ ID 6378

LRGTALNPPSNGLVPPQALQVRISAILIPFVFMCLISEAVEVVFAPAVALAAQNRVGGFHQKPYRQRRRAERQRGDDA

SEQ ID 6379

ATGGATACCTGTATAGCATCATCACCAGCTGCTGTTCCGCGCGCGCGGACGTTGGCGGTATGCTTTTGTGTGAAGCCGCGCGACGCGTTTTCGCGCGCAAGCGCGACGCGCAAGGCG
AAGACGACTTCGAGCGCTTCGATAT

SEQ ID 6380

MDTLLSITALSFGGAATLAVWLLVEADAVLRKRKRGKEDDFDGFY

SEQ ID 6381

ATGTTGGAAATTCGGGAACTGATGAACCGTCAITCCCGCGGATTTCGCTCATTCGCCGAAAGCGGGAATCCGGAACCCCGAACCGCGAGGAATTTATCGGAACCGG

SEQ ID 6382

MLEFRETDESPFPIISVIPAAGIRKPRTRQEFIGN

SEQ ID 6383

GTGATGATGCTTAACAGGATATCCATTGTTTATTTCTTCTTCTGCTGCTTTATGGGTGGGGTGGGATTCGCGCGCTTCGCTCATTCGCGCGAGCGGGGAATCCGGAACCCCGAACG
CGGAGGAATCTATCGGAACCGCTGAAACCGGACGAGCGGATTCGCGCTGCGCGGAATGACGCTTCTGCTACGCTTCTGCTCATGTTGGAATTTGCGGAACCT
GATGAACGCTCATTCGCGCGATTTCCGCTCATTCGCGGAAAGCGGGAATTCGGAACCCCGAACCGCGAGGAATTTATCGGAACCGCTGAAACCGGACGAGCGGATTCGCGCTGCG
CGGGA

SEQ ID 6384

VMLNRVSVLPFPRFYSGSDSRRLRHSRAGGNPETPNAAGIYRRLKPDGPDRLRGNDGVSATVTVFRSCWNFGKLMNRHSRRFPSPFKRESGNPERGRNLSETAETGRTGFPFPA
RE

SEQ ID 6385

GTGATTCGCGACGCTTTCGTCAATTCGCCGCGAGCGGGAATCCGGTCCGTCCGGTTTCAGCCGTTTCGATAAATTCCTGCCGCGTCGGGGTTTCGGATTCCCGCTTTCGCGGAATGA
CGGAANTCGCGGGAATGACGCTTCATCAGTTTCCCGAAATTCACATGACCGAAACC

SEQ ID 6386

VIPDAFVIPAQAGIRSVRFQPPFINSRVRGFRIPAFAGMTIEGNDGSSVSRNSMTET

SEQ ID 6387

GTGCGGGGCGCCCGCTTCAGCGGCAATTTTTTCCAAACAATCTGACACAGCGCGGCCCAACGCAAAATTTGCTTCGCGCTCGCGGATGTAATAAGCGCGGAGATGACGCGAAGC
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GCAAGGCTTTTTCAAGTCTTCGCGCGCGCTTTTTCTTGTGCGCGCAGATGTAATTTGAAGCGCTTCGCGAGGTTGAAGTTGAGGTATTGCGCAAAACCGACGCACTCGAAGCGCGGTT
TTTGTATAGCGGGTTGATTTGCCGCTTGTTCGCGCGCGCTTCCGTCCGACGCTTTCGGTTTTCGCTTTCGGACTGTCATTCGCTATTTCTTTCAAATTTGCGTTT

SEQ ID 6388

VRGPPFRFRHFFQJIFDTGGRPRKIVFAVDVLSGGDGGKQRLRAAVEPAIPQTGVHFFIAAVFEFLRLRAGALAFQVPGFFQVFAPAFFLVPPDVFEVAVEVEVLRKPDLEGAV
FVIAIRVGIALLRRGRPRDGFGLRVSDCHSVFPKFAF

SEQ ID 6389

ATGACAGTCCGAACACGCAAAACCGTCCGAGCGGAAGCGCGCGCAACAAGCGGCAATACCAACCGGGCTATTACAAAAACCGCGCTTCGAGTCCGCTCGGGTTTCGCCAAT
ACCTCAACTTCAACTCGGCAACCGCTTCAAATACATCTGGCGGCACAAGAAAAAGCGCGCGCAAGACTTGAAGAAAGCCCTCGGTACTTGAACGCCAACCGCGCGCGCGCGAA
GTTCAAGAAACTCAAAACACCGCGCTATGAAAAATGTACGCGGCTCTGAAAGATTGCGGGTTTCGACGCGGACGAGGCGCGCTGCTTGCCTCATCTCCGCGCTTATTTACATCCGC
GACGCGGAAGACAAATTTGCGTGGCGCGCGCTGTGTGCAAGATTGTTGAAAAAATGCCGCTGAAGCGGGCGGGCCCGCACCTTGAAGCGCGGATGCCGCTGAAACGCGCGCG
GAGGCATT

SEQ ID 6390

MTVVRNTQTVTEAAPPQGGNTNPGYKNAFECVGFQYLNFLNGLNAPFYIWRHKEKGGREDLEKALRYLERQAGAPFKKLKHRRYKMYAGLKDCGFDGTEAALLAVISAAYIR
DGEDNFAMAAACVEDLLEKMPPEAGRAPHPESPMPPEAGGGI

SEQ ID 6391

TTGCGTTTAAACCGGTTTTTAAATCTCGGTAAGCTGGGATATTCCTAAAGCGTTTACC CGCTTCCCGCTCAAATTCGGCGATTGCGGGGGGATATTTCCCAAGCACCGCGCTCT
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ACCGCGTCCCGGTGTGGTTT

SEQ ID 6392

LRFNAPFKSRVGDIPKAFYPPSRNSAHCGDIPQAPPSFLRLPPMPSETRRRRTDWFAGSTSLPPHSAPSRLSQNRAPACRCWF

SEQ ID 6393

ATGCGTGAACCTGTTTCTATTGCAACCATGCCGACTTCAAAACCAACACCGGACCGCGGTGCGCGGTTTTCGAAATGCGCGAAGCGCGGAATCGCGAGGAAAAAGCGAGTACTACC
CGCGAACCAATCCGTGCGCGCGCGCGCTTTCAGACGCGATCGGGGCGCGCAGTCGCAAAAGGACGCGGTGCTTGGGAATATCCCCCGCGAATCGCGCAATTTGAGCGGGAAGGC
GGTAAACCGCTTGGGAATATCCAGCTTACCGGAGATT

SEQ ID 6394

MRETFCYCNHADFKYNTGTVPVRGFAKCAKARNAEEKATYYPRTNPCAAGAFQTASGAAVAKRTAVLGEYPPRNAPNLSKAGKTLMEYPSLPEI

SEQ ID 6395

ATGAAGTGCTTGTTTTAGGTGCGGCTGTTCGCGCGTATCTCCGTGTGTATCTGCGAGAGCGCGGACATGAAGTAACGGTATCGACCGCACCGAGGGTGTGGCGATGGAACCAAGTT
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CGGCTGTATCAATCGAATGGCTGTGGCGGATGCTGCAAACTGCACGCGAACCGCTATCAATCAATAAGAGCGCATGGTTCAGGATTTCGAATACAGCGGTGAAATGTTCCCGCT
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CGGTTTGAACAGATGCGGTTGTGTCGCGCTGCTGCTTTCAGCAGGACTGTGTGCGCGAGTTGGATCTCAATCTGCCATTTATCCCGTCAAGGCTATTCTTACCTGACCTGCGCGTCA
CAATTTCCGACGCGCACCGGTTGCTACTGTTTAGTGAAGCTACAAAGTCGCGATCACGCGTTTGAACAACAGAAATTCGCGTGGCGGAATGCGCGGAATTTGCGGCTACGAAACCA
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CGGTTAATCGCGCGCACCGCTTTGAAACCTGTTCTGAATACCGGCGCAGCTACTTTGGCTGGAACATGTCGCGGGTTCGCGCAAAATTTGACCGCGGATATGTCGAGCGCGAAGACA
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SEQ ID 6396

MKVLVLAGVAGVSSVWYLAEGHEVTVIDRTEGVAMETSFANAGQLSYGYTPWAAPGIPTKALKRLFKSHPLLFRPDGGLYQIEMLWRMLQNTATRYQINKERMVRISEYSREMPFR
FEAQTFMNFEGRRKGTQLQIFRQTEVEAARQDIIVLERVGVYRRLKPEBCAEFEPALARVTAIKIVGGLHLPLADATGDCRLFTENLYKLQEKGVRFYPNQTIISRIDHNLRIKAVETETG
RFETDAVVCALGCFSRVLAQLDLALPIYPVKYSLTLPVTNSDGAIVSTVLDESXKVAITFRDNRIRVGGMAELSGYETKLPEKRRETLALVVNDLFPEDGDLSQLSWSLRPMTPDST
PLIGRTEFENLPLANTGHTLGTWTPSGSAKLTADIVSGKDTFELRSDDLSLSRQKL

SEQ ID 6397

GTGCCGGAACAGCCCGCCCGCAAAACAATGCCGTCTGAAACCGGAAAAGGCTTCAGACGCAATTTTATCCGCTTTCGATTACGGCG

SEQ ID 6398

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SEQ ID 6399

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CTGAAAAGTTTACCAGCGCGCAACACAGGATTATTTTCCGCGCTGCTGTGATATGGCGCGGCAACAGAGCTATCGACATCATCAGCTGAACGACAGCTGGAAGCGCGCGCGGAGGC
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AGACATTCGCGCAGACCGTTGAGGATTGATTGCGCGTTTGGACAAAAGGCTTGACGCGCGTGCCTTCGATTGCTTACCGGCTTGTATGAAGCTTGAAGCGGATGACCGCGGTTTGGCGGA
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CGGTTAGAGCTTGGCAAGCGCGCATGCGCGCTGAGTGCAATATCCCATGCAAGACCTGAAAACCGCGCAATTCAGCGCAAGCGATTACGCGCAATATGCGGATTACGTCAGCGCAAGCGA
AAGAGTGGAAAGTTTGAAGTGAACCTGCGACCTGCTCAAGCTTGACGAGCTTTGCTTTTGGCTTAAGGAGAAAAAATCACTACCGGCTTGAATTTGTTGCTGTGATCACCTTCACATCAT
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AAGCAGCAGACAAACGCCGGAACATGCGAGACATTCGGCGCAGCGGCGGATTGAGCAAGACGCAACATCATCATGCCGACCCGGAAGCTACTACGACGGAACGAGAATCCGA
GCATTGCCGAGCTGATTATCGCCAAGAACCGGACGCGGAATGGGAACGGTGGTTTCGGCGTGAAGGGCAATTTATGAAGTTCGAGGAAGACGCTGATTGGCATGGCAAGCCCCAA
ACATGATGAATATGACCCCTTACAGTGTC

SEQ ID 6400

MNRTEFEAVQSLASVAGBNLGGILIEPTALARCAILTPEKPYQAQHRILFRALLDMAAANEPIDITLNDKLEARGEAEENAGGLAYLIDLNQTPSAKNI SRYVGI VDRFVERGLLK
ASAAIEKIAVSKDGGTVAEKL SKADELAAVGDVAVKRETKTFGTVEDLIGGLDKRLDGVRFPLPTGLMKLDGMTGGLPDGNLIVIAARPSMGRFVLAENLARFALKQKAVHFQSYEMS
AVELARRGMAECNIPMQLKTGNLTQSDYANMPIYVSQAKENKFDVNCDLLNVDELCLAKEKLLTGLDLLVVDHLHIMPRAGRDEVAELGNTSRRLKNLAELNTPVVLVAQLNRGNT
KQADKRFNMADIRGSGAIBQDANI IIMPHRESYDGNENPSIAELILAKNRDGEKTVVCGWKQPMKFEZEPDLAWQAPKHEIDYDPYSV

SEQ ID 6401

ATGCAATATCAACAGCCCCGAACCTTCAAAATCAACATTCGGGGGGTGGGAACCAACAGCCCCGAAATGCAATATCAACAGCCCCGAACCTTCAAAACCAACATTCGGGGAGTGGGAATCA
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SEQ ID 6402

MQYQQPRTSKSTFGG#TNSPEMQYQQPRTSKPTFGW#INSPEMQYQQPRTSKSTFGE

SEQ ID 6403

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AACGCGCGCTTTTCGGGAAACCGAAATGCGAATGTTCCGCGCGCGCGCAAAACCCACGCGCTACCGCTTCAGGAAATCGCGGATTTGTACACGAGTTTGGGCGCGCGGTTGCCAA
CGCTCAAGTGCTGAACGACACGCGCAACCGCGGATTCGAACCGCTGCTGCGAGATGCTGGGAACCGCGCGCGCAACCGCAAGGTGAGGTTTCGGGACAAGGAACCGGTTTGGCGCTG
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SEQ ID 6404

LMKPSSESLRAAGRPJAYYPLAKPLGGVNAAILFGHPFYWDRKTYVESGIYRTABEIEITGLSVQEQRTARAKLRERGVLIETEKRIEHRIYKINLDAFDDMLQHSGGGEPTAPKCN
INSPELQNHSGGSEPTAPKCNINSPELQNHSGGSEPTAPKCNINSPELQNHSGSESTAVIRTEIDTETEDLAVYTPPLPNAENGKGLNADAFVSADBTGREGTGEPTSPKAESEDSMG
NGGLSGPKNANVPRRRKTHGVPLQBIADLYNEVLGRLPSVQVLNDRKRALANRWCEMLGTAAAPNGKVRPGDKETGLAWFAGPFRKVMNPFWMGENQTGFVGFDMFLKAGNPFVKILE
WHPPKTNQAARGRA

SEQ ID 6405

ATGAGCCGGGAACAAAGAAATACGCGGAGCCCGCTTCCCGGTCCCGCTCATATGACGGCGGAAGGCGCGGCAAGGCACGGGAAGCGTTCGACGCGCGGTCGAAGAAGTGAAGGGGTTG
ATGATGAAGCGTC

SEQ ID 6406

MSREQRIRGARLPVPAHMQABGAGKAREALDGRVEEVKGVDDAEV

SEQ ID 6407

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GAATTGAACCA

SEQ ID 6408

VTQLAARITDLEGRGFVFAKPKYKVGNCNPNVAHYSIAKSGIEP

SEQ ID 6409

TTGTTTGCATTCGCTTTGTTTTGATTCATAATCGCTTTCCCGTTTACCTGAACCGCTTCCCTGCAATTCAGGGGGATTACCGCGCGGTCGCGGTTTTCTTTATCGCGCGCGCTG
TCCGGCGGTCAGCGCTTTTCCGATTTCGCTCACCCGTTTACAACCGGTTTCCACACAACGCGCGACGGAG

SEQ ID 6410

LPALRLFLIHNRLSPLPELPCNSGGLPAPCGFFFI GRPSVRAVSRLSDLPSPRYNRVSTQRPTE

SEQ ID 6411

ATGCCGTCGACTTATCTTCATCTCGCCAAAGAGCTTATCCGCGAGCGTTCTATCCGCTTAAGCGCGAGTACGGCCAAAGGACAAGCGGAGATTTGGCGGTATTCTCCGCAACACTTC
GTCAAAACCCGAAAGATCGGAGCCAAATACCGATGACGAATTTAATCGGGCTGCTTTCCAAG

SEQ ID 6412

NPSDLSPILAKELIRSGSIRLSGTAKGAGELAVFIRTLRQKPESEPNDDDEYLIGLLSK

SEQ ID 6413

ATGAAGAGCAGGACAGAAACCGCTGTGGAAGAAAGACAGACGCGTGATTAAAAAGCGATGCTGAAAGCCGCCCAAGGGTCGGATGAGGTTTACAAATCGCGCGGTTTGAAG
ACGGCTTTGAATTACTTTGAAAGCAGCCGAT

SEQ ID 6414

MKQDRNLSKKDRRLIKKAMLAARAGCDEVYKIAPGLKDFELLGKQPD

SEQ ID 6415

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TCACTTATCTCGCGCTTTCGGGCAAGGCTGCTTTCGCTTCGCAACGCGCTTCGCAAGCGCGCGGTGCTGATGACTTCGTTGTCGCAACGACGCGCAATGCCGT

SEQ ID 6416

LLDSRLRGNDENRCKNSKFKKAIPLGLLFDYDFWIQTALADVDIRAGMQVAVQVDCGLSGFLLEDVLPFGHGLADTFLRRAGIAHFVQFDDVPALGRDRRADLSGFERVDGPFKGNHYA
VGKPAQVAIARACVLGISACQTCIRAVARLVDFADGTFRADGGVFAVGPNQDVLGAVLAQRCAFOQGDALFLRLLEGINFSAHAAVLHHCLLADFFGNDVVGKLAALGAEVPEGG
ILCDGIDFRFTCLNVAFAFARLYNQLVVDKLLHQLSGQLGFTTLRVPGCGGFGNGFGKPAVGDFVVGNDGNV

SEQ ID 6417

ATGGACGAACCAAGAGATTAGTGTGTTTTGAAAGAAAAATGAGCAGCGCGCTATCGCAAGAGGTTGGCTGCTCGAAAGAGTTTATTAATAAAATCGGTACCGCGAGCGAAAA
ACCCGCGTTATCAATTTGTTGATCTTTAAGGAGTTTATACAGAAAGAAATCAAAACCAACCCAAA

SEQ ID 6418

MDEPRDLVLFLEKEMSSAAIAKEVGCSEKFEINKIGNGERKNPRVQIVDSLRLSYRENQNPQK

SEQ ID 6419

TTGGCAAACTGGCAGAGTAAGTCAATCAACATCGCAGCGTTGGAATCGGTAAGAAATAAAGGCTACCAATATCGCAAACTTGCCAAAATTTAGATGTATCGGCTTTTGGCTTG
AGACAGCGCGAAGGCGAGCGAAGCGCGCCCGCTCATCAACCCGACCTGCCCGACGAGTCAAGACATCCACCGCCGATGATGTGGAGCAGCAACGCCGCTGCCGACGATGATTA
TGTTCCTGCTCCCTACCTCAAGAGAGCTGCTTCAAGGCGGGCGGGCGGCTATGAATCCCGACTACACCGCTACCGCTGCGCTTGGCAATCAACGTTAAGGCGCAAGGCGATC
AACCCGACACACGCTTCTGCTGACCCGACCGCGACAGCATGGAGGAAAAATCGCAGAGACGCGCAATCGCGTAGATACGGCGGAAACCGCCATACCGGACGGCAAAATATACG
CCTTTGCCCAAGACGGCATGTTCCGCGTCAATACCTGATACGGCAGCCCGCAACAGCGTGTGATACGACGACACACAGCGGCTTCTATCCGACGAAACCGCCCTTTGGACAGCT
GACCGTTATCGGACGGGCTTTTGGTGGACGCTGTTGGAT

SEQ ID 6420

LAKLAESQSTIAALESGRNKAATNIAKLILVSAFWLETGEGSRTPALINPDLPEHVKIDHRPMWSSNDPLFDDYVFPYLLKESCFKGGAGAYEIPDYNVRLFPFKSTLRRKI
NPDNVFCCTLTGDSMEKIAEDAAIAVDGTETAIKIDKIYAFADQGMFVKYLIRQPGNSVLIRSHNSGFYDETAFLDSLTVIGRVFWNSVLD

SEQ ID 6421

ATGCTGAACCGCTACGAGTGGCAGATTCTTCCTTTCCCTTTTGAAGAAGAGGACGGGAGCAAAATCTCAATCTCAAACTCAAAAACCTCTGTATTACGCACAAGGCTACGCCCTTG
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CGAACCGGACAAATATGCGGACGAAGAGTTGTTGCTTCAACCGTGTCCGTAAGAGCAGGGCTGCTACACCGCTTGGGCAATTACGCAATAAAACCCATCAGGAAGCGCGCTGGATACAG
ACCCGCGAGGGCGAAGTATAGGATTGCGCTGATGGGGAATATTTCGCCCATCGCTGCGCAGCAGGATTACAATTCAATCTTGAAAACTCAAAACAGCGCTTGAAGACAGCTTG
TCAGCGTCCCGATTTCACAGCGCGCAGACTTGAATAATGTTGGAGCAG

SEQ ID 6422

MLNAYDVADFFLSPFEEDEBQISNLKILQLLYYAQYALAILNRPLFAENTIEHQHQPVPVPCIVRTYKRYGGSPLPAHIEPKYADEELVVLNRVRKEQGCYTAALRNKTHQEPWIO
TRQGEVIGIALMGYFRHALPQTDYFNLEKILTAVEDSFVSVPHPNGADDEKWLQ

SEQ ID 6423

ATGCAGGTGCTGCTGGCGAAGACTTCAAAAGAGCTTGAATACTACCCCAAGAGGACCGCAGAAAAATTCGGAATTTATCGCACAGTCCAACAGAACGGCTTATCAGGGTTACCGG
GCAGGAACAAATCCAGCGAACGTTACCGGCAGACGATCTCAATGGCTGGAAAAAGTCCGATTTCGCCAACGGCACAACTTTGGCACTATCACATCGGCAATTCCTCAATACAGCGCG
CAGGTATGGCGATTGACATCCGCTATATCTTCACTATACCTTTGCGCAGCGCTTATCAAAATCATCGGTTTGGACAGACACCGCGCTTTTATCTGCCGATATTCCTCAAA

SEQ ID 6424

MQVLLGEDFKRALKNYPKEDRRKIAEFIAHVQNGLSGLPGRNKSNDVPPADPQWLEKVRFAQRHNLWHYHIGIPKYNGRGYDULTSAYILHYTLCDGFIKIIGFDRHPPFLLPDIK

SEQ ID 6425

ATGTTAGACAAATATCCCGCGGAAATCGAATCAAAACATATCAAACTGGGAAAGCCAAAGGCTATTTCGCGCCGATATGGATTGACCAAAACCGCTTTTCCATCAACTCGCGC
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CGCGGCTATCGCCAGCAATCTGTTGTCGAGCGTCACTTGGCGCGCAAAACGTTGCTCCGCTCAGCACTTGGGCGCGAAAAATCTTGGAAAAAGTGTGGAGTGGAAAAAGTTCCTCGGC
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SEQ ID 6426

MLDKYSPABIESKHYNWESQGYFRPMDLTKPSFSIQLPPNVGTGLHMGHAFNQTINDGLTRYRMKGCTAWIPGTDHAGIATQIVVERQLAQNVSRLDLGREKFLKVVWKEVSG
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SVIEPMLTSQNFVMSATPNNGEPDNEFKGLSLADKAKKAVDSGAVRFIPENWNTYTNQWNNIQDWCSRLQWNGHQIPAWYDEAGNVYVARNQAEAEKQAGTGLTREDVDLDTWFS
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SMGADALRFTMASYASLGPFQ

SEQ ID 6427

ATGGACAATCTGAATCCGAGGAAATTTCCGTGTTGCGCGAAAAATCTGCCGCTGTATTGCTCGGACCGGCAACAGCAGTGAACGGGCATCCGAGGTTGTTTTACTTTTGGCGAAG
GAGAATCGGCGAGCGTTGCCGTGCCGTAATGCGGCACCGCTTACCGCTTGACGGCAAGATGCGCATCATTAACCGC

SEQ ID 6428

MNLANPQEISVLPENLPLYCSGPDNEQWNGHPRVFLPLGEGESGVACPYCGTRYRLDGKMPHHYA

SEQ ID 6429

TTGCTGCTTGGCGGAGGCGACGCGATTGATCGCCCTGCTGCTGCTTTTACGCTTGGCCAAATCAAAACGCGCGCGCTACCGAAGAAATCCGCTTGAAGAAGCGCTGACCTTG
ACGACCGCGCAGACGCGCATAAAAATCACTTTGCCGAAGTCGAAATCCGCAACCGCGCAACCGCTCCGAAAAACGATGTAACGACACACTTGCTTTAGGTGGGAAATCGAAGA
AGAGTTATCGCAAAACAAACGTTGATGTCGAAACCGGATACGCTTCAACCCGATCGACTTGGATTTCGACAGCTTGGCAGCGCGCAAAACGCGCTTTTGTCCGCGCACTTACGCG
GATGAAGAAACCAAAACGCGCGGATGCCGAT

SEQ ID 6430

LLLAGGGTALIALLLLLLRLAQSKRRRTESVPEREPDLDDAADDGIKITFAEVETPATPEAPKNVDNDTLALGGESEELSAKQTFDVEITTPSNRIDLPDSLAAQNGILSGALTQ
DEETQKRADAD

SEQ ID 6432

SEQ ID 6433

SEQ ID 6434

SEQ ID 6435

SEQ ID 6436

SEQ ID 6437

SEQ ID 6438

SEQ ID 6439

SEQ ID 6440

SEQ ID 6441

SEQ ID 6442

SEQ ID 6443

SEQ ID 6444

SEQ ID 6445

SEQ ID 6446

SEQ ID 6447

SEQ ID 6448

SEQ ID 6449

ATGATGAAAAATCAAAGCCCTGATGATTGCCGCGCGCATTTGCTGGCAGCAGCCGATGTCACGCGCCACCGCAAAGGCAAAAAACGCGCGCCGCCAAAGCGGTCAAAGCTGCCGCCACGGGCGC
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SEQ ID 6450

MMKIKALMTAAALLAAADVHAAPQRAKTAAPAKAVKAAATAQKEAAPAQOQGGTRISDGIADVADNEVTNNRLAEAVAEAKATLPEDAQISESZLSRQVIMQJLVNQSLIVQAGKRRNIQAS
EAEIDAVVAQNPAKLNLSPTQRRLEADNTLAEKVRQAAVMQNSRVSEAEIDAFLEBAQKQGITLPEGAPLQRYAQTLLIKADSKNAAVGABSTIRKTYDQARNGTDFAGLARRYQDASA
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SEQ ID 6451

ATGAGCTTCCATCCCGAAACCGTTTATAACGGCGCGGAGAAACAGAGCCGTACGGACCAAGCCCCGAAGAAATCAAAATACCGGCAAGCCCGGAAACCGCGGATGACCG
AAAAACAGGCAGAGGCCACATTAAAGCATTATCAGA

SEQ ID 6452

MSFHPETAYNGGGETEPYGPSPERIKYRQSPETAETRMTEKQABGHKSIIR

SEQ ID 6453

ATGCCCTPGCGCGGGCGGCTTATCTGATAATGCTTTTAAATGTGGCCTTCTCGCTGTPTTTCGGTCAATCCGCCGTGTGTTTCGGCGGTTCCTCGGGCTTTCCGCGTAATTTGATTTCCTGGGGGCTT
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ATTTCAGATGCCGCTCTTCCAGCCAAATCTCGGGGCTCAATTCCGCAACCTGCGCGTCTCTT

SEQ ID 6454

MPCAAALSDNAFNVAFCLFFGHPPCFGGFRALPVDFFGANSVRLCFSAAVISGFGMEAHSLPSGTSASPC¹⁰⁰TRQPASSSAFRCR¹¹⁰SSSQISALNSATCACP¹²⁰

SEQ ID 6455

TTGCTTTCGTCTTTCACACTTAAATCAATGACATTTTCGGTCTCCTGTAAAGGTCGTTTCGTCTATCGGTCTCGCGCTGTTTTATGCCTTGCGCGCGGGCGTTC

SEQ ID 6456

LLSFTLKINDIFGLLLKVVSSIGLALFYALRGGVI

SEQ ID 6457

TTGATTTTAAAGTGTGAAGAGCAAAAGCAATTTCAAACCATGCCCGGACGGCAGCCATCAGCCACCTGCATCCGCATCATCGATTTTGGGTACGCAGCTCGTCGAGTACCAAAACGAAACAA
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GAGAGGGCGCGCGGAACACCCCAAGGCAATGCGCGCGCTGCCGGAAGCATCAGGAGCAGCATCCCTTTTAAAT

SEQ ID 6458

LILSVKDESNFKPCPAGSHATCIRIIDLGQOLVFEYQNBQRQHKILVQWEIDPEGDPMLMPDGRPYLISRRYTASLHKSQSLATDLKSWRGDFTPFEERDNFDLNLWLGKPCLLSTIAHQ
ESSDGKTTYANISAI SNKMSYTPPKHPDNVFAFDLSDPDMANYGLLNEKLRBQIAKSPEYAEAVNGRQPPAPPQKQAQAEAGRPEHPQGNAAPEADIEDDIPFN

SEQ ID 6459

TTGCAACTGCTTCGGGACGGCAACAGAGAAAGGAAAACAAAAATGGCAAAATCGACCTTGACCCAAATGGGACGGGAAAACCATTTGGCGCCGCCCAATCCCGAACAGGGATACATCAACA
TCACCATCGGCAGCGACGACCTATTCAACAATCTGAACAGGCATACGCCATACACGCCCGCGCTTGGCGAAGCGTGTGCCGAATATGAGGGGGGGGCACAA

SEQ ID 6460

LQLLRTATEKGNKKMANIDLTQWDGKTIGAAANPEQGYINITIGSDDLFINIBQAYAIHAALGEAVAEYEGGAQ

SEQ ID 6461

ATGACCGCCCTCACACTCTACCGGTGCGCGGCAGACGTACAGCGGGGCTGGATTACTACTTTGACAGCGAAACGAGCGCGAAGACACGCTGGAAGCCGTTATCGGGCAGTTTCGAGGTCA
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TTAGA

SEQ ID 6462

MTALTLYRCAADVQAGLDYFFDSETEREDFLAEVIGQFEVRAQSVIAYIKNQEITEKMLEGHIRQMTGKLKAAKARVQSLKDYLRNNQAAGTTEIKADDGTFKASFRKSEAVVILDEAQI
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SEQ ID 6463

ATGAGCTATTTTGGAAGATGTAAAAAACCCATTAAAGGTAATAGATAACTTATGCAAAAGACCA'TTAAAGAGCC'TGAATCGTTAGAGGGTTATATATAGACGAAAATTAGGGATAAAGCAGACG
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SEQ ID 6464

MSYLEDVKNALRVIDNLCKEALKEPESLEGYIDRDKADEADTSLEFLKDVINYGISDLKNVIEVFEDCV

SEQ ID 6465

TTGATGAACACCGAAAACCAAGACTGCGGCTACGGCGCAACCGTGCCGAACCGCGCGCCATTCTCTCCCGATATGTGGATCATAGGTCGTGAATCAGACCATCGAGCAGGTTACGC
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SEQ ID 6466

LNNTENQDCGYGATAAEPRGHSFPDMWIIIGRLNQITQEVQAYETTRFDLAAETLYSFWWNDYCDWYLELAKVQLQTCASRQRATRTHTLLRVLEAALRLHPIIPFITEKLMTVAPMCD
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KLOKALDKLNKLSKPGYTEKAPAHLEVKDKADLAEEDKMAKVOMOLAKLRD

SEQ ID 6467

TTGATTTTCCTTTGCGTGGTTGGCGTGCGCCATTTTACGCCATCGGCAGGCTAAAGGATATTTTCGGCGCAAAGCCGCAATCCGCTATAATCCCCACTTTTCAGACGGCATACCATGACT
GCGCTACCCCTTC

SEQ ID 6468

LIFLCVVGVPRPFYAIGRLKDIFGAKPOSALIPTFOTAYHDCAYPS

SEQ ID 6469

TGGCTCGTTPATTTTTCACCTCAAACCACCTGCTGCTGGCAITGGGCTTCTGTTTCGGCACGCATTCGCGCCGCGATACCGTTGCGCGCGAAGAGGCGGACGGCGGTGTCGACAGAAAGCGGTGCGACGGGCGGTTCGGAATCCGCACAACGCTTCGCGATTTCACCTTCGGTTTCGACCTGCTGTTTTCAGTAACGAAAGCGGACGCCCCGAGAGAACCGAAGCCGCGGTCCAAGGCAGCGCGGACGATCCGTCGCCGAGCATATACGCGCATTTGCGCGACAGGATGGAAGGACAGTTCGAGGTTTAAGGTGCGCGCGGAGGAAGCGCTTATCATCGAACGGGACGGCGAGTCTCTAATACCGATTGGGCGGATTACGACCATTCGGGCGACACCGTTACCGTAGGCGACCGGTTTCGCCCTCCAACAGGACGGTAGCGTGATTTCGGGCGGAAACCCCTGACCTTACAATTCGATCAGCAGACCGCGAAGCGCGACAGCTCCGTTGTAATCGCAACGAAGCGGACCGGCTGCAAGCGCTACGCGCGCACCGCGCGAAATGTTGGGCGAAGGGCGGTTACAACCTGACGGAAACCCAATTCAACACCTGCTCCGCGCGAGATTCGCGGCTGGATTCGTAATTCGAAGCGGCTCTCTGTCGAGCGGATCGGGGAAAGCAGTACGGGCTTGCCAAACAGCGCGCTTCGTGTTTCGGCGGATTTCCCTTTCTCTATACGCCTTGGGCGGACTTCGCGCTTGACGGCAACCGCAAAAGCGGACTGCTGCTCCGTCGTTATTCGCGGTCGAGCGGCGCTTCCTTTCCGTCGCTTATTTCAACCTTTCGCCCTGCTGATGCCACTTTTCGCCCCCGGCAATTATCGCGGAACCGCGCGGACGTTTGACGGACAAATCCGTTACCTGCGTCCCGATTACAGCGGACAGACCGACCTGACCTGGTTGCCGACGATAAGAAAGCGGACAGAAACAACCGCTATCAGGCAAAATGCGACGACCGGACGACATTTCGACACGCTTCAGCGGGGTGTCGATTTCAACCAAGCTCCGACAGCGGCTACTACGCGGACTTTACGGCGGCGAAGAAAGCAATCGCCGCAACGCTCAACCTCAACCGCGCGCTATGGCTGGATTATGTCGCGCAGGGCGCGCGGAGGACCGCTGAATGCCCGCTTTTCGGTTTCAGAAATACCAAGCTGGGCAACCAAGCGGACTACAAGACGACCTTACGCCATCATGCCCGCCCTTTTCGCGCGATTCGCGCATAAAAACCGAGGCGGCGCAAAATCGCGGTGTCGCGCACAATTTACCCGCTTCAGCGACGAGCGCGCGCAAGCGGACGACCTGCTGTGTATTCGCGGTATCAATGGGATTTCGACCAACGAGCTGGGGCTACGCTCGCCCAACCTCGGGCTGCAAGCCACTTATTACAGCTCGACAGTTTCGGCGGCAAAAGCATCCCGCAGCGCTTCGGGCGCGGTTTTCGCCGTGTGTCAATATCAGCGGCGCACCTATCTGCAACGCAATCGCGCTGTTCGGGCGGAGTCTGCGCAAACTATCGAGCCGCGCTGTCTCACTATATTTCTTCGCCAAATCTCAAAAGCAGCTGCCAAATTCGATTCTGTCGGAAGCAGCTTCGGCTACGGGCGGACTTTTCGCGGAAACCTCTATTACGCGAACGACCGCATCAACGCGCGCAACAGCCTTTCCACGCGCGTCGACAGCGGTATTTTGGACGGCGGACGCGGGGAGGAGCGTTTCGCGCGCGGTATCGTGCAGAAATCTATTTCAGGATGATGCGGTGATGCTTGACGGCAGCGTCGCGCAAAATCCGCGCAGCGCTTCGAGCTGGGTGGCAITTCGCTTCGGGCGCATAGCGGGCGTTTCACCTTCGACAGCAGCATCCACTACAACCAAAACGACAAACCGCGCAACATTACGCGCTCGGCGCAGGCTACCGCGCCCGCCCCGGAAAAAGTTGTAACGCGCCGCTACAATACGGGCGCAACGAAAAAATCTACTCTCGAGCGGACCGGCTCTATTTCAGCAAACTCAGCGAGCTGACCTTCGCGACAAATGCGCGCTGACGCGCAACTCTGTCGCCGCTGCTCCGCTACCACTACAGTTTCGTTGAAGCGCAAAAAACCGATAGAAATGCTTCGGGTGCAATAACAAGACGCTGCGGCTGCTGGGCGCGGCGGTGTACGCGCAACCTGCTTATCGGCGGAAACCACTACAACAAACGCGGCTTTTTTTCACCTTCAGTTGAAGACCTCAGAGCTTCGCGAGAAACCCCGCAGGCAGGATGGATGTGCGCGTTCCCGCTACAATCCCGCCACTCTCTTTTCGCGCGGACGCAACAAACGGGCC

SEQ ID 6470

LARLFSLKPLVLALGFCFGPTHCAADTVAAEADGRVABGGAQGASEAQASDLTLGSTCLFPCSNESGSPERTEAAVQSGSEASVPEDYTRIVADRMEGQSKVKVRAEGSVI IERDGAVLNT
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TFWADFPIDGNRKSGLLVPSVASGSDGVSLSVPYYFNLAENFDATTFAPGLI GERGATFDQGIKRLRPDYSGQDTLWLPDHDKSGRRNRYQAKWQHREHDSIDLQAGVDFPNQVSDSGYYRD
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DDAPGQDGSVGKPNR.SRSDVWFAAGGIGGRTFLDSSITHYNGNDRAEYHAYVPAQPKFVNDLMAKRYKGLWYKNEKYLQADGSYFYDKLSQLDLSAQWPLTRNLASVVRYNYNGFEAKPFI
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SEQ ID 6471

TTGACGGCGCGTTCCTGCCCGGTGATTCCCTTCCGCCGCGCGTTTGGCGGCAAGCATCTGTTTTCGCGTCGGTTTGTGTGCTACTGTTTGCAITTTGTTTTCTCGATTTTTTGATGCCGTCTCTCAATGCCCAATCATAAAGCTGTAATCTCTCAGAGGTGCGCGGAATTTAAAT

SEQ ID 6472

LTARSCRVDFAARLAASICFAVG FVATVCILFSRFFDAVLSMPNHKAVSLTRSPNLN

SEQ ID 6473

ATGTTGTCCTGGCGCAAGGTTATCGGAAGACGAAGCCCTGACGTGCGGCATCATGATGCGGCTGTCCCTGCAGGATATGCGCTATGCCGTGCAATCAGGAATTAATCAACTTCGCGCAACATA
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SEQ ID 6474

MLSGAKVSEDEALTCGIMRLSLQDMRYACNQELINFAEHIVKQVQRGLGYNFTDDPANGESVLFPACREASQAVAQWTKDFDNLSPNQRLVLRPLSNLPAAYEFLKDAFARLIAEVSAY
SLAVRVAKKAMAFLELDGLI SAVGKVNGADSRABARRLKMPYAEFTGRIILHAANLLYDVGIGADKELSAMYGKPLNPNVRPRISDVRPMMKMLVADKGGALVRAVKDSSEDEVIRKHCNG
AGFSCFNWTEHPKRTANLISLHRRAAA

SEQ ID 6475

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SEQ ID 6476

MRTHIRTCVUHDGSGTKGSNTASGISGTAAGAAEQAFFSAAKTANRASAASANAPHPDKPKNGRKPMTFQGHNNRKKAGGYAEYITGGELRLLLQQTACRFKAALETAANKHYVRAIKES
PVPDAEARRRKKQAA

SEQ ID 6477

ATGGTATAGCGAATACCTAGACCCGAGCAATGCGCAGATATTTTATCGTAAAAAAGCGTACATTTTATAGACGGGTACGCACCCCGTCCGGATTTCCCCCGCGAATATCGTATCGAAGA
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SEQ ID 6478

MDSEYLDPOCCADILSVKKRTFLERYAPRPDPARISVSKKRFWKKKEEVEGALDROKEKRPIM

SEQ ID 6479

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SEQ ID 6480

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SEQ ID 6481

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SEQ ID 6482

LGMPAALIKDFLLTQGLKPLDEVRAAYLTAQTVMDMNASIDRSVLCNDEGWLADYLPCDDVREDALKRLFMALDSVTSRSTGVRSAAYVYALMPSENAALRLVCLSQQEGLENIWQ
DGNITDVSLSACRSAQSGMMNVASDVRRNLNLGELSGERNHASAAQISIPVCTESGGVLGVVHVEFBCAECADTAAQAENVALALALEPLKQLLIGITAABGDENV

SEQ ID 6483

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SEQ ID 6484

LSENKRAKIAPQVGLFVRIVFIVTRNARILLCNKPN

SEQ ID 6485

GTGTTCTGCAAGCAGGGCGAGGCTTGTTCGGCGGCTCTGATGATGCGCGCTCCACTTCTTCAAAGCTCGGGAACTGTTCGCGCAGGATTCGATGCTGCGCTCCGCTCGCGCGAGGCTT
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SEQ ID 6486

VFCQGVVLFGGVVCAVPPFKVGEFAQGFVCAVSGVERFDGFAVLVVEGFGVQDFRHFDFPAAQAVGKRAENVFAVAGGDKLYEAAFPDLAVEVAECQORVLVVGAGGFFVAGLG
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SEQ ID 6487

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SEQ ID 6488

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SEQ ID 6489

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SEQ ID 6490

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SEQ ID 6491

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SEQ ID 6492

LIFMIFSIIVPIYVNEKYLRCCVSVLAENFADYEMILVDDGSPDGGCKIDCEYAGKYPHIRIVPCVTP

SEQ ID 6493

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SEQ ID 6494

LIYPIILRRYANDYPIMRIFACIFVANLPAAVRRTVIDQNHFIIGKIPGKHGIIHAAKVFFHTVNRDDRENHXYQYVVLRLVCLKPALAMRLHPHPAT

SEQ ID 6495

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SEQ ID 6496

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SEQ ID 6497

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SEQ ID 6498

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SEQ ID 6499

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SEQ ID 6500

LIAAPTRNPSETANGLQTASSSTVIPAQAGIQNVGQRQYSKAV

SEQ ID 6501

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SEQ ID 6502

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SEQ ID 6503

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SEQ ID 6504

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SEQ ID 6505

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SEQ ID 6506

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SEQ ID 6507

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SEQ ID 6508

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SEQ ID 6509

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SEQ ID 6510

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SEQ ID 6511

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SEQ ID 6512

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SEQ ID 6513

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SEQ ID 6514

SEQ ID 6514

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SEQ ID 6515

SEQ ID 6515

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SEQ ID 6516

SEQ ID 6516
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SEQ ID 6517

SEQ ID 6517
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SEQ ID 6518

SEQ ID 6518
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SEQ ID 6519

[illegible]

SEQ ID 6520

SEQ ID 6520
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SEQ ID 6521

SEQ ID 6521
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CAAGCGAAAAACGACGGGAAGGGAATATCTGAACTGGTCGAAAACAAGGCAATCAAGAAAGACAATAAGACATCAATAAAGCATCATACAAATTGAATGTCGCGCTGTACGGAACAGGGA
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CGCGGGAATAATCTCCGCGACGCGCAGCGATTACCGCGTGGGCGGTACGCGAACCCGATATATGGGGCTTTGCGCGCGCTTCAACAGGACGGGGTTCGCGCATAAATGGATTCAATACAAA
GGGCTGATGCTCCGCCACCCTCAATCGTCTACGCTTCCGAAGACTACGTCGCGACGCGCAAAATCTTACGCGAGGGCGGCGAGTGTATTATTCGCGCTGGCTCAACCGGGAAGCAGGGCT
TATTA

SEQ ID 6522

SEQ ID 6522
MSNGARWTVTND~~SL~~KELDLSEDAQVEPSDNNKPKVSVSKLKG~~GG~~VFKMYGDIVKGESDKLITRKGSE~~TH~~IIEYMDDAKARTTGREYIKLVENKGNQEDNKASNKASYKLNVC~~TE~~QG
GWC~~F~~ALGESGASKVNI~~ST~~DGRDFLYLPD~~LT~~PPGASSSVLFG~~EAL~~YQLNAVSD~~ET~~LVQRNGEIHADGMPQEDANNWIKRVGGKFGSGRSDSYRVGGYGNRYWGFGAGGPNRTGFGDKWIHYK
GLMLRHL~~OS~~SYASEDYVGS~~G~~KILRQGGRC~~L~~FLRLAQPGKQGLL

SEQ ID 6523

SEQ ID 6523

TTGGTCGGCAACATCGCCCGATATAAGGGCAGCTACGGGGTACCAATTACGCGGGCAACGGGTGCAATCGGACGAGCGCGCCTGAATGCCTATATGCTTTCCGCGGAAGCCGGTAGGC
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ACTTTCGCGACGCTGTATGGGGCGGTTACGGCTTTCCGGCGGGCGTGGACGGTTTGGACGGCGGCGAGCTGAACATCTACGCGAAGCTGATGTCAAAACGCGAGTTTATTCGGCACGATCCGCCA
CAGTTTCAACGGCTCTGCCGTGGAGGAATCAACAACCGGGCGGCTGGTTGGAATACGGCTTTGGCGCTGTGTCCGCCAATGCGCGAAACGGACGGCAGCTTTATTT

SEQ ID 6524

SEQ ID 6524
LVANIARYKGSYGLTNYAGKRVESDEARLNAYMLSAEAGRMERQDGGKNSVAAGSAVLLVYARLRLSAVKRAVCRDQLPQPDCAVRLSGGRGFRGQRQAHLRQADVQTRVYRHDP
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SEQ ID 6525

SEQ ID 6525
ATGCCATATATGCTTTCCGCCGAAGCCGGTAGGCGGATGGA AAAACAAGACGGCGGCAAAAACCTATCGGTGGCAGCCGGAAGTGCAGTTGTCTTACTGGTTACGCGCGGCTACGGCTTC
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GTACAAACCGCGAGTTTATTCGGCAGATTCGGCCACAGGTTCAACCGGCTCTGCCGTGGAGGAATTCAAACACGGGGGCGGCTGGTTGGAATACGGCTTGGGCGTGGTGCGCCGAATGCCGGA
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SEQ ID 6526

MPICPPKPVGGWKNKTAATYRNQPEVQLSYWFTGYPPLSNGLSABTUNFSLMGRFGFRAGVDGLDGGRLNLYGKLMYKREFIGTIRHRFNGSAVEEFKHRGGWLEYGLGVVRNAG
NGRQLYFEAQRSSMHTMRQNMVNHGVRSMF

SEQ ID 6527

TTGCCGCTTTCATAGTTCCCGCTGACCGGAATGACGATTTGGAAATACCAGAAACCAAAACAACTGAAACCGAACAGCGCGGATTCGCCCTACCGCGGAATGACCGGG
GGCGGATGCCGTC

SEQ ID 6528

LPLSNGLSRLHNDLEITRNPKTTETBQAGFLRGNDGADAV

SEQ ID 6529

GTGGGCTTCAGCCACCGCTTCAGACGGCATCCGCCCCCGCTCATCCCGGTAGCGGGAATCCGGCTGTTCGGTTTCAGTTGTTTGGGTTTCGGGTAATTTCCAAATCGTCATTCC
CGTGCAGCGCGGAATCTAGACCATTTGAAAGCGCAATATTCAAAGGTTAGCTGAAGCTTTAGAGATTCTAGATTCCCGTTTTACGGGAATGACGAAAGGTTGCGGAATCCAAACCAT
GAGCAACGCAATATCAAGATTATCTGAAAGTTTGAAGTTC

SEQ ID 6530

VGFSPPLQATASAPSPFPRSGNFACSVSVVFGFRVLSKSSFFCRRESRPLESGNIQRLAEALILDSRFHNDERLRESKPLSNSNIQRLSESLRF

SEQ ID 6531

ATGGGTGCGCGGTGATGAATGTTGATTTGACCGCAACCGCGCGGAANTGCCGTCTGAAGGCAGATTTTGGCTTCAGACGGCATTCGCTTCAAGACTGACCGGGA

SEQ ID 6532

MGRVRMKHIVPQPAEMPSEGRFCVQTALRPFKTRRG

SEQ ID 6533

GTGAGGCATGTACGAAAGTGGAGTGAAGCAACTGTATTTCCACCCGTCGGGCAAAATACCAAACTCAAACTAAGCCGTCGGAATACCGTTTTCGGCGGTATCGTTGCGGCAAAA
TAATCAGCATCCGGCATTCGATATCGTCGCGATTTGCGCATACATGCCGTAACGGCAACCTTATACGGCTTACCTTGTATGCGCGGATTAACAAATCAGGACAAGCGCGCGCGCG
CAGGCAGTACGAATGTACGGAACCGGTTGCGCTGGTCTGGCGCGCT

SEQ ID 6534

VRHVRKSEKQLYFPFRRAKIPKLSSRPNTVFGGIVCGKIITHPGIRYRQFAHTCENGLRL/LVWRINKNQDKAAGRQYQYWTGSPGAWAP

SEQ ID 6535

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ACGCCATTGCCAAAGCGGTGGTATCAAGACAAACCTTATCGCTACTATGATGCCGCCAAACACTGCTTGGATTGGGACGGCATGATTGAAGATTGAACCAAGCGCAAAAGGCGGACAT
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SEQ ID 6536

LRLFPARVQRKIGKPELSSVPIKEQAMFFKHLIAPADPILGLGEAFKAETREPKVNLGIVGYDKASGATPIVKAVKAEKRLLESETTKNYLTIDGVADYNBTQILLFGKDEHIIASR
RAKTAQSLGGTGALRIAFAKRLQAQTIWISNPTWPNHNAIAKAVGIDKPYRYDAAKHCLWDGMIEDLNQAKGDIVLLHGCCNPTGIDPTPBQWETLAKLSAEKGLPLDFAY
QGFNGLEEDAYGLRFLKHNTELLIASSYSKNFGMYNERVGAFTLVAEDEETAARHSQIKTIIRTLVSNPASHGANTIALVLKNDLKAQWIAELDEMGRIRKMRQKPVVELLKARGST
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SEQ ID 6537

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GATATGCTCGCGCGCAAGCAAGATGTGCGCAACAGCCATTTTCGATGCGATGGTCAACCAAAATCAAGCTCAAGAGCGCGGAAGTCTCAAAATATGGCTGGCGCAACAAACCG
CCTTTCAGCGCAAAAGTCTTGCAGCTTACGAATCCCGGAAAGTCAAGCGCGCGCGCGCAAAATGCAGGAGCTGACCGAAACCTTCCAAATCGACGGTACCGCCACGGTTATCGTCCG
CGCAAAATATAAGTCGAATTTGCCGATCGGAGTCCGATGTAACCATCGACCTTTTGGCGGCAAAAGTACGTAAGAACAAAGCGCGCGAG

SEQ ID 6538

MKSRHLALGVAALPALAACDSKVQTSVPADSAPASAAAAPAGLVEGQNTYVLNPIPOQAGKVEVLEFFGYFCPHCARLEPVLKSHAKSPKDMYLRETHVVQKEMLEPLARLAAV
DMAAESKDVAISHIFDMVNVQIKILQEPVLKWLGEQTAFDGKKVLAAYESPESQARAGKMQELTETPQIDGTPPTVIVGGKYVEFADWESGMNTILLADKRVREBQRAQ

SEQ ID 6539

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CGTCCGCTGCAAGTTCGCGCGGACCTGTTCAACATCCCGCGCGCATCGCGCGCGTCCGTTCCAGCGAATACCTCGAATACCTCAGCCCAAGCTCGAAAACCAACGAAACCGCAGCTT
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GCAGGCGCATCAGCGCATCAATGGCGGAGGCTGCGACATTCGCGCGCTGCTCGCGCGCGGAGCGGCAACCAATTTATGGGACCATACCGAAACCGTCATCAAGACGGTGACCA
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SEQ ID 6540

VKILLINGQVSTVAQNLAATWNVVIDIDEKALQETGSRLDVQTVFNGASPTFLERAGAEADLLALLSRSEDTNIVACKVAADLPNIPGRIARVRSSEYLEYLSPKLENNENGSL
SIFGTETISPEQVTEQLAGLIDCPGALQVLRFPADRVNRVVIQARRGGLLVGRSADIADQDPDAGDCQICAVYRNRLIVPAPQTVIIEGDEILFAAAENI GAVIPBLRPKETSTR

IMIAGGNGIYRLAKQLEHAYNVKIECRPRRAEWIAENLNTLVLQGSATDETLLENEVIDEIDVFCALTNDDSENIMSALLAKNLAKRVIQIVNRSYVDLLBENKIDIVVSPHILITI
GSLIAHTRRGDITVAVHPIRRGTAEAEVVAHGDKKTSATIGRRISGIKWPEGCHIAAVVRAGTGTIMGHHTETVIQDGDHIIFFVSRRLINLEKRLIQVKGFFG

SEQ ID 6541

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AACCGCGCTCTTGGGCGATGATCGGCAATCCGAGCGCGCGCGCCACCTCGGAAGCCATCGCGACAACAAGCGCGTGATCTCATGGCAGTCGCGCGCGCGGCATACCTCGTGGCAAA
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SEQ ID 6542

VASWKTGVDLLNGKILITGRDAHKLRLVNLDKGEELPVDFTNRLIYYVGPVDFVGEVVPAGPTTATRMDFTRQMLKQTLGLLMIGKSERGAATCEAIADNKAVILMAVGGAAVLVA
AIKSSKVLAPPELMEAVVEFEVKMPVTVAVDKSGESIHATAPRWQAKIGIIPVES

SEQ ID 6543

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ATCGAGCGGCACTCTCGCTTTGTCGAGCATATTGACGAGCGCTTTGTGCGCGCATCGCGCGCGGTGAGGATTTTGGCGTTCAACAGCAATACGTCGCGGTTTCCAGCTTGGCCAT
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SEQ ID 6544

VDGFAPAVHGDGYGHIPDFKPVNGPHTQFGERQDFGRDFGFCHEVCRAADCHEVHGLVVGDFAGGRAALGFADHAQEAQLFEHLAGKFVHAGGCGRTCGTDDFIADRIDGADVNVQAVGE
IDGQLLAFVBEHIDEAFVRGIAAGEDFAVQQYVAGFPACHFFFGQLIDIDAFVAVGVSQIGSVFDDARRREFDRT

SEQ ID 6545

TTGCTTCCCGTACAACCGCTGGCACTATTTCAACCTGATAAAAAACAGCCTTCAAAAAGTGTGTTTAAACAGCAGCAGACACTTACCGCCACAACTTTGAAAAGGAACACAATCATGA
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ACACCAAGACACAACCCCGCGCTATCCACATGAGCATCTGCGCGCGCGTAAAGTCGAAGTAACTCGCGCGCAAAAGGCGCGCTCTGAAAACAAATCCAACTCGCTATGCTCAA
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CGGAAGAAATCCGTGATGAGCCACATCGACATCCAAGAAATTCAGGAAAAGCGCGCTCGCGCGGGAATTTGCCACCAAGCGCTCGCGCTCGAACTCTTTGAAAAGGTCAACCGC
TGGCATCGCGCGCAAGGCTTGGCGGTCTGACACCGTGTGACGCTGAAAATCTCGATTACCGCAACCATGCCCTCCAAACCGATTGCCATGATCCCACTGTGCCGCCACCG
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SEQ ID 6546

LSSPYKRWHYFNLIKNSLKQGLKQQQTLTATTLKRNITMTVIKQEDFIQSICDAFQFISYHPKDYIDALYKAWQKEENPAKADAMTQILVNSRMCAENNRPIQDGTIATVFLKVMIV
QNDADMSVEKVMVNEGVRRAYTWEHNTLRASVLADPAGKRQNTKDNTPAVIHMSIVPGKVEVTECAKGGGSENNKSLAMLNPSDNIVDWLRTIPTMGAGWCPGILGIGIGTPEKAVLM
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SEQ ID 6547

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SEQ ID 6548

LFINRSTHNCILLISPYRKATGDKYQNPNTVFF

SEQ ID 6549

TTGATGAATATGAAAAATGGATTGCCCGCGCCCTTGCTGTTCCGCACTCGCGCTGTCTGCTCGCGCGGTGAGGCAAGATGCCGCGCGCTGCCGCCAACCCCGCAAGGTATCC
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SEQ ID 6550

LMNKKHIAALACALALSACGGQGDAAAAPANPKVYRVASNAEAPFESLDSKGNVEGFDVLDLMAKAGNFKIEFKHPWDSLPALNNGDADVMSGVTTIDDRQKSMDFSDPY
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SEQ ID 6551

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SEQ ID 6552

MPSENQVSDGIFDTGLLRGLFFTYFVRQKVDGVHTGLPVGKDFDIFAADNRGRFTDLEGFQQLHFAGARLTPGGFVGGKDFPVGKGLFAQPFDFRLLQLDLVDHRIENMAVRHI
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SEQ ID 6553

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SEQ ID 6554

LYGSRRLPCAQTDADGAQKKTAAAYKGQDPAKVHYLTTRPAGSDCQRVCPDETGFDRRLFRPYARSLKGMAKARISGRYRRLSLVSAQADNRPIAPVVQNTVAGVFFEARFQCCLLPA
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SEQ ID 6555

ATGGGCAGTATCGAACAGCGTTTGGGAATATCTGGAAGAAGCAACGATGTCTGCGTATGCGAGAACCGTCTGTCCACCGCTTCAAAGCCCTGATCCGCGCCCTTCCCGCAGACACCG
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GGAACGT

SEQ ID 6556

MGSIBQRLEYLEANDVLRMQNHVLSAFKALIRALPADTARIAVESIQLEPEDALAEISYEDSPHTDLPHDVTYAFPREKER

SEQ ID 6557

ATGATGAATCCTTATGAATCTGTTAAATGCGCCATTATATCAAACTGCGCTTTGGGCGCGGGTTTGGCCGCTGCAAAAGATTAAAGAACCGGAAGCCGAAAAATGGATACAAACAATCAG
GA

SEQ ID 6558

MNPYEVSKMRHYIKLRFGGFARLQRLTGSRKNGYKQSG

SEQ ID 6559

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CGGTCCAATCAATATCTTGAACCGGAAAGCGCTCAACCGCGCGAAGTGTCTGCGTGTCCGAACAGGAGCTGACCGAAGCGTTGATCAACCGCTGCGCCCGCATCTGACCGATACCGT
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SEQ ID 6560

MDTNQDKPNWSEKLENLRTTRMTAPAYVLPTRPSEVGKEEPIKLLDANRDRVLKAYLKKWQEEHNSAVADCGEEVETDPMIVLQENWLNQAASLQMPVSEKHISRRIRFADAKD
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KILNDIKYELKYR

SEQ ID 6561

GTGACCCGTTGTGTTAATTATTAATATTTTGGCGCTGTTCCATGAGGCTTTCAAGTCGGACGGGCAGGAAAAATGCCGTCTGAACACGGCTTTCAGACGGCATGGCAATCAGCGTTTGTAT
TT

SEQ ID 6562

VHPLFNLLIFCACSMRLSSRTGRKMPSEHGFTAMQSAFVF

SEQ ID 6563

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ACCAAAATTCGCGCATCGGAGTGAGCGCGGTGTGCGCGACTGATATAAATGAATGGAAAGCCGCGCTCAAGGCCAACACCAAACTGCTGTTTGGAAACGCGGTCCAAACCTTTGGGCGAAG
TGCGCGACTTGGAAAGCTTGGCGGAATTTGGCGCACGGCATCGCGCGCTCTTGTGGTGGCAACAGCCTGCTGTGCGCGCTGCGAGCTTTGAAACACGCGCGGATATTTCCGT
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TGACTACACCGGATGCGCGACCATCGCAGCGCGAGCTTATCCGAAACAGCAAAACGCGCGCGCATGTCATCGGTTTGAAGTCGCGGACCAAGCAGCGCGGTGGAAGTCGTGGA
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GTGCGCGCTGTGCGGTGGAATATGTTGGCGATTGATTGACGATTGGAACAGGCACCTCGCGCGC

SEQ ID 6564

MSKLLHPQTLAIRGKEITGYREHQAFLTSSFMWDNAQAADLFSKKIKGTYTTRANTPIAEPKRIAALEGAERAVATSGMSAIQAAPFTFLQAGDHVSSRLFGTIVGVFINNV
TKFGLGVSRVSPDINENKAAVANKLLPLETPSNPLGEVADLEALAEALHIGALLVVDNSLLSPVGSQPLKHGADI SVSSATKAIDGHRVGGVLAGSEELMAQVAVYCNCSGLAHS
PPNAHQLLSGVETLSLRMEQFDNALRIAQLBQPVQVAVYVYTGLEDHPQALIRKQNGGIVIGFEVDAQAAWKVVELFSRTANLGDVRSTTINPMTTHGRMQPEKLAAGIRPGL
VRLSVGLEYYGDLIDLKQALAR

SEQ ID 6565

TTGCGTGTTCAGAGCGCATCGCGGAAAAATGCGCGAGATGCGCTGAAACCTTATTCGCGTATGGCATACACATCAACAAATAGGAAAAAATATGGA

SEQ ID 6566

LRVSDGIGGKMRQMPSETLIAVGIHINNRKRYG

SEQ ID 6567

ATGGATGAAGCGGTTTTTGGCGATTGGCGGTTGAAAACTGCGCTGACCGGTTGATTATTTTTTGGGTTTTATCGTTTGGAAATTTGGGCAAGGATCCAAAGCGGGCAAAATTCGGCATCG
CGTTTTGTTTTTGGGCTTGGGTGTGTTGCGTTTGTGTTCAAAGAGTTATGATTAAGTTTTTGGTATTTGCCCAA

SEQ ID 6568

MDAVFADWALKICITGLIIFLGFIVNWLKESKAGFGIAVLVLGLGVFGFVKELLIKFLVLPLK

SEQ ID 6569

TTGCGGAAAGATGATTTTTTTTGTCTATAAAAAACCGCACCTTAATCAGTTGGCGGTTAAATCAAACCTTTAGGGTGCAGATTCTTTTTATGATTCAGACGGCATTTTCGACAGACGGC
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SEQ ID 6570

LRKDFYFVLIKTRTLISRLNQTFRVQITFYDFRRHFDRRTYLGNTKRLINNSLNTKPNTPKPTKNTKAMPNLPALDSLKPQFTIKPKRIKPVQIFNAQSARTASSIFPPIVDVYAI
RNKGRFRLPHPSADAV

SEQ ID 6571

TTGGTGGAAATCCCGAATAAGCGGTTCAAAACGTGTCGCTCCCGCGGCAGOCATATACAGTTGGCAACTGTCCGGTTGTGCCGATGGGTTCGCCCTGCCCTCCCTGAGCTAGCAACGGTT
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CCGCCCGCGTCATCCCGCATAGCGGGAATCCAGACCTGTGCGTCCGGAACCTTATCGGA

SEQ ID 6572

LVRIPNKRFKTCRCRSHIQLATVRLCRWVLPFLPELRNGCLPWAGAGGGRVCRVYDEVPIYKGLQPAKSTNSARSTDSRRHSRISGNPDLVSRKLI

SEQ ID 6573

ATGTTTATTTTCTATAGTCTCAATCCGGAACAGTATATTTCCCAAGCATACATCATGAAAGTGTTCAGGATAAAGGCTACGAATCCCAATGCATCACAACAGTTTCTTTTATATCT
GCAATCCGACTTTGAAGCAAAAGACCGAAACGAGCGTATGAATACCGCAGATTGTTGTTAAGAACTGATGCATAAGGAATGCAACCGTGAAAGCCTT

SEQ ID 6574

MFIFTVNFPHVYPIKAYIMKVPKDKGYESQCIITVSVFYICNPILKQKTENEAYEYGRILFVKELMHKBCNRSL

SEQ ID 6575

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SEQ ID 6576

VKAFEDKALAVSADMALADGAAATAVGCPPLRIGGEQNKTPNPKGAERTENQEPQFYFPHVSDGKGRFIEIPLRRGRDDGAFIDQITFTIHENSMKVTGKGLVSDTEFVVRYSEL
LEEILPGITKLPFGKFFYQSCYQPGPDNVEYGVHYGGQCTMLVELNGTGMALPGENRLEFLSKCVRPKITRIDVAHDFPNGEYTPDQANLHDHNGHYDVHMRPKSECRGTA
WRNEDSGKTFYIGKRNKSKFTRVYKGRQLGDVDSFWVFEGDIEIPLDVLVSSYLGAYPICKBIFTEAKRMEVKVKNVNLIPDVKLPHARNVQKMNPLRDIGWDDSRIVDELV
KGVGYPKGLQPEYDCKNQTPQYIHEBQKAINALNIETLFDLLIERECAPPDREW

SEQ ID 6577

ATGTTTGAACCAAGCCAGTAACCATATACCGCCACTTTGTTGGGCGCAAAAAATTCAAAGGCGAAATCGACGGTAACAAAATCGATTATGACCGCTCTTGGTAGCGAGCCCCATGC
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ATCAACAGGAAAAGCCTTAGTCGAGAAATTTGTTGATTTCAGTAAGGCGCGACACCTAAAGCC

SEQ ID 6578

MFETSQVFTYATLIGAKPKGEIDGNKIDSCVTLVASPMPNNGNAVGTSESMPGDSHNFELKLNLFCAVDLTVAMESTGKGLVQLKLLDPVKGAPKA

SEQ ID 6579

ATGAGCAGATACCAACAGAAATTTATCTGACAGGAATGGAAAAATCAGAAATTCATCTATCCGATTCTGTTGGCGATATTGGATTACSTCGAACATCAATACAGCCGGTAAATATGACA
GCTATGAAGACGCTTTAGCTCGGCATTGGAAGAGATAGCGGGGAATTTGTAATTTTCGGATTCTACGAAAAAGAAGAT

SEQ ID 6580

MSRYQKFTIVQLENEHFIYDPSFGDIGFTSNISAGKYDSYEDAFSSALREIGGEFVIFPGYKED

SEQ ID 6581

ATGAAATTTATTACACCTGCCGTAATACGGCCAAAATCGGCTGTTGTAACAGCGCCCGCGCTGGCPTTGGCGGCACAGGCAAAACCGAGCTTCCCCGAAACGGCAAAAACCGCTTTGG
AAGCCGCAAAAGCGGAGGTATGGAAGCCGGTTGGATTGTAGTGGCGCTTTTCGCCCGCTTTTGTATTTTCATCGTTAAGAGGGTGTATGAAG

SEQ ID 6582

MKFINTCRKYGAKLVVTPAFLAALAAQANAALPETAKNALBAKADGNEAGWIVGVFAALFVFSIVKRVK

SEQ ID 6583

ATGCCGCTTACTTCATACCTCTTAACGATGGAATAACAAAAGCGCGGCAAAACGCCACTACAAATCCACCGGCTTCCATACCGTCCGCTTTTGGCGCTTCCAAAGCGTTTGTG
CCGTTTCGGGCAACGCTGCGTTTGCCTGTGCGGCAAGGCCAGCGGGCGGCTGTTACACAGCCAGTTTTCGCCGATTTTACCGCAGGTGTTAATAAATTTTCATGATATTTTCCCTTAC
GAAATTTTAAAAAATGTGTTTGGCGCTTTGTGAAGGTTTGTAGAGACCGCTCCCGGGCTCTTAAACTTAATCTTCTTTTTCGTAGAATCCGAAAAATACAAATTCGCCGCTATCTC
TTCCAATGCCGAGCTAAAAGCGCTTCAATAGCTGTATATTTACCGC

SEQ ID 6584

MPPYFITLLTMENYKSAKTPPTTIQPASIPSAPAAKAPFAVSGNAAFACAASGAAVTTASAPYLRQVLNFMIFSFTKFLKKCVGLCEGFRDLPLGLNLIPFVSENYKFPAYL
PQCRKASVFIIVITG

SEQ ID 6585

CAGGATAGCGATTCTGAGCACTGCATCCAACCCCCCCCCGAAACACTCCCAAAACAGCGCGCGCGCCCGGGCGCTTGGCGTTTCCCTGCAAAATCTGCGATACAATGCAGTCTGAA
CATTTATCCGAATCCAAACCGGATGGATACCGCACAAAAACAA

SEQ ID 6586

QSDS*QLHPTPPPEQLPKQRRAPRAVSLQNLRYNAV*TFIRIPNPDTAQKQ

SEQ ID 6587

GTGCTTCTCAAGACATTTATTTCCGACTTGGCAGTACATGCCGCTTACTTTCATCACCTCTTAACGATGGAATAACAAAAGCGCGGCAAAACGCCACTACAATCCAACCGGCTTCC
ATACCGTCCGCTTTTGGCGCTTCCAAAGCGTTTGTGCCGTTTCGGGCAACGCTGCGTTTGCCTGTGCGGCAAGGCCAGCGGGGCGGCTGTTACACAGCCAGTTTTCGCCGCTATTTAC
GGCAGGTGTTAATAAATTCATGATATTTTCCCTTACGAAATTTTAAAAAATGTGTTTGGCGGCTTTG

SEQ ID 6588

VLLKTFISDLAVHAALLHPLNDGKYKRGNAHNPFGPHTVRFVCFQSVFCRFQRCVCLCRQSRGGCYNQFCVPTAGVKNKFDIFLYEIPKMKLRL

SEQ ID 6589

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TCCGCCCGCTCCGCTTCCCGCTGCTCAAAAACAGCGGGGCTGGACACCTCGAGCTGACATCGAACCGATGCGCGGGCTGCCGCTTATTGTGCGGCAACAGACTTCTCCAGCT

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CTTTACTCGACGCGCTGACATATCCCGGGGATACGGCATCGTCCGCCCCAAATCCCGAAATGGCTT

SEQ ID 6590

MDTAQQRWAIITLSYDGRFYQWQKQAGGVPTVQALETALARIAGESVATTVAGRTDTGVHATAQVVFPTAAVRPAQAMIRGVNAHLPEGIAVLHARQVAPGFHARFDASGRHYRYLLE
SAPVRSPLFLKNRAGWTHLELDIGPMRRRAALLVGEQDFSSPRAAGCAQSPVKTIYRADLTQSAGLVRLDLHGNAPFLHMMVRNINAGLVVYVSGRSLVBEPAALIQERSRLKAPPTFMPDG
LYLTGVDPGAYGVIRPQIPHEL

SEQ ID 6591

ATGAATATGCTTGGAGCTTTGGCAAAAGTCGCGAGCTGACGATGGTGTGCGCGCTTTTGGGATTTGTGCGGATACGGTCATTGCGCGGGCATTCGCGCGGGTATGGCGAGCGATCGGT
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SEQ ID 6592

MNMLGALAKVGLFWVRVLFVVRDVIARAFGAGMATDAFVFAKLEPNLLRRVFAEGAFAQFVPIIAEYKTRSKATEAFIRHVAGMLSPVLIVVTALGILAAFPWVIYVSAPGPTKDA
DKPQLSISLLRITFPYILLISLSFVGSILNSYHKFIPATPTPLINISIFVAFVFPVDFPVTALANAVFVGGILQGLFQLPWLAKLGLPKLPLNFKDAANVRVMKQHPAILGVSV
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SEQ ID 6593

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CGCGCGATTTTTCAGGCACTTATCTTCTGATGGAACATCAGGCGCTGAATTTCTTTTTCGCGGAGTGTGGCATGAATACGCTGATGCTGGCAGTATGTTGGCAACGTTGCTTC
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SEQ ID 6594

MLNPSKRLVELVRLDEGGFVSGDPVQATEALRRVDGSTEKIIIRRAEMIDRDLRLDRLERVRAGSFWLVVVASMMFTAGFSGYLLMDNQGLNLFVLVAGVLGMLNMLAVWLATLP
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RAMSGLLVGSIVCYGLPRLLAWVCKILLKTSENGLDLEKTYQAVIRWQNKITDADTRRETVSAVSPKIVINDAPKWMLETEMQDQGWFEGRLEQWLDKGVANRBOVALETEL
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SEQ ID 6595

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SEQ ID 6596

LMVRNPSERCIRKALISGTLANAIMLQAAFFLIRTPQQYLAKLQTKLLITADLPSKIRSNF

SEQ ID 6597

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SEQ ID 6598

NPISFFGRFFRAYIRARIARVETGRTGCRITWAV

SEQ ID 6599

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TCAAGAAACAGCTTTACTGCGGATTCGCTTAAAAAACAAACAGCAGCC

SEQ ID 6600

MAYSADLRNKAHLNGLTKIRTRRRTAGSTNGTEFVRPALHHLRESFPLGRGGATFYRLLIRYITDNAKTPAKPQQLTCQETRTFCGALKKQAA

SEQ ID 6601

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SEQ ID 6602

MKSLIAL/LAALFVAAMADVLYGAIKAGVQTYRSVEHTDGKSVKVTGSEIADFGSKIGFKQEDLGNGLKAVWQLEQGASVAGTNTGWGNKQSFVGLKGGFGTIRAGSLMSPLKNTGA
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SEQ ID 6603

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SEQ ID 6604

MLFPDPFPFLRNHNDTIAAKFLQHPAPAYRREMLPDSGTGKTKTAYDPSAGGISPDAPLVVLPHGLEGSSRSYAVELMLAVRNRGWHGAVVHFRSCGGVANTAPVPHYLGDTARIAFA
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SEQ ID 6605

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SEQ ID 6606

MSEQNHQPTSPQLDENQIIALRREKLNINRQORNAYPNDFKRSFAADLQAQYGEIGKEELDFQAVPVKLAGRMHLKRMGKASFATIQDVITGQIQLYLNKGVSEVLDDFNHNDLGDIV
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LKRLVVGGLERVFIEINRSPRNEGMSVRHNPETMIEFYRAFSDYERMMQMAEDIIRNASRTVNGTANTITYNGKEVDLESPPERLTILEAIKKNPHYDEQLNDAEWLKEIVKHGESLFP
SPGIGSLQLALFEGCABGKLNWPTFIVDYPVEVSPLARASDTKQGLTERFELFVVGRELANGYSELNDFEDQAEKFSQVAQKDAQDDEAMHYDADYIRAMEFGLPPTGGCGIGIDRLVML
LFDLQITIRDVILFPQMRPE

SEQ ID 6607

TTGCGGATGGTTTGTTCGCTCATAGGGTTTCCGAAAAATAAATCAGCGCAGTCTGTTTCAGACGACCTGACCGAATCACAATAATTCGCGTATTTTACGCGATGTCGGTGTTTTTT
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SEQ ID 6608

LRMLVFAHRVFRKNKSGAVCFRRPDRTKFAIRILRDVGVFPQERAMPSENADGIIQLKMPKVR

SEQ ID 6609

GTCGTGGATAAACTTACCCGTGAAGCTGCGACTGCATAATCGCGCGCTTCATCGCGCGCAACCGCTTCGGACGGACAAAATTACGGCGATACGCCAATACGACCCGCGCGCTTGGCGGC
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CGCGCGCGCGCGCGGCAATGACGCTCTTGGCGCACTGCGACGATGATCCGCAATTCGGTTAAAGGTCAAT

SEQ ID 6610

VVDKTYPVKRLHNRRLHRRQRLRTDKITAIROYDPPAWRRTPKRNNAEQHMLVIGRGRQHQHADCQTADGHMADCIDRAALQCIQGPLYALFRROFGTA*EYLIPIHTVAFRQQNLLITQ
HPGRNGIQLK*MPFRDNHEKRFVIQPGNNARLLKRFNGDNRVNPAPERLQSHRVLVLFQHRHFRCTAQRDNQFRQVVRNRKNQPEFERTLQLVLPFIQMPDLRLFLQYLTRLCN
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SEQ ID 6611

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TTGCCGTTTGTTCCTGTTGAACCTTACCGGACTTTTGGCA

SEQ ID 6612

MSEQHISTWKSINALPGIMMASAAGVGGSHLIASITQAGALYVQQLALIIILTNLFKYPFFRPSAHYPLDTGKSLIEGYAEKSCVYLWVFLILCIASATINAGAVAIVTAIVKMAIPSLM
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LALVFLALGAFVQYNGEAVMGAGKYIQLINMYAVTIGGWSRPLVAFIAPACMYGTTITVVDGYARAAIEPVRLLAGRDKTGNALFPANWIWAGSLAVIWFWDGAMARELLKFAMIAA
FVSAFVPFWNLNVLKGRHRITAGNALAIVGLLYLAGFAVLFLNLTLGLLA

SEQ ID 6613

ATGTTGTTCGGACATAAAGTCTCCGTATTTTAACTGTGTTTCAACACACAGAGCCGATATTTCGGACACAGCCCTATCTATTGTCTCAATTTGGCGGGATTGACCCCAACAAACCCA
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SEQ ID 6614

MLFGHKVFRIFNCVSTHRAAYSDTALSIAPIWAGLTPNPKSYRLQKQDTAR

SEQ ID 6615

TACCTTTTTCGTTCGCGCAAAGTAATGTTCAACTCAAGCACATCCATACCTCTGCTTTTCTTGGGAAATACGGATATTGTCTAATGAAACATTCACATATTGGACAGGACTTCCATC
AACTCTTTACGTAAAGTCGGCAGGTAATCCGAGTCTGACCTTCTTGGGCGCGCTCTTGGGCAATGATGATTGAAGCGGTGCGGGCAACGGTTGCCGTTTCTGCTTTCTACCGAATA
AAAGTTCGATCAATGACAT

SEQ ID 6616

YLFLEFRQSNVQLKHIHTILLFLGNTDIV**NIHIFGQDFHQLFT*SRQVIRSLTFLGALLGNDLKAIVAGNGCRFLLS*EPDQ*H

SEQ ID 6617

TTGGCGCGCAACTTCTGTGCTTGGTGCAAGGATTTATTGAGGATGTCGGTCATGTCGTGTTCCGTATTTGTCCGGGAAAGGGGAATATTAGCATCAAAACCGT

SEQ ID 6618

LGGNFLCLGGKDFIEDVGHVFRICPGKGGILASNR

SEQ ID 6619

TTGTCCGTACTGACCGACGAACCCCTATTTCCAAGGTTGCGCCGAATACCTCAACAGCGCGCGAAGCCGTATTGCTGCGCGGTGTCGCGAAAGACTTCATCATCGACGAATACCGGTT
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GCACGACGAACCGCAATTTGGAAATGCGCAACCTGACCAAGCGCTTGTGGGCGGTAAACACCGCAACCTGCGGACTTTTGAAGTCTCCCTCGAACCAACCCCTGTCGCTGCTGCCCGG
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SEQ ID 6620

LSVLDEPYFGSPFYLKQAREAVLLFVLKDFIIDEYQVYQARAWGADAVLLIAALEQGQLERFEALAHELGNTVLLLEHDETELEKCRNLTPPLWGVNRRNLRTFEVSLDQTLISLLPA
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SEQ ID 6621

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SEQ ID 6622

SSEQTPEAPFLSPQETHFTVLAQKTGNVILICLSRYAVLMDRFSIGICGLQDVIGFNGHTQQRNTQNIANILYRQHFACHTFGRITRN*QMFNRTALLRLTGFALQNSQNPVGVTHF
GNLRIGRYNGFISKIQRHQCTLLNTSRVANNILKAHFLAGQLLHFFYALACQSVFIPSLGSRQNKQVFTIPFNQSLVERRLTINDIQVINDTTLATHNEVEVAQTHIKINYSFISA
*CQTCNCTGSRFTDIALA*SYNNPCH

SEQ ID 6623

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CGGCGGTATCCTGTTTGAAGACGGTAGGATTTGGGTTGTTTGGGGTCAATCCGCCCAATTTGGAGCAATAGA

SEQ ID 6624

MPSFGSNTENIVRFEHEVLIVCVGRYLDYVTIRAFIRISLPGGILFLKTVGPGFVNGQSRPNWSNR

SEQ ID 6625

CTCTGAGCCAATTGCATGATAACCAATCGGTTATCTGCAACAATATCTGTACCGGCTGCTGTGTCAGATGTCGCGCAAAATCTGTTCAAATAACGTAATATCCCGCGACAGAAAC
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SEQ ID 6626

L*ANCTDNQSVILQYVLYRLLVQWVRQILFKITVNPDRNQRLHGVDKYAGRSITFGAGQSTPSHRRINMHIAICNQFRPLADRPRNQIAIFGINLLTGTDRGCNQYCFPCFLITLRF
HLNLTQFFNIFRMQTKQQMILHSHSPTPIRMLQTNLHMP*KQRNQCSKIQRLGIILKFNQNKWNTRLLKLLAQPDQHIQIKQV*CMQRYRQVHLRLTYBEGIHYNHHRIP**
CKPTAQ

SEQ ID 6627

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SEQ ID 6628

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PFNFVVFSPFLIGKDSAVILPTEQCRLNARAAAALQTGATVPEYQVADKLAQIGGALLIEPNKTAVSTVLRLPESARLIEGINPSTFFKSVKSEADIAIRIIRAMEQDGAALCGFFAEFED
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SEQ ID 6629

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SEQ ID 6630

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SEQ ID 6631

TTTCATTATAATTTTAAACATGATAGCCAATACCATATTATCTATCAGATATTGCAAAAAATACGCCACCTGCTTTTCGGCAGATGGCGTTATATGACTAAAAATTACTCAGCAGCGGTTT
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SEQ ID 6632

FN*YFKHDSOYHIIYOILOK*RHLLFGRWRYMTKITOOPVCOPIO

SEQ ID 6633

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SEQ ID 6634

MIQHGNHAVCVDPSEPSVFLVLRNRIMLAQTWVTHPHDPHEGGAAALWRGYMESPVYGESDIEAATHVTVAGTRFTFTGNGQVTVWATPGHTDRHTSYLLETSDGIHVFPGDYLFSAGCG
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SEQ ID 6635

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SEQ ID 6636

VNDLLFAYTVNILENACVKICFLFSDGILC

SEQ ID 6637

CTCAGCAGCGCGTGTGTCAACCAATTCAACAGTGCAGAGGTGCATTTATACCTTTTACGGAAATCCGTAATTTCAACACTCGAACAATAACCCCGTTACGAGCAGTAAAAACGAGGACCCAAATCGCCAAACAGTTTTACTACAACATCAGCGTTCGGAGTACGGTCAAAATGCCAAACGGGGCGTTGCCAATGACGGCTTTTATACCAATGTAACTAACGGCTCTACTACACGGGCGCAATTTCTCT

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CAT

SEQ ID 6638

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H

SEQ ID 6639

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CGGATGGAAGTGAAGCGTTTCCCTGCTGCTCTGCTGTTTCTGACCAAGTGGCATAAAAATCTATATGAATATCTGGAGGAATATCCGTTTATACCCGATTTGTCTGGAAGAACCG
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SEQ ID 6640

LDWRGNKPLGAELADLKPLKYDFMYWERGLHMYKASAVVPTGYVVGNTAPLCEGDTQRYASFWDGYDVYRQLRWQRQIPEKQKAFKKAASKNTVMFAGREYGISKQNLSDVDDDFED
AMELKAPCLSSFLTKWHLNLYELEYFPITRLCLNHGQTVLDFSNTRITDLSVDMTGVSLSYLNELGLSLNLKGBLEKENCVCPTAGKGAGLILEVGKSVPIVGRLENLFAVNVGIA
DFDMQNLSETPYKLTIRLWGPKNIANPFAVSGFEDLEVFTAVDLFGFGADDIHPHRLPKLHRLMNSLPEREAAKAVKLYKKRKEDGLDPWIEKARKPEHLQNFDPNFRDWDGAET
PKSHAKAELRYKTRAGVVKLLGNPPENIGELAEAVKAYTGGFNKMDKHPIDTVEREDJAELEFILDLIPDGSCADKEKLEIFEDENRNF

SEQ ID 6641

AGGCTTTTCCAGCCTACAGGTGGCCATGCTTCCAACTTAGAACCCAGTGTCAAACTTTAGATGCCAATACTTCTTAATCTCATTCAAAGATTACGTCCCAAAATTCGGCGTTTAAAGA
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SEQ ID 6642

RLFOAYRWPCFQRLTQCQTFRCQYFLNLIQRFTSQIRRFKLGFSALNQIANIINILSFQTS*TYCQFIHRHQKRVDR*FFPFLHRSITLQISKHRLINQNTCTAYSFRLINRT
VGFIDIQNLIRPLLYTCTFPNLKANPADGRKARTQLDCTNLVFLITNYLIT*NRLLPTTLLYFNFHPLNLTIVISQMTNMDTRIQNFYIMRQIATIGRYDT*T*FLQHLNLTATMEFKHNT
FNIQQNVNINPLATNTSRLPVQYTGNSYFSRSKTIHQ*Q*DTAQST*GMTFTFFKWLHRYFCTSCRKSIYINLTFRQKFGCAILH

SEQ ID 6643

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TAACCGAAACCGAACCGACTGGATTCCCGCTCCGCGGAATGACCGGAAAGTGGGCTGTGGCGGAGTTGGTGAA

SEQ ID 6644

LPQADTPFCGRCTKNPMPSETPNRLQASVADENSKAYRHSCENSSQPSGRNLYEIPSPFRKWSRNEKQDEFGHNRNRTDWIPACAGNTRKSLWAGLVE

SEQ ID 6645

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TATAACGTGCCAT

SEQ ID 6646

FRVELYHQLFINITGQFRAIRHVFEHTLKFCIYRNPTQADLSCQTCPLNTYLPFGFFTN*DNITSFHLERRNIDNLSIYNLSLRNKLSCFSSGRTEHTPTINDIIQTRFQQLQQLAS
RTFTALSFCEITTELFF*YAINPADLFFFLQITIV*QTRFPCTMLTSGSINFTFRIQRAARTLQKQIRTFATCQLTFRANITCH

SEQ ID 6647

TTGGAAACGGCTTCAGACGTCATCTGCACATCATCTTTCGGAACCAACGACCAAGCTTCTCCCGCTCGGCGAGCAGCAGTTTTCAGCGGCTGTCCGTACACCGTTTCAGCGTAATG
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SEQ ID 6648

LEFASDVICTSLRKKTHHVLPLRQHQFFHGVSVHRFQRNAQTAFPPYRPGTETRGVVFVVRHPRPNAQRVHVRPRLFVVQHLRRIQNVIVKAVFGEHIAQVHVHGHAAAFNAV
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SEQ ID 6649

AATACGACGTTTTTAGGCGGACGGCAACCGTTATGAGGCAACGGGGTAACGTCAGTAATGCTGGTAATCTTGAAACCAAGAGCATTCAAAGCACGTACAGAGGATTCGCGACCTGGACCT
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CGCCAGAGGTAGCCCAAGACAACGCAATTCCTTGACGGTCAGTGATTGTATGATGGTATGTTGAAAGATGCATGAACGTGCACAATACCTCACTCAGGTTTTACGTACTTTTTACG
TACACGTGAAGCTGTGTTTTCCTTAGCCAT

SEQ ID 6650

NTFFRRRTATVMRQRGNVSNAGNLETKSIQSTYRGFATWTFWTFNL*IFNAILGNFTSCFCCNLCKNCTFTRTFKTSAAAGSPRQRIALTVDNDGIVERCMNVHNTLTHGFTYFTT
YT*SCVCFSH

SEQ ID 6651

ATGTCCGTGCGCCGTTCCCGTCCGTCATCCCGCACAGGCGGGAATCCGGATTGTCCGACAGGAACTTATATTCGTCAITCCACCAATCCCGCCACAGCCCACTTTCCGCGTCATT
CCCGCGCAGCGCGGAATCCAGTCCGTTCCGTTTCGGTTATTTCGGATAAATTCCTGCTGCTTTTCATTCCTAGATTCCCACTTTCCGCGGAA

SEQ ID 6652

MSVRSRPSFPHRRESGFVRTETFISSFHQSRRPQPTTFRHSRAGGNPVRVSIVISDKFLLLFIPRPLSRE

SEQ ID 6653

GTGGCGGGATTGGTGAATGACGAAATATAAGTTTCGTGCGGACAAATCCGGATTCCCGCTGTGCGGGAATGACGAGCGGGAACGGCGCACGGACATTCGCGGGAATTTTTATGTCT
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ACCGCAAATCTGCTCAACCTGCCCTCCCGCTGGGGGAGGCGCGGAGCGGCATTCCTCAAGTTCGCGCAACCTTTCCCAACAACCTTAACCGCCCAATACAGCCTTGCCTGCT
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SEQ ID 6654

VGGIGMTKYKFPCCQIRIPACAGMTDNGARTFAGIFYVSLILFLMYRYSKIGCAGCPYFSDDLKSTVVPNICFSNRLQPPNLQPPSPVPGEGGGILQVAATFPNNLTAPIQALRL
VALSPALSHGERGRCGCG

SEQ ID 6655

AAATTTATTTCTTACCAGCAATCGCTTTACGCGGACCTTTGCGAGTACCGCATTTGTACAGTGCCTTGACCGCGCATGGTAAGCCGCGACGATGACGGAAGCCAC

SEQ ID 6656

KFISYQQLYADLCEYAHLYECVDRGMVSRDDGSH

SEQ ID 6657

GTGCGCGGACTTTGTGGAAGGGGTTGACATGAATCCGCGGACAAATGCTGGCAGGTTCACCGCATCTTCCCGAACATACCGACCAACGCTGACACTCGTCCGCAACGGCGCGGGC
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SEQ ID 6658

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AAEQILFVLHNARALKTDGLLFFTCFGRDTLAELKSLKENGIESRSVMFPDMHDLGDLAENGFDYDPTDTAKLVLDYKRAETFWADMFTLGVWRAVANDDENAARSCAGAIPIREGGL
GITLBTVYGHAVKILVLPQGENVVRFPFKR

SEQ ID 6659

GTGCGGACAAATCCCGATTCCCGCTGTGCGGGAATGACGCGGGAACGGCGCACGGACATTCGCGGAATTTTTATGCTCCATTCTCATACTTTTTAATGCGCTATTCAGAA
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GGGAGGGCCCGGAGGCGGCAATTCCTCAAGTTGCGGCAACCTTTCCCAACAACCTTAACCGCCCAATACAGCCTTGGCGCTTGTGCGCTCTCTCCAGCCCTCTCCACGGGAGAGAG
ACGGGGAGGCTGTTGGGGTTAAGGGTTTTG

SEQ ID 6660

VRTNPDRLCNDGRERRTDIIRNFCLHSHTLFNALFQENRLCRLFLFRPEINGCKSNLFFKPPATAKSAATCFLPRGGGPRRRHSPSCNLSQQLNRPNSTSLAACPLSSPLPRGR
TGRLLGLRLV

SEQ ID 6661

TTTTCTTCCAGCAATCGCTTACCGGACCTTTCGAGTACCGCATTTGTACGAGTGCCTTGACCGCGCATGGTAAGCCGCGAGATGACGGAAGCCACGATAGCAGCCATGTCCATC
AATCGTTTGATACATAGTACTTACGAGCAATCACTTCTACTTCTATCTTGGCACTTGATCAGCAAGCATCTAATTTGAGTCTCGTCCAAATCTTTTGCTTTAGTATCAGGCG
CAATATTGCGAGCTCACAATCAATTTAGCACGAGTAGCACAATACCGTAATAGCTGAAAGACCAATTACGATGTGCGTTATTAGGATATTACCCCTGCAATACGAGCCAT

SEQ ID 6662

FLTSNRFTTTFASTRICTSALTAAM*AAATMTAATLAHVHQSFDTHTSYPTTQITFTYFILGNLITQSI*LSLVQIPCFISIRRNICSLTNQFSTSTNTVNSLKTNYDWCIVIRDIYPCNPSH

SEQ ID 6663

GTGCGGAAACTTGCCAAATCGGTATTCAGCCGCGCGAGATGCCCTCTGAAACCGCGGACGAAACCGTGGCATAATACGCAACGCTGATAGTGGCGCGCTTCCGATGCGCGCCCAACAG
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CGGATTACACCGCTGCGTATGGCGAGTATCTGCACTCGGCATTGAAAGGAAGCAGGCTGTTGTGATGAAAGGCGGCACACGCGCGCTTTTGAAGCCATGCGGAGCGGTTTGGCGCGC
TGTCCCGGACTTTGTCGAAGGGGTTTGACA

SEQ ID 6664

VRKLAKSVLQPAQMPSETPDEPHWNTQRLIVGASAMRROQERKMPDAAKVYLHGWANRHFDDLMPLPATWPFVSAVDLPGHGDAFPAQPFIDIEAADGIAAQIDTSADILGWSLGG
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SEQ ID 6665

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GCGAGGAGGAAACGGTAGATTGGAGCATCTACCTCTCGGAAGAAAATATCCAAAATAGCAGATACCTGTGTTCCCTCGGAATCTGTAGGTTCTGACGCGCTTCCGAAGCGAAATACGA
CCTTCCCGAAATGTATCTCGAAATCGGCGACCGCGATGCCGCTGCCGAGACAGTCGAGAAATGCTGGAAGAAGCGGAGCGGACGTACTCAACGTCGCCCAAGCATTTGCCGCGAGGAATG
GGTATT

SEQ ID 6684

VYEPETFPNPVPEVIDTPEPESVAQTAENKPEVDVDFYNNLFSNNHIGTEETASAKPAAPSGLAGFLKASSPETILEKTVAEVQTPERLHDFLKVYETGAETAPEPDPFNAADDL
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GI

SEQ ID 6685

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CGGACGGCGGTATGCTGTACAGCGTCGGCATTTACTGGTTGTAAACGATGAAAAATCCGACACGGGACGGAATCTGGCATCTGTTCTGTAATGGCGCGGCAGCATACCCAATTTGTCAG
CGGTACGGTTATGTAATC

SEQ ID 6686

MYAGERFNTYSHLSGLILAAAGLMLMLLKTIGHGDIYRIFSVSVYGISLILLYLSSSLYHGIAGKLSILKKTDECHYVLIAGSYTFPALVSLRNGPGWTVFSLSWLLAAAGIAQELFI
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SEQ ID 6687

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ACCGCAAGCGGTCGCGCGGCTACTTGGCGCGGCTACATGGAATCGCCCGTTTACGGCGAATCCGACATCGAAGCCGCCACCCACACCGTAACCGCGGCGACACGATTCACTTCCGCA
CGGTGAGTTTACCGTTTGGGCAACACCCGCGCACACAGACCGCCACACAGCTACCTTCTCGAAATTCAGACGGCATACAGTTTCTGCGGGCGACACCTTTTTCGCGCGGCTGCGGA
CGCGTGTACCGGCAAGTCGACAGCTTTACGACAACCTTCAACGGTTTCAACCAATTAACCGAAGGCAACCTGTTCTATCCGCGCACAGGAATACCGCGCGCAACCTGCGTTTTCGCGG
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CGTC

SEQ ID 6688

LLGFRCILTFPGYFTQASEPSRNTHEHYPRQSPDRQLHLDFTARQPCRLRRSFRTLARLGIPTPTOPHARPNLGNAPPSEPRRCGGTLARLHGTARLRRIRHRSRHPHRNRHTIHLRQ
RSGYRLGNTRPHRPPHLPNSRNFRRHTRFLRRHPFFRLRLTRVYRHGRTALRQLPTVQPIRTRHPLVSGTRIHRQPAPFRFPYRAGQRRHSDGIEGGTHAHPARYPRARTPRQPVLTDRN
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SEQ ID 6689

TTGTGCAGGCTGTTTTTGTCTTTTCAGACGACCTGCATCAACGGTTGTAATCAACTCTGTTTTTCAAAACCGCTGCAACCGCAAAACCTGCCGCAATCCGCCCTCCCGCTGGGGAGG
GCCGGGAGAGGGCATTTCTCCAAGTTGCGGCAACCTTTCCCAACACTCAACCGC

SEQ ID 6690

LCRLFFAFQTTICNGCKSNLFFKPPATAKPAAIRPLPRGGRGEGILQVAATFPNNSTA

SEQ ID 6691

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AACCTGCCATCCCGAGCATGTGCGGTAAACCAACCAAAACCGGCAAAAGCGTCATCGTCCGCTCAACGACCGCGCCCTTCCACGGCAACCGCATCATGACGATATCCAAAGCC
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SEQ ID 6692

LTLFRKTLFLTAAPGTHSLQTSADAVVKPEKLHASANRSYKVAEFTQTGNASWYGRFRHGRKTSGGDRYDMNAFTAHHKTLPIPSHVRVINTKNGKSVIVRVNDRGPPHGNRIIDVSKA
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SEQ ID 6693

CATTTCATCTTACCACCAACATCTCGATAGCAGCTCTCGCACTTTGCTTAATTAATACCTTCAAAAGCAACTGCTTGAATAATTTACACAGAAGCAATACTTTAATATTAGAGACT
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TTTTAGGGAGGCGTGTGCAAGGCGATTTGACACCTCGAAACCCACCTTATGAAACCCACAGACCGGCTCTTTGACCTTTATGACCAAGCAGCAGCCCGTTTTGCCAAGACCACTACC
AATACCGCGTCAACACGACGACGATGCGTAGCACCACAGCAGGTTGAATTTGATTTCAAAACAT

SEQ ID 6694

HFNLATNILDSSSTFGNFNTLQSNCLRNFTRSNNFNIRDCRNQTCLL*D*NINLINSN*PQFT*TKLCIS*YC*RFKTSFRESLQGHLLTLETHLMKPTRPALLTFMTTTRFAKTTT
NTASNTTSMRSTNSRLNCIQKH

SEQ ID 6695

AGACTCCACTTTCAACAAGTAGCTGATTTTATTAATCATACCAAGGTTTTCAGAGGTATCTAAAACCTCTACCGTATGCTCGCGACGACGCAAACTAAACCGCGTGACATGACAGATGA
GATTCATTTGATACCAATCAGGCTTTAAACCAATGTAAACCTAATCTTTTTTGTTCAGCCAT

SEQ ID 6696

RLHFQVADFINHFTVFRGI*NLRYMLATTQT*TACTCTMRFNCTQAPNQNPNLPLFSH

SEQ ID 6697

TTGTGCAAAATTCGGGAGCCCTCTCCCGACGGGGAGGGGAGGTTGGCGGAGATTTGGCGGTTGACGCGGTTTGAAGAACAGATTGGATTACAAACCGTTGATTTCAGGTCGCTGA
AAAGCAAAAGCAGCCTGCACAAACCTGAT

SEQ ID 6698

LSKFGESPFPGRGQVAADLAVAGGLKNRLDLQPLISGRLSKKQPAQPD

SEQ ID 6699

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SEQ ID 6700

MNIKHLILTAATALLGISAPALAHHDGHGDDDDHGHAAHQHGKQDKILSRAQAEKAANARVGGKITDIDLEHDDGRPHYDVEIVKNGQYKVVVDARTGRVSSRRDD

SEQ ID 6701

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SEQ ID 6702

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SEQ ID 6703

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SEQ ID 6704

LPPASTNPFNITDPAIAADSVKSINSAESRLFPKNLDAAG

SEQ ID 6705

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SEQ ID 6706

EA*TIPTSSPSQSLETTVILET*TIKSNLFYTCCFSLLSNTFTNYCSCFNIAIRFQTTAHLSPQCRGLSQYFITFTSNYLSINMIASEPT*SYHFWNTSTGFACTPESGCMFIH

SEQ ID 6707

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SEQ ID 6708

LMRRABARPATLSMHLASPTLRNLI RTHPVKNTRTFVPIHRNPKTRHSRAGGNPVRVSVISKNCRSVKFLDSHFRNDADVQSVRTDSSPHRQSGFVRAETIAPSPFHRREPRSVGIGTYRIKRLPQPCVLDSHFRGNDSDGIPNSNPPQPTYAHPHLPSVPERADKVRERRAS

SEQ ID 6709

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SEQ ID 6710

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SEQ ID 6711

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SEQ ID 6712

PFLGPFPHYHYFATYANTPTFIRLSTERTNLSNLTNNLFIAS*NNILCLARSLNGDTFRHFYIDRMKTRQRIQDFTLCLSTITHAQL*FLLETF*WTFNHIAD*CASSTRHCICLFTAIIIRKNSQPAIIKPNYIIRMQRKQFTVLINQCLCKSFYFTSGNRHNVFCDT*H

SEQ ID 6713

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SEQ ID 6714

VQADLAYAYEHTTRDYPEATGAKKGTITSTVSDYFKNIRTSVHPRLALGYDFGWRVFSAPAVAAGLHQSLQYRSRHCRRFRQIHQPRITPIPKP

SEQ ID 6715

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SEQ ID 6716

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SEQ ID 6717

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SEQ ID 6718

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SEQ ID 6719

GGCTACAATGCATAAACAACCTCACCACCAACACCTTGAGAACGCTGCTTTACGATCAGTCATTACACCTTTAGAAGTACTAACCAGTACGAAATCCCAAGCAATTCATAACCTTGAATCTCATAGACGCTTTATAAATACGCAAAACCGGGCGAGATACGCTTGATTGTTCAATTACAGGACGACCTGCATAGTATTTTAAATGAATTCCAATATAGACTTACGTGAGTAACTG

SEQ ID 6733

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SEQ ID 6734

LMFYNINALNNFTQHSNYL/LLTFFILTSNYNPIAFNDFIHRAPYNTSGANETIFINRSVRNSRVTPKIRVPKSSLLFSNTAALLSNLINAPSGRRTPLAVRTTTLTYTSPFLTR
PRGTASLTATLIISPTA

SEQ ID 6735

TTGTTTTCGCGGATATGATTTTTTTTGTAAAGATGATTTATTTTTTAAATTCGGTGGCGGATCGGATATGGCGGATTAACAAAAATCAGGACAAGGCGGGAAGCCGACAGAC
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SEQ ID 6736

LPGRDHFFVKECIYFLKPRCGDRWRINKNDKAAKPQTVQIVNRNFTWCFSTLENESL

SEQ ID 6737

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SEQ ID 6738

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SEQ ID 6739

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CAT

SEQ ID 6740

*YPRCQ*NDPHKLSLSTQFTGYRTKDTSTQRFKFIQHGIGVIEFN*RTIRTTHTLSSTNNYRIITYIAFFDTATRNRIFNCHFNINRVSATLRSQYLDTHYATRTVISHI*DGLHLN
H

SEQ ID 6741

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SEQ ID 6742

VSSFPIHRNPETRRHSRADRNPDLSARKIMRRHSREGNPDORSVSVISDKFLLLFI PRFPLSRE

SEQ ID 6743

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SEQ ID 6744

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SEQ ID 6745

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SEQ ID 6746

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SEQ ID 6747

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SEQ ID 6748

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SEQ ID 6749

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SEQ ID 6750

LNPTNDLKAWQRAQTELLERFLPSGNEIPRTHEAMRYAALDGGKRLRPMVLAASELGGAMADAVQMAAAIEMHIVYSLVHDDPAMONDSLRRGRKPTCHKYGEATALLTGDAL
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SEQ ID 6751

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SEQ ID 6752

LSTFFS*NGFMSNIATYTFQPTWFA*LTGSVLHT*AKLSFQQVQICQLNGFVQFICFH

SEQ ID 6753

ATGTCCTGTCATCAACCGCGCTGATCAGCTGTCCGACAAAGGCGAGGCGGTGCAATTTGCCAAACCTGCACAAGCTCGGTGTCGAAATCCTCTCCACCGCGGCACGGCGAACTGC
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GCCAT

SEQ ID 6754

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SEQ ID 6755

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SEQ ID 6756

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SEQ ID 6757

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SEQ ID 6758

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SEQ ID 6759

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SEQ ID 6760

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SEQ ID 6761

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SEQ ID 6762

LFACLFVVARVPKIPPHETREGENEVQADDGGVKLPTLIVVRSRTGFEDVGKRGQRETCRQLDQVVSFALERGHAEQSGREBGGVGKDECDQDKVHVGCGHGLSVWLSAAMPSELI
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SEQ ID 6763

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AGTCGGTACTTTTAGCAAAACATTTTGAAGCCAGCTTTAGTTACCGCAGGCGAAGACCTGTAGGGTTAATCTTTTGCCCAT

SEQ ID 6764

VGCSTTSCLSLFTLNFRRFGRFNIAFRINPNFQTYTTCGVRFAGCIIYICT*SMQWHAFTTIPFATGNIRTIQTA*SHNLNAPSTRTHCILHCSFHSHTLNAFFQLGDTVSNLSIQI
RTANLFIYINRYTHQDLQVTFQNPDIITFTDNHRTSGVGNACRFRANFNYSNRSIQPLQIIANIDILLQNSRKVGT*SKPF*SPVFSYRQAKACRWLISH

SEQ ID 6765

GTTTCAGAGCTGCGCTTTTGTTAAGATATGCGCTTCGCAATGCACTTCAGAGCGCATCGCCGCCGACAATGCCAAACAGAAAGCCCATCATGACCGCATCCATGTACATCTTTTGG
TCTTGGCACTCATCTTTCGCAACGCCCTTTCCTACGACGAGACTGTTGGCGTGGCGCGCTCAAGCGCAAAACATTCGGACACCCACTGATCGAGCTGGCGCGAGGTTTCGCGCTGAC
CGCTCTCTTGGCTACATCTCGAATCCGTCGGGAGCGGTACACAATCAGGGTTGGGAGTTTACGCCACCGCTGCTGCTGTACTCATTTTCGCTTCCGTGTTTCGTCGGCGG
TATTTTGGCACACGCGCAACAGGAA

SEQ ID 6766

VSEAAVFKICRSANQFRHRRRQCENRKPIMTASMYILLVLLALIPANAPLITRLFGVAALKRKHFGHLLIELAAGFALTASLAYILESAGAVHNQGWEIFATVCLYLIFAPPCFVRR
YFHTFRNR

SEQ ID 6767

GTTACCCACTGTCACATGATATGACAAGTTGTTTTTCGATGCGGTTACCGCGACCTTTGGCGCGAGCTTGAAACGCTTTCAAGCTTGGACCTTTGTCAACAAAGATAGTTACCACCTTC
AGTTCATCAATGTCGCGACCGTTATATGCTCAGCATTAGCAATAGCTGACTCAATATCTTTTGTATCAGCTCGGCACCTTTTTCAGGCTGAAAGCCAAATATTCAAAGCTTGGGCAA
CGCTTTTACCAAGATCAATCAGCTACCAACGAGCCCTTTGAGCAGAGATACGGCATTTTATGTTGTCATTTACTCTCAT

SEQ ID 6768

VTHCHIDMSLFFDAVTATPGASLKTQAMTFVNKDSYHPQFINVRTVIMLSIENS*LQYFDQLGTFPRAESQNIQSLGNVFTTQISYQTSLSLSDTGIFHLCTYSH

SEQ ID 6769

ATGCCGCAAGCCCTCGCTCTCCAAATTCCTCCGCGAAGCCCTCGCTTCGCACTTCCTCCAGCCGCGCCGAACCTGATTATGCTGATGAAAGCGTATCGCTTTTATGTTGAAGAAG
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GATTACCATCGAATGATATGATGAAATTCGCGCAGGTGTTGGGTTTGAAGGCAAGTAGCGGAAATACCGAGCGCGCATGCGCGGAGAGTTGGATTTTCGACAGCTCTTTACGCGCGCG
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CAGAATCATCGACGCGCAGGCAAGCGGATTTATGCGCGAATACCGCAGCGCTCGGATTCGACCGCATCAGGTGTTGGCGATGGCGCAGGTGCGAAGCATATCCGATACTCATA
GAAGCGGCGATAGCGTGGCTTACCGCGCAACCGCAAGCGCGCGCGCGCGATGCTGTATCAACTTCGCGCGTTTGGAGCGTGTACGCGCGCTGTTGCGA

SEQ ID 6770

MFQALVLPFSAEALPSDFPSRLPEPDYADEKMRMFIIVEGFSLSKDAALLDSRQIDHAVLPNMAPGELGLIVSDMDSTLITIECIDEIAAGVGLKGVAEITERAMRGELDFOQSLSR
VALLAGLDEQILADIYENVILKSPGAFLDDECKRHNVRFLVSGGFTTPTERLQRLGFYQHANILEIENGRLTGRKGRIDIAQAKADLLREYRSRLQLPHQVLAMGDGANDIPILK
RAGIGVAYRAKPKARAAADACINFGGLERVGLFG

SEQ ID 6771

GGTATTCGATAGGCAACGCAATCGTCGCGCTTTCTTTTGAACGAATCGATTTCGATCCGTGCGGCTCTCTACGAAGGCTATCAGGTTGTGCGGTGTTTCATCAGCGCGGCTTCG
CGGACGAGCTTTTCGCGCTGCGCTTCACGCGTTCGCGAGGCTTCGTAGGATCTCTCCATTCACCCCGATGTGTCCGTAGGCGTGGCGCAAGTCTGATCGTTTCGATCCAGTGTGCG
TCAGTTCCAAACCGTGTGCTGCGTTTCGTCGCGTAACCGACGAAGGCAAGGTAATCTCGCTTCGGGATAGCTTTTCGCGCGAGCAGCTTTTCAT

SEQ ID 6772

GIRIGNRIVAAFLNLNEDFASVGVFYEYGHCAVPHQAGFADDVSALPLHAFAGFVGIVHFNDRDVSQVAVQVVSFRIIPVVRQFQNRVAVGFVAVTDEKKGSAFGIVFSABQPH

SEQ ID 6773

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CATATGTCGCGATGTTCAACCAATCTTTACCGCGCTTCAATCCGAGCGCGTTTGGCGGCTGCTGCGGATATCGGTATCGGTGAGCGATACGTTTCGCGTGGCGCGCGCTGCTGT
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SEQ ID 6774

MENTLSLVGTVNRFMLGYLLIYALLGIGLFFTLYLGAPOITKLGAGFKSVFGLFAKGDKDKSLSQFQALAVASIAQIGTGNVAGVATAITAGGPGAIFMMWLSAVLGMSTIFARALLA
QKRVVSHGKYGPAFYITHGLTPKIGRGAARPLSGFPFIALIVALGFIQNAQANSIASAVTAPDVPSLAVGIVFAVLAMVVIIGVNRNIANIRPVFPMAVVIILCAVILLFEFSD
HIVPHFHLFTAPNPEAVLGAAGIGMREAIRFGVARGLFSEAGMGSTPHAHATADVKHPVQGGMTAFVGVFIDTILVCTATALLILLTDANLSEGGAAVTPAFNKAFFPGFSQLLA
MCLFFPFTTIIIGWYFESNIRFLFRGRLGIYRALVLLAIVLGLKGVLDVLSLDMFNGFVFNILIALFLLRKEIRAIYDYLKQKAGQDLSYQYEFHFHDEQ

SEQ ID 6775

TTGGAGGACGAGGCTTCGCGCATACGCGCGCTCAAAAATCGGATTATATAGTGAACGCGCAAGAAATGTTACGGCGGCGTCCCTGCAATCGGAAACGACTTCAACGCAAAAGCGC
AGTATGTGTCGCAACACGCGGAAATCGCAACTATTGCCAGCTGATGAAATTCGTTATATAGGGGATTATC

SEQ ID 6776

LEDBGLRHNGSKNADYIVKROMLRRACLSSENDPKRKQYVSDFTGKCATIASLKKIRYKGI

SEQ ID 6777

TTTCTTTTACGCTTTTATCGGGCAGGTGGCCTTTAAAGGTACGGGTCAATGAGAAATTCGCCTAATTTATGACCAACCAATATTTCGCTGATAAACACAGGCACATGGGTGCGACCGTTG
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CTACATATGGGCTTTTTTCAATGAACGAGCCAT

SEQ ID 6778

FLFSLFIGQVAFKGTGQ*EFA*FMTNHIVADKHRHMGATVVHNGGQTDKIRQNGRTTRPGFNRAFVVACANSIYFFQQMQVYTWAFFQ*TSH

SEQ ID 6779

[illegible]

SEQ ID 6780

MKIGIPRESLSGETRVACTPATVALLKGLGFETVVESGAGLAASLDDAAAYQTAGATVADKAAVNACPLTIYKVNAPSEGEPLLLKEGQTVSVFLWPQNEALVEALRAKKVNALAMDVPRI
 SRAQALDALSSMANISGYRAVIEAANAPGRPTFGQITAGKVPPAQVLVIGAGVAGLAAIGTANSLGAVVRAFDRLIEVABQIESMGKKFLKLDPLQESGGSGDYAKVMSDEFIAEMKL
 FAEQAKEVDIIITTAAPGPKAPKPLITKEMVESMKGSSVTVDLAATGGNCELTPGELSVTNGVVKIIGYTTMANRLAQSSQLYATNLVNLFKLSPNKDGETTLDPEDVIRIRMTVTRD
 GEITPPPPINQISVARQPTSEKAAPKAPEKPVPLMKKLAPAAIAAVLVLWVRAPAFAFLNHFIVFVLACVIGYHVWNVNWSLSLHETPLMSVTHAISGIIIVGALLQIGQNGFVSLLS
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SEQ ID 6781

ACCTTTATTTGAGTACAGCGCGACGAACAATCATATTATCCGTGCGTTTGTATTACGAGTGCGGTAGCCTTTAGCAGGAGTACCCCATGGACTAACCGGTTFCGGGGCTTCGCCGGTACGG
CCTTCACCAACCACCATGCGGGGTGATCGACGGGATTTCATGACAACACCGCGTACGGTTCGGACGAATACCGGCCAACGGTTAGCACC GGCTTTACCGAATTTTTTCAGGCTTTTGCTCTTGCT
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SEQ ID 6782

TF1*VTATNNHIIIRAFVITSAVAFSRSTPPIINRFAGFAGTATTMTMRVIDGIHNDNTAYGRINTAFTVSTGFTDFFQALLFVTDFTDGRTAIYVDFTNFARAQDTLSVCTFFSQQYRRSTGR
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FKGCIACITCFVOTFCYHANHAATACRGLHFNDCH

SEQ ID 6783

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SEQ ID 6784

MNWSDILNLMLPALPEVALLSLVLVLLPADLWASDDKCRWTHYGALATVAVTAAVQLAVWBGQSTSSFGMYIADGMSRLAKMVLVYALFVFLVYAKPYNQVGIKFGFVTLSLFALLGMSV
 MVSAGHFLTAYIGLELLSLALYALIALRRDSGFAEAALKYFVLGALASGLLLYGISMYVYATGSLSEFAGVLASSFNEEANEWLLKLGVLVIVAVFLKAVPFFHMMWMPDVYHGAPTSVT
 ALVGTAPKIAAVVFAFRILVTGLGTVHHDWSLMLFALLAAASLLVGNLAAITMOTNIKRMLAYSTVSHMGFILLAFMAGAVGFAAGLYYAITYALMAAAGPGVILVLSGDGNECENISDLGL
 NOHRVWLAFILMLLVMSMAGIPLMGFYAKFGVIMALLKOGYVWLSTVAVVMSLVGAFYYLRVVKVMYFDESGRARPAAAGGNAAKSLLSVNALLVLNGIMPOTVLDWCAKALEPTL

SEQ ID 6785

ATGACTTTCGGCTATTGGTGCATTCGATTGCCCTGCCCTATTGGCGCTTTTTFGTGCGGGCGATGCGCAAAAAGCGGGCGGATTCCGGTTTAAAGACAACCAATCTCGCGGTTTCTCG
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CGTCAACACGCTTCGCGGATTTGTTTCATCTCTGCCCTCGCCCTTATCTGGTGTACATCGCAGACAAAGCAGCATTGGCGCTCGCTGATGTGGCGGGCGGATTTGCCCTGCACCGTCGGA
CTGTTTGTGCGCGGCTGCT

SEQ ID 6786

MTFFAYTCILIALCLPLFCAAYAKKAGGFRFRDNHNPRGFLAHTQGAAARAHAAQQNGFEAFAPFAAAVLTAHATGNAGQATVNTLAGLFIILFRLAFTWCYTIADKAALRLSLNWAGGFACTVG
LEFAAA

SEQ ID 6787

TTGAAACAGATGCCGTCGTGAAACACGAACGTCAATTTTTCAGACGGTATTGAAAACAAATCATCGAAAATCGGAGAATTTCATGTCTTCAGGA CTGG

SEQ ID 6788

· LKOMPSENTNUNFSDGIENKSSKIGEFPCLODS

SEQ ID 6789

TTCTTATCTGCAGCTGCAGCAGCGGCTTCCAAATCCAACCTTTGACCGTCAACCAAGCTTACATAAGCTTTTTTAAATCGCTCGGGGACCCAAAATACGACCAAAACGCTTAGTTTTCCTTTTAGTGGTAAACGGTAGTTACAGAAGCAACTGGAACACCGAACAGCAGCTCGCAGCAGCAGCTTTGATTTTCAGGTTTGGTTGCATTTGCCAAGACTTTAAACGTCATTTGGTTGCATTTTCAGCCAAACGTTGCTTTTTTCAGAAACGACAGGCACCAAGATTACTTGAGTCAAAACGTTGTTGATTCATAACCAAT

SEQ ID 6790

FLICSCSSGFOIQLLTVNQAYISFFNLAATQNTTKTLSFAPSGNGSYRSNLNTEQQLDSSFDPRFGCICQDPKRHLVAFPSQYVAFPRNDRHQDYLSQTLLETH

SEQ ID 6791

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CGGCGGTTTCGATGGTGTGGCGGCAAAATTACGCTGAAACTGGGTGGGTATGGTTTCTTGCCTTCGCGCTTTATGCTCGCCAGTGTGACCGGAGCGGGCTCGCTATTTGCCCCGGTAATCATGTTAT
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SEQ ID 6792

[illegible]

SEQ ID 6793

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SEQ ID 6794

MSSGLVTAAYIAAILFIFSLAGLSKQETAKGCGSYGIAGNAVALFVTVPSDNTHGLWIIIAMLIGAAGIHKAKKVEETPELIALHSHFVGLAAVLVGFNSYIEPGNVSHDMHTIHL
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SEQ ID 6795

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SEQ ID 6796

YPLL^LL^LLCNRI^FSD^DYFF^IITQQA^VRIN^LLS^PQNQ^VYV^QVA^ASQ^VN^LLV^EFP^GYK^QHL^LQS^IIP^LFG^KN^FGF^GSG^FGS^QRL^NHK^QTL^VTR^QLG^DSR^HTG^TVH^FTV^FY^LSE^VVF^GV^RERAT
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SEQ ID 6797

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SEQ ID 6798

EQ ID 8798
LQEFKPIFGQDPLGSKKEAIRKVLKWLPSHLKPTLMVAQGIQGFHPKAVPWKNDKNFYALIGSSNLTHAAFNSNYEANILTKISEQDFIKVKSWADEIAMKSSIPVSEDLWLEFYQEAETNY
KKS2VRQSVMDKGLPMEMPHYINQBELLAARRKQMRNHQTVCNQLNLTKQCAAGKIDMNDYGFENKLSWSKSENKGEVGNRPQDKTWKRTGKSSDFKLCIAIQSVFDPAPLTERDNNVAKQ
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SEQ ID 6799

CGACCACTACTTTCACGCTGGGACGAACCTACAACATCGCTGTGTGACCGCACCCGGGAACAGCACCCCTTAAACCAACAGCAGTTGGCGTTCATGCATCAACACGGGACAACTTCCAAATTTTGAACA
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GTTGGGCACCGAAGTTATACGCTTGATCGTGCCGGGAAACCTTTACCTTTAGAGGTACCGGTATACATCGACCAAGTTGACCGCACTTCAAACATAGAAACGGTGATTTTCGTACCGGGCTTT
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TCATACCAACTTTGCGCTCAACACAGACCTAAGATCATGATTATTTTTCCTTTTAAAGTAAAGGGACAGGCTGCGATTGGCTGTCTTTTCAGACAA

SEQ ID 6800

RTYTHAGTYNIADVDRTRNSTLNQQQLAFCLNFDNFQFLNSCPGVAVLGHALTGEHATVRLRHDRAMNAVRTGTVGVSTGLTGEVMTFDRAGETTFPTFGTYIDQLDTFKHRNGDFVTGF
QFSQFFPSQSKLNQATGCFMTCCKVSGFGFVDITGFFLTGKNLNGGLAVSIFGFYLCNAVGRHIQNGYRNKNTLLVEHAGHTNFAASQPT*SHDYTPPKVKVQQAATGLSFRQ

SEQ ID 6801

TGGTTTGGTTTCGTTGATTTTGGTGTCAAGTTTCAGATGTGGGTGCTTATCCGGACGGGTGCTGTGAAAAATGTTTGCCCCAATGCAAAAAAATCACTGCAAACCTTCACAAACGGGGCTGCTAG
 TGAATTTTTTCAAATCAACAGAT

SEQ ID 6802

LFVSLILCQFQMWLIRTGR LKMFAPMOKNHC KPSQTGLVVIFSNQTD

SEQ ID 6803

ATGTTGTAACCCAAAGCGGTGAAATAGCCAAAGATGCAAAATTATCTGTTTCTAAAATTTTATAGGCAATCTCAACAAATATAGAGGAGTCAAAAAGGGATGACACAGTTATTTTTACATTCAGAT
ACACCAA

SEQ ID 6804

MVPNRREIANMOIICFLNFLGNLNKYRGVKRDDTVIFTFRYTK

SEQ ID 6805

TTGGCCCTGTCTTTTCAGACAAAGTTAAACTTGGCAAAAATGTACCAAGCTTGACATTATATATCCGACAAGTCAAAGAAATATCAACAGAAATATCAGAAATATCTTCAATATGCCGCTCTGAAG
CGTTT

SEQ ID 6806

LACLSDKVKLGKNVPSLTLYPTSORNINRNINRNIFNMPSEAF

SEQ ID 6807

SEQ ID 6807
ATGAAATATTTTTATTATTAGACGGCGGCAAGCGTTCGGACATTCTCA CGGCGGGTTAAACCACACGCTTCACAAAAAAGCGAAAGAAGTTTTCAGCGCGCTCGGCACAAATGTTCAAGAAA
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GGA CGAAGTCTTTACCGCGGGACA CGGCAAACTCTACCAAAAGCGAGCGGCAGACACCGCGTCAATCCGATGAGGCTACCGGCACAGGCGCGTGTGTGCAAGGCAAAAAACATATGCTTTCA
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TGCGGACATCTCTGTAAACAGTGTGGTTTAAAAATCCCGACATGGAAAACTTGCGCAGATTATCAGGCACACTTGGAAAAAGTGTTCGGC

SEQ ID 6808

NNTLLLDGGKAPGHSHGGLNETHLHKKAEKVLTAIGHNVQETVIDAGYDVEAEIKFVWMDAVIWQMPGWVHEHPWTVVKYNDKVFTGGHGKLYQSDGRHRVNPTEBGTGCGLLQCKHKHLS
 LTNNAPIEAFTRGDDFFBEGKGDVLYMHFHKANEFIGLSRLPTFLCNDVVKNPQVERKYLADYQAHLEKVPFG

SEQ ID 6809

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SEQ ID 6810

SEQ ID 6810

MKTNSEELTVFVQVVEGSGSPRAAEQLEWANSASVRSIVKRLEELGVNLNRTTRQNLNTEBGAQYFRAQRILQEMAAETEMLAHVHEVQGVLRKVDASMPMWLHLLAPLAAKFNERYPH
IRLSLSVSEGYINLIERKVDIALRAGELDDSGLRARHLFDSSHFRVVASPEYLAKHGTPQSAEDLANHCQLGFTPEGSLNTWAVLDAQGNFYKISPHFTASSGEILASLCLSSCGIACLSDF
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SEQ ID 6811

[illegible]

GGCAGCGCGCATTTGGGAACTTCTTCTGGAAAGTCGGGATACCGCCATTATCGACAAACGGCATCGTCAACGGCTCCGCCAACTGGTCGCGCGATTCGCGCTCAGGTACGCAAGCCC
AAACGGCTTTATCTACACCTACGCCGCGTATGGTGTTCGGGTATTTGCTCTCGGCATGACCTTCTGGGGCTTGTTCAGA

SEQ ID 6812

MNDMTLYLIALVPLAGSLIAGLFGNKIGRAGAHTVTILGVAVSALVSAYVLWGFINGSRKTFDENVTYTWLTMGGLDFSVGLVDVTMTAMMVVVTVGSLMVHLYITIGYHDEKVGXQRF
SYISLFTFSMLMLMSNFIQLFPWEAVGLVSYLLIGFYFKRPSATFANLKAFLINRVGDFGLLIGLVLAYFGGSLRYQDVFAFLPNVQNTIQLPFGVWLSLITVTCLLLVGANGK
SAQFFLHVLPDSEMEGPTPISALIHAAATMTAGLFMVSRMSPIYMSSTALSVMVIGAITALFMGLVQNDIKRVVAYSTLSQLGYMTVALGASAYSVMFVMTHTAFFKALLFLAAG
SALIGMHQDHRHMGNLKKYMPITWLTMLIGNLSLIGTPFSGPYKDSIIIRAVKYSTLPGSGVAYFAVLASVVFYAFYAFRQYFMVPHGEEKWRSLEPHSDGHGEEHGLGKNDNPH
SPLVVTLPILLIAPSVIIGYLAIEPLYGDFKDVIFVNADAHPTMHIMKEZFHGALAMVSHSLTSPVLYLAAAGVAAANLLYVKLPHLPKIAQAQFRPVYVLFENKYLDALYFNVFAR
GTRALGNFPWKVGTALIDNGIVNGSARLVGALAAQVRAQTGFITYTAAAMVYFVGLVLLGMPFGLFR

SEQ ID 6813

TTGGCGGCGCGGTATCAGGTATTCGCATAGGCAACCGAATCGTCGCGCTTTCTTTTGAACGAACCTCGATTTTGCATCCGTCGGGGCTTCTACGAAGGCTATCAGGTTGTGCCGTG
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TCGTATCCGAGTTGTGCGTCAGTTCCAAAACCGTCTGTCTCGGTTTCGTCGCCCTAACCGACGAGGCAAGGGTAAATCTGCCCTTCGGGATAGTCTTTTCGGCGGACGAGTTTCATACCCAA
AACGTTTTCGTAGGAATCGAGGGATTTTTCGAGATTCGCCACGCGGAGCTA

SEQ ID 6814

LAAVSGIRIGNRIVAFLNLDPAFVGVFYEYHGCAPFHQAGFADDVSALPLHAFAGFVGIVHFNDRDVSQVVAQVVSFRIPVVRQFQNRVGFVAVTDEGKKSAPGIVPSAEQPHQ
NVLVGIEGFPFIAHAEL

SEQ ID 6815

ATGAGCATCGAACACACTCTCCGACACACGACGGCGAAACCGGTCAAAACCATGCGCAACGCCCTTCGCGCGATTTTCGACCGTGTCACTCCCTCTCGGAAATCTCGAACCTGCTTTG
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GCCGCGGACACCAATATCTTTGCTCTGCTCAAAACCGAAGACGACGCGGAAGTATTCGTCGAAGTATCCGACGCGGTCCGAGAAACGCTGATCGAGTCAATGGACAAAGGACGAATTG
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SEQ ID 6816

MSIEHTPTTHDGETQNHARPSADFDVHSLCEILEPAFEQIENGTFLEDAFLDKLTELVTLLARLHPADVADVLESPPRERNIVLLVKPEDDGEVLLLEVSDAVRETLIESHDKDEL
LAAVDLDDADELAELADDLPHQVVEALQTRDEEBRAQVKAAMSYEDNQVGAIMDFELVSIIRADVACEVVLRYLRFPDLPDHTDKIPVVDENDVLQGLPIRKLVLVADPEDLVENVHARD
VVRFAEDDVEEAQAPEFYDLVTAPVVDENKLLIGRITIDEMVDVIREESEADMLNMAQLQEEEDLFAVLDSVKNRMMWLAVMNLCTAFASRVIGAFEGSIEKIVLALALHPIVAGIGG
NSGNQITMTIVRAMAMQQLTDMQAGRLKKEVGVALVNGIITGTVMGAVSWLLYSGISLGLVMAAMTALLAATVGVLIIPVMEKFRGDPALGSSVLITAVTDSGFLIFLSLATIFLL

SEQ ID 6817

ATGTCGCGCGTCTGTAAGAACTCTCCATCCATTACCGCAAAACACTTTTGAAGGAAATATCATGAAATTTATTAACACCTGCGGTAATACGCGCAAACTGGCTGTGTGAACAG
CGGCGCGCTGCTTTGGCGGACAGGCAAAACGACGCTTGGCGGAAACGCGCAAAACGCTTTTGAAGCGCAAAAGCGGACGATGGAAGCGGTTGGATTGTAGTGGCGTTTTCGC
CGCGCTTTTGTATTTTCCATCGTTAAGAGGCTGATGAAG

SEQ ID 6818

MFGRLEKNSPSTAKHPLKENIMKFINTCRKYGAKLAVVTAAPLALAAQANAALPETAKNALEAAKADGMEAGWIVGVFAALPVFSIVKRVK

SEQ ID 6819

TTGGCTCGCAATTCAGGCAAAACGATGAAGATTACCTCAAATCTTATGGGTTTGGCGTAAAGACGCGCGGAGACCGAAATTCCTTATCCGAGACCTTTACAAAACCGATAAAT
TCAAATTTATAAATAACCAAT

SEQ ID 6820

LRRQFRQNDQEDYPQNSYGVGVKDAKTEIAYPETPKPIFKIITN

SEQ ID 6821

CGGCTATGCACTTCTCCGACAAACGGGATGACGTGCGGTCTCTGCAAGATCTTAAACGCGCGCTCAAATCATGCGGTTCTTCAAATTCATCTTTGTTGTTAAAAATAGTGG
ATTAAATTTAAATCAGGACAAAGCGACGAAGCCGACAGTACAAATAGTACGGAAGCGGAGGCA

SEQ ID 6822

RRMHLSPNRRDVRVLQDLNRPLQIMPFFQIQFVV*NI*V*IRTKRSSRBQYK*YKARQ

SEQ ID 6823

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GTCGCTGGTGTACCGCAACGACAAACGATTAATGTTGCGGATTTGGACGAGTGAAGGG

SEQ ID 6824

HTTLTHYLVGLALLFGISAMGIFMNRKNVLVLMSEIEMLLAVNPNFIAPSQHLGTAGQIFVFFVLTVAAESAIGLAIMVLVYRNQITINVAIDLDELK

SEQ ID 6825

TTTACTTGAGAAATAAACATCATCCATCTTAGAATCAGATGGATGCTTCTGCCAAACCAAGCCGATTTACCTTTTTTCGGGGGCAAGCTTAGGAAAGTTATGGATAAAAAATATC
CTGTTTTGTCTACTAAAAATGCCCTCGAAAATCTTTGAGGCACAA

SEQ ID 6826

PT*E*NIHP*NDASATKPDSTFFRGASLRKVMKKYFVLPFKKRLKILEAQ

SEQ ID 6827

TTGAGGTAATCTTCATCGTTTTGCTGAATTCGCGACGCAAGCGATTATCGCGGTTGTGTTGAGCGTTTGATTCGAGCTTGCCCAATCTCAAATATTTCTAAATACCAATGAAAT
TCAATATTTTA

SEQ ID 6828

LRVIFIVLPFLPQSDLSAVVFERLIAACPISNISKYQLKFNIL

SEQ ID 6829

EQ ID 68229
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SEQ ID 6830

SEQ ID 6830
MTFSVILFYTLAAVILYGAVRTVTAKNPVHAALHLVLTFCVSAMTMMMQAEFLGVTLVVVYVGAVMVLFVFMMLNIDIEENRAGFWRHAPVAGVGTLLAVALILILVNPKTDLAAG
LMKDDIPADVNNIRDLGSRITYTDYLLPFLEAAVLLLGWVAALVHRKTTNPKRMDPADQVKVRADQGRMLRVKMEAVKPQVESAESEVSDGLKTEGEGKA

SEQ ID 6831

SEQ ID 6831
ATGGATGCTCTTCGCCAAACCAAGCCCGATTCTACCTTTTTTTCGGGGGCAAGCCTTAGGAAAGTTATGGATAAAAAATATCCTGTTTGTTCACATAAAAAATGCCGTCGAAAATCTTG
AGGCACAAAATAAGCCGATTTCACCGACCGCACTGTTTTTTGATTTTGTGTGTTTTGCGCT

SEQ ID 6832

MDASACTKPDSTFFRGASLRKVMDDKYPVLFTKKCRLLKILEAQNKPISTALFFDFVVL

SEQ ID 6833

SEQ ID 6833

TTGAGGGCAACAATAATATGGCTAACTTAGTAAAAACCTTTCTGCTTGGCGAACTGGTCAAAGGCATGGCGCTAACGCTCAAAAACCTTTTTTGCCCGCAAGACACAATTTATTTTCCCGAAG
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CGTAAACCGC

SEQ ID 6834

SEQ ID 6834
LREHNMANLVKTFLLGLGLVKGMGVTLKNFFPARKDTIYFPEEKTQSVRFGLHAQRYPNGEERCIACKLCEAVCPAMAINIESEEREDGTRRTTKRYDIDLTKFCPGFCEEACPTDAIVE
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SEQ ID 6835

SEQ ID 6835
TTGAGGCACAAAAAAGCCGATTTACCGACCCCACTGTTTTTTGATTTTGTTGTTTGCCCTAAATCTGTTTGCCCGCCGCAATTTTCAGACGGCATAACA

SEQ ID 6836

LRHKISRFHRPHCFLLFLCLKSVCRRI FSDGIT

SEQ ID 6837

SEQ ID 6837
ATGCGACAATTATTGATTTCATCTCTGAAGATTAAATAATACATCTACGGATATTATCGCGTCTGCCGTTATCTCAACCGACGGATTGCCGATGGCGACAATGCTTCTTCACATTGGA
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SEQ ID 6838

MOOLLISILEDLNTSTDIITASAVISTDGLPMATHLPFSLNSDRVGAI SATLLALGSRVQELACGELEQVMIKGKSGYILL SQAGKDAVLVLVAKETGRGLILLDAKRAARHTIARAI

SEQ ID 6839

SEQ ID 6839
CCGAGCGCAGCTGTTTGTGATTTTGTGTTTGCCCTTAAATCTGTTTGCCGCCGCATATTTTCAGACGGCATAACATAAAAAATCCCCAA

SEQ ID 6840

PTALFFDFVVL P* ICLP PHIFRRHN IKNPQ

SEQ ID 6841

SEQ ID 6841
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SEQ ID 6842

SEQ ID 6842
MRTKWSAVRSCSRADTADITDNLNLYRLQKLEFLPYGDENGHSDGINLSDQQLPLMBQLSGSGKALLVDNRGLYLANANFHHSRAEELGLLAAEVAQMEKKYRLLIRNMLTYNNNANGVC
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SEQ ID 6843

SEQ ID 6843

TTGATTATGCAGGAATGGTTCACAAACCTCTTTGCCGCAACGCTCGGTCTGGGCGATTGGGCATCACCGTAGGCTTGGTGGTATCCGTCATCGTCAAAATCGTGATTATCTGATTCCGC
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SEQ ID 6844

SEQ ID 6844
LIMQEFQNLFAATLGLGDLGITVGLVVSIVIKVILIPILITVAYLTYPKRVIGFMQLRVGPNVTGPRGLIQPFADVFKLLFKEVTRPKLSNKALPYTIGPIMSLAPSFAAMAVIPFNE
EMVLVHNIGILLYILMTISLVYGVILAGWASNSKYSFLGAMRASQSSYSYELAMSAALVCCVMVSGSMNFSDIVAAQAGKIAGGSVFSWNWLPFPPIIVYLISAVAETNRAPFDVAGE
SEIVAGHIVEYSGFAPALFPLAEYTFMILIALTSLMFLGGLNSLPPQSGWIGVTPSAFMFMVKAAVLYWYLWLRATFPRTYDQIMRLGKVLIPIGPATIVVLGVMMISPLNWK

SEQ ID 6845

SEQ ID 6845
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TCACGGGAAGTTTGTTCACGTCGGGAGAACGCAAAATGTTGAAACGCTCGATTTTGGTCGGCAAGGAATCGGGCCCTTTTACAACAGCACCGGTACGTTTTCGACGTTTCAACGATTCTCT
GTGCAGAACGGTCAATCAGGGCGTAATCATAGCTTTCAGGCGGATACGGATTTTGTGTTTGCCAT

SEQ ID 6846

SEQ ID 6846
LDNFNYINTGROIOLHORIGSGFIGPIHDVHOAQMGADFLFTGSPVHVRRTQNVETLDFGRQRNRAFYNSTGTFCSFNDFLCRTVMQGVIIISPOADTFLVCH

SEQ ID 6847

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AGCGCAAAATGGGTCCGGAATTTCCAATTTGTTACGGGAAGTTTGTTCACGTGCGGAGAACGCAAAATGTTGAAACCGCTCGAATTTGGTCCGCAAGGAATCGGGCTTTTACACAGCAC
CGGTACGTTTTCAGTTTCAACGATTTCTTGTGCAAGACGGTCAATCAGGCGTAATCATAAGCTTTTCAGGCGGATACGGAATTTTGGTTTGGCAATTTATCAATATCTTCAAT

SEQ ID 6848

LLGDFRQSELLDFNYINTGRQIQLHQRIGSFIGPIHDVHQMGADPQLFTGSFVHVRTQNVETLDPGRQRNRAFYNSTGTFCFNDFLCRTVNGVLIISFQADTDFLVCHLSISFN

SEQ ID 6849

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CCAACCTGTTGAAGATTGGAATCTTTTACATTCGTTTCGAGGGCTGCTGGAGAGGCGATCGTCTGTCGGTATTACCAAGATGGATATACGCTCTCAGCCCGGTATCGACGTGA
TCACAAATATCTTGCACAAACATAATCTTAATGTTCGGTTTTGAATTTGATGCCCGTAAAGGAAGTACGCTAAACAAATGGTTAGCGCAATGTTATTTCTATTTGATCCGGACGAG
GTT

SEQ ID 6850

LDLDTKVLHLYSTPQERFNFPMWEILLSQSMGLVLLLDNARTNSLKDLEFFLHSPRGLLEKASVVVGITTKHDIRSQPGIDVYHYLAKHNLNVFVFEIDARKEDVKQLVLSAMLSIDPGLB
V

SEQ ID 6851

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SEQ ID 6852

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QSIRESLADNDVILVVGANLRKQPLPARLRAAKDRMALSVLGSKSELPFLLSQEAHPDEWAGRLKNLSADAHAHVASLKNAEKAAVILGAEVNHPDYAAIYAAQELADATGAV
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SEQ ID 6853

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SEQ ID 6854

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SEQ ID 6855

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SEQ ID 6856

LINNFLMRSSKHWASDGLLSFDINQYCLKRLPPCRHSRTGGNPFEPFRLLPKYRL

SEQ ID 6857

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SEQ ID 6858

MKNQSSDLHDQILQNLRFHIFQKRLEI

SEQ ID 6859

AGCGATAACAGAAGAACACCGCGGACCCACGGTACGGCGCGCTTCGCGAATCGCAAGCGCAGACCTTCTTCATAGCGATAGGCGCAATCAGTCTTACAGTAATGGTTACGTTCTCA
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SEQ ID 6860

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SEQ ID 6861

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CGCGGCCCTCTCGAAAGCATGATGAAAAAATCTGTTGGGCAGC

SEQ ID 6862

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SEQ ID 6863

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SEQ ID 6864

VVFWVSFRPTISISSPTMIPRSTRPVTTVPRPENGHEVFDROQEWVHGTLSRDVAVQCSQFEDFFVSGIAPQGFQCGTLYDRAVVAGEVAVGQVADFFHNFQQLGIVDHFVAFVH
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SEQ ID 6865

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SEQ ID 6866

VGRVVMVEAKIFILYGAANKGKSTTILWFLNQICRKFSLVFFERYGNGLDFVAVFDHEGQRIGFYSSGDNVEYVRNLYKLYSHNCDPILARQGHGVVVMQ

SEQ ID 6867

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SEQ ID 6868

MAGHSKWANTQHKARQDAKRGKIFTRLIKEITVAARMGGDPGANPRLRLALEKAENNMPKDNVQRAIDKGTGNLEGVVEYELRYEGYIGGAALMVDCLTDNKTTRTVADVRHAFPTKNG
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SEQ ID 6869

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SEQ ID 6870

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SEQ ID 6871

CCAACGTGGATGATACCTCGCTCTACACGGCCGCTGACTACGGTACCGCGCGGAAAAATGGAGAACAGCTCTTCGATAGGCAGCAGGAATGGTTTTGTCCAAGGCACGCTCGGGAGTCGGG
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SEQ ID 6872

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VFAGLRHRAVGSRTYQDCTVHLCGAGNHVFNVVGVTITVYVCVAGFGFVYVVRVNGNTACFFFGCVVDLVVSFCSAAEFFS*NSSQSSQGGFTMVNVTGNAVYVRFATFEFFLSH

SEQ ID 6873

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SEQ ID 6874

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SEQ ID 6875

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AAAAATATGTGTTTGAACACCGCAGCAAGCGGAGCCGGTACATTTAAAGACCGGACATCATATGTTCAATCCCTCATGCCCTGATTGAAGGATGATCATTTCCCGGTTACGCGATGGGC
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SEQ ID 6876

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SEQ ID 6877

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SEQ ID 6878

LDLHLHLVCRHSRAGGNPSSMVSNNVLSSETESYRWIPACAGHTAFQYPSRAD

SEQ ID 6879

GCCFTTACGGGCTTCAGTTACAGCAGCAGCTATGTGGGCGAGAGCTTCAGATATTTCTTGAATCCATAGAGTAAGTAGCGCGCTTGGGTTGAGAACGCGAGTTCGGTTCAGTAACCG AACATTCTGCCAGAGGTACTTCGGCAGGACTTTTTTACCGCGCATACCGTCATCCATACCAATACACACCGCGAGCGGTTCAAGTCGCCCATTTACGTCGCCCATGTATTCCTT CCGGAGTTTCCACTTCACTGCCATTAATCGGCTCAAGCAGGGCAGGAGATGCTTGACGCAATACCTTTCTTAAACGCTTGAGAGCAGGCAATCAAATGCCAATTTGGGAAGATCGCATC ATGGAAGAACCGAATACAGAGCGGATACGTACCTCACTACAGGATAGCGCGCAACGATACCGTTAGGCAACGTATCGCGGATACCTTTATCGACAGAGCAATAAATTCGCGAGGAATC ACACCACTTTAATTTTCATCGATAAATCGTAACCTTACACACCGGTTCCATAGGTTCCATTTCAATCACAACGTGACCGTATGACCTTTACCAACCGGATTTGTTGCAATGTTGATTC CAGCTTTAAGCGCTTTGCGGATAGTTTACGCTAAGCCACTTGAGGTGACCGGATTTGCTTCCACACCGAATTCGCGTTTCATACGCTCAACAATAATTTCCAAGTGCAGCTCACCCAT ACCGGAATAAATGGTTGACCGGATTTCTGCTGTACGAACGCGGAAGAGGGCTTCTTTAGCCAAAGCGGTTACGCGGATACCCATTTCTCTTGCTGCGCTTTGGTTTTCGCGCTCA ACGGCAATATGGAATACCGGCTCGGGGAATTCATACGTTCCAAGATAATCGCGCGCTTTCGACACAGAGTTTACCGGTAGTAACGCTTTTCAGACCGATAGCGGCTGCGATGTCGC CAGCGCTACTTCTCGATTTTCACTACGCTGCGCGCAGTATTTGACCAAAACGACCGATACGTTGCGGAGTGCCTTTTACAGAAATTCAGTACGCTATCGCGGATTTTACTACGCTGA GTAACGCGGATAAAGGTGAGCTGACGACGCTATTTGCTGTTCAACATTTTGAATGCCAATGACAGAAATTTCTCTTCATCGCTGCGCTTGACGCGCTGCTGCGCTTCTTCAGGTTAGGATTA ACACCTTGAACCGGAGGAATATCGGTAGGAGCTGGCAGCAATTCACAACCTGCGTCCAACATACCTTGAACACCTTTGTTTTAAATGCAGAACCCGACAGCATAGGCTGAATTTGCGCTG CCAAAGTACGTTGACGCAACGCGCTTACGATTTCTCTTCGCGCAGATCTTACCGCCCAAGTATTTGCTCCATCAGTTCTTCTGCTGCGCTTCGCGCTCGCGCTTCAATCATATTTGACGCCA TCTTTCGCGAGTTTTCGACCAATTCGCGCAGGAATTCGCCATAGGTAAAGGTTGTACCTTTATCGGCTTCAATTCAGATGATAGATTTCAATTTTCAGCAATCGCAACACCGGTAAGACTG TCTTTCGCGCTTACCGGAATGACGATAGGTACGCGGTTTTCGCGCAACAGGGTTTTCATTTGCTGACACACCGGAGAGTGGCAGCTTGGCGGTCCATTTTATGACAAACGCCAAGC GCGGAATTTGATATTTGTTGCGCTTTCGCGCATACGCTTTCAGATGCGGTTGAACACCGCCACCGCACAGTAAACATTACCGCGCGCTTCAATACAGCATAGAACGCTCTACCTCTAC GGTAAAGTCAACGTGCGCGGGGTGTCGATGATGTTGAAGCGGTGCTCGGGGAATTTTTCGCCATACCGGACAGTAGGAAGTAAACGCGAGCGGAGTAAAGTAAATACCGCGCTCTTGC TCTTGTTCATGTAGTGGTAGTACCGCACCGCTATGCATCTTCGCCAGCTTGTGGGTCAACCGGTATAGAACAAATACGTTCTGCTGCTGCTGTTTACCGCATGATATGCGCGG AATACCGATGTTGCGGTACAGGCTGATCGGGCTTACAGGACAT

SEQ ID 6880

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SEQ ID 6881

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SEQ ID 6882

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SEQ ID 6883

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SEQ ID 6884

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SEQ ID 6885

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SEQ ID 6886

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SEQ ID 6887

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SEQ ID 6904

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SEQ ID 6905

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SEQ ID 6906

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SEQ ID 6907

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SEQ ID 6908

YFYCKQTVKHNDKKDDFLVCR*IPTDI PHNQSDGWRKYCQVVSII/INH

SEQ ID 6909

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SEQ ID 6910

MEKRCAGMTBGLKGFITTSADTVLNHMRGSLWPVTFLACCAVENMHAGMARYDLDRFGIIFRPSRQADLMTVAGTLTNKMAPALREVDQLAEPRWVLSMGSCANGGGYHYSYS
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SEQ ID 6911

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SEQ ID 6912

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SEQ ID 6913

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CGCTGGAATGGGA

SEQ ID 6914

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ALEHE

SEQ ID 6915

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SEQ ID 6916

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SEQ ID 6917

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SEQ ID 6918

IRFFHTDKPSLAANRIKGGHIAVVLVVTETIYLCKSPFPQFMP*SRAH

SEQ ID 6919

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SEQ ID 6920

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TIDQTRALVVLRLQPKDARALFADRIERIHCFFVVDGFFVFAALTVPKPAEGVQIILRLPAVDDFRLPFCRAPAVAVDQSVQAFIKSRRDAPCLLYGFHIIHAGGKPAHREEDSQKINRQ
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SEQ ID 6921

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SEQ ID 6922

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SEQ ID 6923

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SEQ ID 6924

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SEQ ID 6925

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SEQ ID 6926

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SEQ ID 6927

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SEQ ID 6928

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SEQ ID 6928
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SEQ ID 6929

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SEQ ID 6930

SEQ ID 6930
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SEQ ID 6931

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SEQ ID 6932

SEQ ID 6932

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SEQ ID 6933

SEQ ID 6933

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SEQ ID 6934

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SEQ ID 6935

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SEQ ID 6936

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SEQ ID 6937

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SEQ ID 6938

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SEQ ID 6939

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SEQ ID 6940

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SEQ ID 6941

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SEQ ID 6942

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SEQ ID 6943

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SEQ ID 6944

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SEQ ID 6945

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SEQ ID 6946

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SEQ ID 6947

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SEQ ID 6948

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SEQ ID 6949

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SEQ ID 6950

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SEQ ID 6951

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SEQ ID 6952

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SEQ ID 6953

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SEQ ID 6954

SEQ ID 6954

MKTKFYHNQGEHLILYPAGWMPDPVANHLLIPENHDLLICYDQDNLNLDPDFSAYRHRRLVAVSMGVWAAERALQGIRLKSATAVNGTGLPCDDNFGIPCVAVFKGTLENLNTENTRSKPER
RIGGDA SFSEYDOOF PARFPEDLHOB LPA LPA M I G D R R R T D L I R W T N A L F G S G D K I F I P A N Q H R Y N T P R C T V Q E T D G G H Y L F S R F T H M S A L N N H

SEQ ID 6955

SEQ ID 6955
TTGCGCATACATATGCGCTAACGGCAACCTTTATACGGCTTACCTTTGTATGGCGGATTAAACAAAATCAGGACAAGGCGGGCGGCGCAGACGGTACAAATGGTACGGAAACCGATCCGCCGTG
TGCCTTCATCACCTTAGGGAACCGTTCCCTTTGAGCGCGGGGCGGGGCAACGCGGTACCGGTTTTTGTGTAATCCGCTATACAGCAGGCGTTGGTGAAATCCCGAA

SEQ ID 6956

LRHIAVTATLYGLPLYGGLTKIRTRRRRAADGTNGTEPIRLVLHLHLREPFPLSRGGATPYRFLIRYTAGVGGNPE

SEQ ID 6957

SEQ ID 6957

TTCAATCCGTTTCTGGGTTTCAGCAGTCTCTGCTCTACCCCTTGCCATTGCTGATGACGGCTCGCGGTGATAAGTCAAACCGGTACCGGCAGGAATCAGGCGACCGCAGTACATTCCTCT
TTACAGACCTGCGCAGTCTGCTCTTGTGTGCCATGATGGCAGCTTCGGTCAACACACGGGTGTTCTTGGAAAGTATGCGGCAGAAATGAAGCTGTCTGGTGGACAGGGAGGCTTTGGTAAATAC
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ACGGGTATCGGGATCCCAAGTTCGCAAGGTTTGACCGGCTTTAATGGCCATACCGCTTTGTACACGAGGATGGCACCGTAAGGTACTTTGTGGCGTTCGCGTTCACGGCGGATGTACATG
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CGCATACCGGATCTGTTTAACTTGAGCGCGACGAACCAACCGGACGGCTCCGCCATCATATAAGATTGAGTCTTTCATGACTCTGCTGCGGCTACCGGTCGATTAACCTTTT
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TGGTTCGCGGAAGATAACCGTATCGCGCAAGCGCACAGGCGGAACGATGCGTTAATCAGCTTTGGAATTTCTTTTCTTCAACGCTTTGTTGATCATATTCAAACCGGACGGCTTCGCGCA
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SEQ ID 6958

SEQ ID 69558

FIRYTLGSSLLLYPLPLMLTAAVISQGTGRNQATDDDLFTQAQFVLFANDGSFGQHTGGFLERCGRNEAVGGQGGFGNTQQYVFTCLRLFAFFQSPFFIGRHHIAAPDLLSGNKGFA
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CQQLGNARQTAGNAVAGPGRGLRNTRQYVAPDTDLFTAYGNHRTNGECHRNSRGRTGMDFAHVFVQEPHSRTQQFGSTRGTAPTAVNHYSQSGQTYIITGLFCNGNALFHVLEPHHTCMFGNHR
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ARQAAVTTVRAQTVAGFTSNRSTDFDITDLGVNHHIQHTQSTQGTGFNQSLAA**RIDNRHNGTNTQNTIAQCFNHTLALVCLHDKAV*STVAIVNDIQVLSYHTQVGTQVGTGVRGFGQRI
RQFLTVTVGRNKLVIQGYCTFAE**GNRRPNNRSVRFKHTQHTQGLQNLRSRTQTVGRHHNQV**LLIDPVAVTVNDNLFQGVVHHRFSNLIACTTPNIDHFVVAFVAGNQTLFVLVFD
FQNTGIGFSGSQGRFFPNWPHFVLVNGNGNTAFCKRSETGVHGVVGEDNRIAQAAQAERCNVNLGNFFFLQRQFVDIFKRQAFRODFAQOCTADGCPVTVDNRKLKTCFVFHFAAQTVYGFDFCTQL
DLFGMVCIMHFFHIGKQAAALAFGIDTVAGHVQQTQYDVLGRYDNRFAVGRRQYV**SQHQRACPHLRFAQAMVVTCHLVTVVKVGIKCQTHQWQLVQVPTDQNLRLBNTLTVQGRRTVNF
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LQHTFFVADDDVRNMFPQQAQFTVVAVDAAVQIVQIGSKTAAVQRNQRQTQIRRQYQRIHNNPLQLHTGHEGFGYQAFSDIFPDGVTGRFGLKLAQDQDFDACYIQSGSQPADTFRTH
PQIEVAVAFVQYVVVDFVFSQQLTLQRSHAGIGHCECFKVAQYAFDITQRHVQDQYRQGRQGFQEPNMGNGCSQFDMAHAFAAHFGQGNFYATFFTYGAFKQSFVSFAQAFVVDRAKDFG
ABGAEVGLFPERTVTVVDFRFPNFAIRP**ADGFGRGNTDFDGIKLFPHTCGLQRK*VQQIH

SEQ ID 6959

SEQ ID 6959
ATGGCTGCCCGCGGACGACACGTTTGAACCGCTTATTGGGATTTCCACCAACGCCTGCTGTATAGCGATTAAACAAAACCGGTACGGCGTTGCCCGCCCGGCTCAAGGGAACG
TCCC

SEQ ID 6960

MAAAAATRFEPLIRDFHORLLYSGLTKTGTALPRPGSKGTVP

SEQ ID 6961

SEQ ID 6961
 ATGCGCGGTTAATAAAGCGATGAAGAAGCTGGTAAAGAGGGGAAAATTACCGCGGTATTGCTGCAAAAAGACCGGGGTAAGTTTTTCATCTGATGCCAACCCCAA

SEQ ID 6962

SEQ ID 6962
LPVNRDEELVKEGKLPPYCCKDRRKFSDDANPK

SEQ ID 6963

TTGGCAACTGTCCGGTTGTGCCGATGGGTTGCCCTGCCGCTCCCTGAGCTACGCAACGGTTGTCTGCTTTGGGCGGGCGCGGGTGGCGGCCGGGCGGTTTGTCCGTATGATACGGAAGTTC
CGATATACAAGGGCGGGCTTCAGCCCGCAAAATCCACCAACTCCGCGGAATCCGCGGATTCGCCGCCGCTCATTCGCCATAGCGGGAATCCAGACCTGTCCGTCGCGAAACTTATCCG
A

SEQ ID 6964

LATVRLCRWVALPLPELRNGCLPWAGAGGGRAVCRYDTEVPTIYKGLQPAKSTNSAESADSRRRHSRLSGNPDL SVRKLIG

SEQ ID 6965

GTAGCGTTCACAAATCGATATCCAAACCCAGTGAAGCAATCTCTTTGACCAATACGTTGAAGGACTCGGGCATACCGGCATCGATTTTGTGTTCGCTTTGACGATGTTTTGCTACATTTTG
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CSTCTTTTACGCGCTTCCACAGAGCCAAACCGCTCGGAATTTGGTTTTCAGTCAGCTGCTCACCGACCGTACTCGACCGTTGCCCAGTGAATGTCATGTCGTCATTCGCGCTGCGCTGATGTC
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GAAATAGAATTAATGCGGCTTCGACAGCGCTCATCGGTACGTTTGTCAAAGCAATTTTCGACGCAAAAATTTTCGATAGAATCAATTTGGGTTGCCAGTAGAAAAGGAATTCGCAAA
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SEQ ID 6966

VAQPIDIQTQ*ANLFDQYVEGLGHTGIDFVFAFDVVFVHFGTAHVHVRHSQHLLQRCVACVFCQCPNLHLETLAAKLSFTAQRLLSNQTVRAGRTRVHFVFNQVVQFQI VHHTDCNLAV
 KCFA*TAVIDRQLSFTVVEAQFLMLRIFAWVSQVQHFAFDRPLFRTEYRGERCTFTQIGSQDFDFPISQAVQIFPLTAAVVEFVQBLAQLAGFASLFQHTVDALADTFRCRTPQVNFQMLT
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 QIFGRDFAAQGLHRAAVGLFDTNHLDTVECVVENTQLVWQIQITVAPQLGIDNGLGAFVALDAFAGKDLVNDRNTAHTGRHTQ*SIIFYVRRFV AEDGQAQFFFRRLQGFAPRRYLAQR
 IAGFYPTDNDTGFTVQLYHLTGLQVRNIAGNVTRTDLGIAGNDITQLLVNRSIAVLRSHFPHNQRRVFTVTPVRHGEDGHI/LTQSQVFIQIGRAVGHQAALQNLACIADFLSDVWGR
 IGTGFNPQIVNDITGFTVGTSGRVFVMDTDHNAVGTDLQIHASAGNDCCSSRVNMGNTLDTGTDHFNQFTQTRHCLTLHVGHGTQACVRAVTPQERNQOGRNGYHLTGCHVHILDVAVGRCHNGFA
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 GLIHLTLQLAGAEERFDGGRNGFRINQVVRHQV*FRLIQTFYGTFTTSQTAELVFSQLATRPYSTVAQVIDIVHFAMAVTQLDQSRNRGDNITPAQDITAVFGSTGKRLVQQAAPRV
 LLGFGQFLPVCARLKPHYTAAGQIVAVFTEBAQVKLLDLRLPGGRPARTHTVNRNTRRLPAGSLIRAQGINSTILQILQIDVGRNFFYAVNIKFGQQLFCNFIIGRSQYLAGFRINQIG
 SQCAQQAFLFYIQTGQACIGNITDIFRSNALTFGNQYIAFFIQDIDLGSFAFQITACQIGLNTV*RQIKRFFVVENIQDLLVVAQSLQONRYRHTAAVDTEIQQIFRIKFKIQP*TFV
 GNDAGGE*QFAGRVCLTIPVLEKEETGRTVQLGNHHTICA VNHKTRTARGHQRNFHAFVTFNFFRYRRFRPLIQNHQTDTRIRAGSISDSAQLTRFDIEQLRLAQYIKLQTSITVVAHR
 ENRILCRLOTQITVFKSIFMOLKZTRIRINLNGC*KRNQNPPIPLCKTLQDTRFHLGKRVHTHT

SEQ ID. 6967

TACACACTCCGAAAAGTAATTTTCAATAATAGGCCGCTGAAAACAACGGTACGCATCAATCTGATATTACATTTATTTGCAATGATTGATAAAAACATATGCAAATAAATGTAAACAA

SEQ ID 6968

YTLRKVIFNNRPSENNGTHOSDIYTYLQ*FDKNYANKCKQ

SEQ ID 6969

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GGGAAGTGGCGCATCGGACGCAAAATATGCCGAGCGAAACCTGTATCGTCCCTATATTTAGCGGGGAATGAAGCCACCTTGCCAAAGCGGAATATCGCAAGGTCAGGGTTATTATTG
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SEQ ID 6970

LIHQGRYITRENRKMLNMSNDYLGLASDENLRSPLOQYGNFPSTSSSRLLTGNFIYTDLEELVAQRFQRESALLFNSGYTHANLGLPALTTKSLILADKRFVHASMIDGIRLSRC
APFRYRHNDYEHLLKNLEKNVGRFDRFTVTVESVFSMDGDVADLKQLVLKQPPNTYLYVDEAHAIGVYQNGLGIAERDNLIAEIDLIVGTFPKALASVGAIVCNQVLKCLINQMRP
LIPSTALPPFNVAWTYIFERLPQFSKERSHLEQLSAFLRREVAHRTQIMPSEICIVPYILGGNEATLAKAEYLQGGYVCLPIGPPTVPKNTSRIRLSLADMTTDEVROFAACL

SEQ ID 6971

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GAACCTCCGTATCATAGCGACAAACCGCCCGCGCCACCCGCGCCGCCAAGGCAGACAACCGTTGCG

SEQ ID 6972

LSENGKGNFAAAAIVIPANLHSVIPTKVIRNAKSKETVLSDFPHRQVNIPIAYAGMTAAGIGGFGVGPGGLKLPALVYRNFRIATNRPAAATRRPRQTIVA

SEQ ID 6973

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SEQ ID 6974

LRIWEAHPSPALFSRRPQPSYRHPNQSEKIMNQTAIRNADARTRFIFDDMPVRGLHVRLNVWHHIVKQNYPAAIRCALGELLAAGVLLSGNLKNEGLIVQVQGGKMLVBAETS
RTVATARWDETAIEADDESLDGLLGGNGVFLTLQPKDGEPWQGVVPLEGGSIQMLVNYMKRSEQLDTHIALSASDEAAGLLVQRLPEEVLDEEAWHSTLARTLTAEELAEIDAGH
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SEQ ID 6975

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SEQ ID 6976

LMNQIRNETILILRAELFKLLSKNFHYDVIPELKPEATQHQTIX

SEQ ID 6977

TTTGATTTTCGACTTTAGCGCTGCTGCTTCAGTTGTTTTTGGATGCTTCGCGCTCAGCTTTAGAAAACACCCCTCTTTAATGGTTTTAGTTCGCGCGTCAACGATGTCTTTAGCTTCTTTC
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AGCCAT

SEQ ID 6978

PFDFPSACCFQLFLDVPFGFSFRNTLFGNFRCAVNDVFSFFQTQTSNCTDNFNHADFLIAGRSQNDIKFGFFFSIGSTGTSRTCNCSNRNTEFFFKSPNQVIQPHYQRTNCFQNVFPSN
SH

SEQ ID 6979

TTGCGAAATTGGAAAGCGATGTAATTTGAAATGAGGCGCGGATATCGTATCGACAAAAAACATTTGACGCGTTTATCGTTTCCGAAAAACCGCTGTTGAAATGTGGATTTCGAGAA
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SEQ ID 6980

LRNWRCKFEMQAGYSYPTKKTFTDAFIVSEKPLLEMSDSRIRPAKNRSKDKANSCLKTGRAILPQPSPSFRITYIPSPFRKWSGTQNLKKPFYPISFRTDRSGFPLMBE

SEQ ID 6981

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SEQ ID 6982

LFLDVPFGFSFRNTLFGNFRCAVNDVFSFFQTQTSNCTDNFNHADFLIAGRSQNDIKFGFFFSIGSTGTSRTCNCSNRNTEFFFKSPNQVIQPHYQRTNCFQNVFPSN

SEQ ID 6983

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AAACGATTTTCATTAAAGGGCAATTACTTGATTGTTGATGCTGGGTGCTTCAGGCTT

SEQ ID 6984

LCENMRFGTVRTDWMATETNIAEISALDYEGRGVAVUGGRTIFIRGALLDCLMLGCFRL

SEQ ID 6985

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SEQ ID 6986

MICRKPIGHTPPYDMNKTCRTAALLISGFSYANTVIVDVSFVAQGGHVFINIQQRLFLYTDCKLTKVYPVAVGRAMTQTNLGEHKIGAKAYNPVWHIPKSIQKRGDGVKTIAGPDPNP
LGPVVRVLGDPKLGILGHTNAPASVPGIRSHGCVRMKSPDALEFARTLATGSPASVITYQMAINEDADRNLWLAAFPDPYKNNLDASLKKSIGQWAKTQGGKTAPKVDVAVLKDRYGS
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SEQ ID 6987

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ATATTGAGACTCA

SEQ ID 6988

SSFFAGFFLCQSSQTKARKYRSLHNEQQFGQQLFAARNRQSLNLSSIHVFAIVRTGFNDNFVIFPRELVQHFSSNSIPRSSVQRTNHLIGQFYK*STLHCATSQSIFQNAQINAFIT
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SEQ ID 6989

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ACCAAGTTTCGAAATGGAAGCGATG

SEQ ID 6990

MFPPQSAFNLQGLNPEQLSAVTPPQSAVLVLAGAGSGKTRVLTTTRIAWLLQSGQASVSHIMAVTFNKAAKEMQTRLGAMIPINVRAMWLGTFHGLCHRFLRLHHRDAGLPSSPQILDG
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GLTEHYRTQKQDNQRLDNLDELVNAAIEFKPDSNFETLPENISDDPAFPLAFLSNALESSENGAGAGEKAVQLMTVHAAGLEFNAVFLTGMEEGRFPSEMSLABRGGLEERRLHY
VAITRARKRLYTMAQQRMLHGQTQGLASRFVEEIPPEVLHYLSVKKPAFDSYGNTRQTTVQRDKIIDDFKQPQTYAGFRIGQNVRAHAKFGTGVIIIDAAKGRSARLTINFGQKGVKELD
TKFARLEAM

SEQ ID 6991

FTGTTTGGCTTTTCTTACACCGCGCGCTTCCGCTTTCTGCAACATCCAGCGCAACAAATATCGCGCTGAGGCTTTAGACGCGCATATTTACAGA

SEQ ID 6992

LPGFSYTAALPLSATSKRTNMPSEGFRRHISR

SEQ ID 6993

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SEQ ID 6994

MRYFNRRGRMPDNLILISVLAKPSPTHARKTLIGGHIAAFQTDLDGRIDRMADLPSTLWVKLGKPLPRKGGIRIGFDIALSVGENISVCRNLNIGITAPQFANNRNRDTCSDTAKNKRCL
KPLSGFRHFLFRRLPLPRTLPTATIS

SEQ ID 6995

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SEQ ID 6996

VIIA*CNANT*THSAGYSNFFQVLTFSSSRFGFNDVQQRKVLQISFSE*STNRCMNNCLVGLVHLHTCFCIFRYFNGIRGNRTYFKVWHQITRTQDGTQLNDTHCIRRSNNNIK
VQIACDFSSQIFETDDIRTSLSFSCYITLSKYSHGCLTSTFRQND*TTDLNVRPRTINAQVRYVNRVFKFSGSSFFNQNGNCFVDCVQFVSFNRRAKNQAFRYFSH

SEQ ID 6997

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SEQ ID 6998

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SEQ ID 6999

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SEQ ID 7000

YNTLHVQAH*ASRTCYSTNSRIQVSSSQIRLPSFNFQLGTGQFTYLVQRIRTTFLQTGGFPQNRSSRFHKCE*FICKCSNHNRRNQTFHTLGCISKCTFEFHDIQTTLTQSRWN
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SEQ ID 7001

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CTGGGATATTGG

SEQ ID 7002

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GVLAESVGGIGVSGTAAGVILLVLAHYMYAFYMPASTTAHITAMFGAFLAAAVSLNAPMPTALMMAASNTMMLTHYATGTSPIVFGSGYTTMGEWMAKGFINSVVNFIPIFVIGISIMWKV
LGTW

SEQ ID 7003

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SEQ ID 7004

MSDRLDTARRHSLFLARQLDNGKLKPEIFLMLDKALTDEGQAFADWDKIRAESEELARQLRELRYVVSQIIIVRDINRISDLNEVTRITITLFDFAVNTALDFAYAYRDMYGTPI
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SEQ ID 7005

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SEQ ID 7006

MQYSTLAGQTNLSNNGFPLRLPLNMFYSHADWVITGVVDMVSGRSGARFGPEAIRRASVNLAWEHRRFPWTFDVRERLNIIDCGDLVFSFGDSRDFVEKMEAHAGKLLSFGKRC
LSLGGDEFTLPLRLAHARYFGKLLIHFDAHTDYDNGSEYDHGTMFYTAPKEGLIDPSRSVQIGIRTEHKKLPFTVLSPKVNEDSVRETRKIKETVGNMFPVYLTFDIDCLDPSFAP
GTGTFPCGGLSSDRALKILRGLTDLDIVGMDVVEVAPSYDQSDITALAGATIALEMLYLQAKRD

SEQ ID 7007

GTGGCGAGGTTTGAACGGGAAACGGCGGCATTTCGCCGTGTTTTTTATCGGCAGGCATCCGTCGGAATATCGGGGCAAGGTTTCAGACGGCATCGAAGGTTGCTATGATA

SEQ ID 7008

VARFERETAFAAVFLSAGIRPNIGARFQTASKVAHI

SEQ ID 7009

ATGCCGTCTGAAACCTTGCCCGGATATTGCGAGCGATGCCCTGCCGATAAAAAACAGCGCAAATGCCGCCGTTTCCCGTTCAAACCTGCCACGCTCTTTTAAACAGCA

SEQ ID 7010

MPSETLPRYSQCLPIKKQRQMPFPVQTSFSPKTA

SEQ ID 7011

GTAAATCTCTCAACCTTGGCTGAACCTCAGCTCAACGGGTGTTTCTCTACCAATATCTGAACAGACAGCGTAACCTTAFTCCGTTTCAATTTGACCTCTCAACACCCCGTTAAATCC
GCAACCGGTCTTCAATTACAGAACCTGTTGACCGACCTCAAAATCAACTTTTGGTTTCGGCTTCTCTATGCCGCTCTGAACCTGCTGTAAATAATTTACAGCTCTCTCTGACTAATCG
CGTGGGCTTATAGCCCTCCCTCCAATAAAACAGAAACAGCGGAGTGCTTTTACAAGATGCCAAGAGTCATCTGTCAATTTCCATCTCAACTAACACATAACAGGATATGACTTTCT
TTCACTAATAGTCTTACGACCATTTGCGGATATCAACAACTTTCTCTACAGGCACGAAATTTGTCCGAAATAATCTCCATCTCTCAGGGCAATTCGCTCTTCCAATATTCGTTGGACA
TCTCTCTCAACCCCGAATACGCTGTACAACTATCACTTTTTTCGACAT

SEQ ID 7012

VNLLNLAEQLNGCFSTKYLNHA*LIPIIDLLNHPVKIRKSFYITNLLTDLKFNFWFRLLYAGLNL*NNPSLSITNRRGSI SPPSNKTRNTGSAFYKMPRVICHPHLN*HITRI*LS
PTNSLFTIADLNNFLYRHQNLSEIISHLLTGNLFPQYSLDILLKPRIRLYNIPFFRH

SEQ ID 7013

ATGCCATCTCTTACCATCCGTGAAGTGTGCAACATTAATCAATGGAGCATAGGTTTATATGATGTTGACGATTCGCCGCAATCATCTGCCGCCCAATCCCTCGCAACACAATCAAACCTG
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GGCAGCGGAAGAGTTCGGCTATAAGGGCGGTTATGTTGTTTACCTATCAAGGTCAACCAACACCGCGCGTCATCGAGTCGCTTATGTCAAGCGGACAAACCGCATGGTTTGAAGCC
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ACAATTTACCGTATCGATTACGATGAAGGAAACACCGTTGCCGATATGCTCGAATACGTTTATCAAGATCCGAAGAGCTGATGAACGCTATCGCGAACAAATCGAATTCAGACCTT
CTGCTCTCGCAGGCTATGCTCTTCTTAAAGAACTCGAAGCGGGCTTAATGTTATACCTATTTTGAAGACGAA

SEQ ID 7014

MEPIIFIREVCNINHSIGYIDVDDSGEILVRPNPQHNQTVSLQKLTEAVQKQKQARLPVLFPCPQILEHRLRDINRAFTARBECCYKGGYCLVYPIKVNQHRVRVIESLMSGGQPHGLEA
GSKAELMAVLNAHAGTRQTLIVCNGYKDREYIRPALMGEKLGHVYLVEIKLESIQMVLEEAELKIGIKPLGRVRLASQSGSKWQSSGGEKSKPLSASQVLQVLDILKQNRDCLQLLH
PHLGSQNLNRDVAIVGHEARFVYELHKLGVNIRCFDVGGLGVDYEGNRQSDCSVNSLYNEAATVWGI SQACLEHGLPHPTTITESGRGTAHHAHLVANVIGVERYPRLDAPS
PEAPRVLHSMWETWIDSASREKRSLSRWIHEQFDLADVHNQYVNVGLLSLAQRAWAEQLYLANICHEVGELFNEKHSRHTIIDELOERFADKLYVNFSLFQSLPDANGIDQLFPVCPITG
LNEPIARRAVLLDITCSDGTIDHYIDGDIAGTMTFNPEDYPEZEPPLGPFMVGAYQELGNMHNLPDGTADJVVRDQGQFTVIDYDEGNTVAIDMLEYVYQDKELMKRYREQIEHSL
PASQAMSPFLKEAGLNGYTYLEDE

SEQ ID 7015

ACCTTCCCTTCTCAGCAATACATCAAAAAATAACCAAGAAATGCTGTATCTGCCGCATAGATAAATATAGAAAGCACAGCAACAACACTATAACAAATACAGTCATCTGACGGCATCT
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TAACATCTTTTTCAGGCGTATGCTCTGTCAT

SEQ ID 7016

TFPSQVYIKK*PRNCCI CRIDKYRKHSNKHYNKYSHSDGIPTLRPNHLEFPGPRI*EICKKTLT/GIRCFPIILNNQLIHPNLFPRMPCF

SEQ ID 7017

ATGCCGTCTGAAGCGTTATCCGCGCTCAGACGGCATTTGTTTCCGACAGTTTATAACTGTGCTGTTGTTCTTGACAGAAACACGACCTTATTTATTTGAACAGATTGGAGGACATGA
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GCATGAAATCGTAAGAGTGATGTTTAAATAATCCACACGGGAGAAAGGTGCGGCTTATGCTGTTTAAAGAGCGTGGCGAGGTT

SEQ ID 7018

MPSEALSGVQTAFCFPPTVYKLSLPLDRNDLIYLRLEDIMGFWGSGVGAAKAVGEGILRAGNQHKALKMEYAEKSSSELHEIVKSDGFPKNSTREKGAAYAVLKERGEV

SEQ ID 7019

ATGCCGATTTCGTCGATATATCCCGAGATGGCAAGGGAGCAATCGACACCGGCACAGGTGCGGACGATTTCGCTTTTCCGATATGCACAAAACC

SEQ ID 7020

MPILLDISRDGKGRIDTGTGADDFGFPDMHKT

SEQ ID 7021

AGGCTGTTTGGCAGATTTCGGCAGCATTTTGTATCGGCGGTGACAGTCAATTTCTGTCGCTCAAGCGCGCACTTTTCTTCACTTCCGCAACGAGGCGGCTGTTTTCGCGCGCAAGGACAGC
AGCCGCCCGCAACAGGCAACAACTTCGGAACAGATGCGGACGACAAACGCGCGCAACAAATACGACATCAGCGGACAGTTGACACTCTGCCCCGGAAGATAGGAAAGGTAACGGCATCCA
TATTAATGACGCGCAAGCAGCAGGAAGAGCAGCAGGATAATGATTTTATGACGGTATAGATAAGTTTCACTGTTTCTGCTCCGTAATAAAAAACCGCCACGCAAGCTTCGCACTCTGAACCA
AGATTGCGTGTAGTTTAAACGATTTCGACGGTTTCGATAGAAATCGGCGAGCTGTTTCGAGCGCATACGAGTATGCGATTGCGGACAAATTTACCAATACACCGCTCTTCCCAT

SEQ ID 7022

RLPGRFGSILYRRCQFLSAQARTFLHFRQAAPFAAQGGQPPPEQKXSEHADDKRAEQYDNRQIDTLPRKIGKNGIHINDGKQOEQDNDQDDGIDKPHVCSVNKNAARTASHSE
RLR*FKRPARFRJEGSVFGRHTEYALADNFTKYTAPFH

SEQ ID 7023

TTGAGCTATTGGCCTCTAACTTAAGCGATAACAGAGAAACCACGCCGCCACCGGTACGCCGCCCTTCGCGAATCGCAAAGCGCAGACCTTCTCCATAGCGATAGCGCAATCAGT
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TTTTTACG

SEQ ID 7024

LSYWLNLSDNRNHAGTHGTAAPFANRKAQTFPHSDRRNQFYSNGYVLFHYHFTFFQSNRAGYVSGTEVELGTVVGEKRGMAAALFFAQYVHFCFELGVRSDSTRFGQYLTAIFYVTFG
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FFS

SEQ ID 7025

ATGCCGCTGAAGCGCTTCAGACGCCATTTCGCTGTCTCATCAGTATGAGCGAGGCTTTCTTATTAATAAATGACATTCACGCTGATTGTTA

SEQ ID 7026

MPSEAFRRHFACSSSGMRQAFLIKMTFHADLL

SEQ ID 7027

ATGAACCTTGATTTAAACCGCTCAAAAGTCCGCCCTTCTTGGAAGGATATCTGTGGGGGTATGAGATAAATACCTTGGGTGGGCTGATGTGGCAGCTTATGCCGAAAAATGACGCTTT
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SEQ ID 7028

MNLDLTAQKVRSLWKDILMNGYENKYLGWADVAAYARKMTLSHDERVFKLSLTKNSNILELKPVEDLASETRGYSFKNWLILNDVFRKEEFYGPLGEVEKIYADFDYPERIESFVRY
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SEQ ID 7029

AGCGATAACAGAAAGAACACCGCGGCACCCAGGTACGCCGCCCTTCGCGAATCGCAAAGCGCAGACCTTCTCCATAGCGATAGCGCAATCAGTCTACAGTAATGGTTACGTTCTCA
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SEQ ID 7030

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SEQ ID 7031

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SEQ ID 7032

LLCFNGGLEKHLIFNQPIKGLKMKLLAAVVSLSNAATFAGDSAEQIYGDPHFEQNRKAVKNLEBQRYQVYVDADDYWGKPVLEVEAYKDGREYDIVLSYDILKIIKEQLDR

SEQ ID 7033

ATGCCGCTGAACGCACGTTTTCGCCGTCAGACGCCATTTCATAGATTGGTATCGACTGTTGAAGAGCAATCAGCCGTCATTGGAAGACTTTTCG

SEQ ID 7034

MPSERTFCRSDGIFIDWYPTVEAISRHLEDPS

SEQ ID 7035

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GCGACAT

SEQ ID 7036

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SEQ ID 7037

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KFSKKEIDETTKFVGIYGAAGLAYIKVNDAGNLNGEDSGLOSPITVKFLSENALKEIERTAAQNGDIIFPGADAKVVMNAVGAIRIKVGLHEHGKNGYFTDEWKEFLWVDFPMFYDEE
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SEQ ID 7059
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MGRGHEEFUNODAVHRANI-LALRLTVVSDALRAEVGVDFVNFI-ALNGIIGAFGFAYVAVDALVGNKKRHFFSPSTKLSKPGGRGL

SEQ ID 7041

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SEQ ID NO: 10

MAAPFSEHSPVVMYPLARRILFALDAEKAHFPLDALNTVYKLGILPVTINRTKPIKLMGMDLPNPVGLAAGLDKNGEYIDALGALGFGFLEIGTVTRNPQGPNGPQRLFRVPEHQGTINR
HGAFNNHSGIDTAMIRNTEKSKYQGVGLINGINKNAVTPIQNAADDYILCLEKAYAHASYITVNTSSPFTKNLRALQGGGELGALLEALKNQAQLAAAHKGYTPLAVKIAPDLDEAQIEDIARV
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SEQ ID 7043

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MSNTEQOVKKTIAFOLGVNEADVKNESFODDLGADSLDTVELVHALEAFGC EIPDEDAEKITTVQLAIDYTNAHNG

SEQ ID 7049
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SEQ ID 7047

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IRGAAEAVVSGDRI~~LA~~VVGIDVVD~~S~~OLDGGDFFGIFVGDFAAEGFFOSHNLHGIIQ~~RI~~RAQVVL~~E~~GRFVFHVGFVYAQLFSNNFLNLLFDV

SEQ ID 7049
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STRNDPATASTRPDKGRDGFVIGEGAGILVLEELHAKKRGAKIYAEIVGFMSSDAYHITAPNEEGPALAVTRALKDAGINPEDVDYVNAHGTSTPLGDANETKALKRAFGHEACKTVI
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SEQ ID 7051

TTGAGCCACTTGGAAAAACCTTAATTCAAATGTACCTGCCCGGACTTCCCTCCCTATATCCCGTCAGCCAAATCAGGTTTGTCCGGCTGCCGTGCCGTGCATATAACATATGCCCGG
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AACAGACGGTTTGCACCTGCCCAAAACCGATTCGCGGCTGTTTTCTCAAGGGTTTGCACCGTTTGACGGTTGTGTCTGCAATCAGACCCGTTTTCGATTACCGGATGCCGCTCCAT
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SEQ ID 7052

FSHLENP*FKCTLPRLPLIRQPIRFVRLPACLDINICAVIQACAQYIEKTFPTLPRKRRIKEDDIEFLF*VCQIGNAVRTDGLHLPTQFAAVFLKGLHRLTVVVCNHDFFCITRCRLH
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SEQ ID 7053

ATGACCGAACCTGCGCGGAGGCGGCAAGCTGCCAAGCGGTAAAAAATATCTGATTACAGGCACTTTTGGTCTGCCGTGCCGATTCGCGTAACGGTTTGGGTGGTTTCTATATCGTTT
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SEQ ID 7054

MTEPAEAGGKAALKKYLITGLWLPPLAVTVVVSYSVASDQLVNLKQWRPQVVLGPNGLGVIVAVLAVLFTGLFAANVLGRQILAAWDSLGRIPVVKSIYSSVKKVSESLS
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SEQ ID 7055

TTGCCGCTTCGCGCGCAGGTTCGCTCATCTTCTGTGATCCGACAAAGTCCGTACAAACCGCACATTTATACGCGTTTGGCGGATTCAAACGAATTTTATCCGCGCCGCCAAACCGC
CGCGCGCTTCAGACGCGCAGCACT

SEQ ID 7056

LPPSAAGSVLLDSKVRTNRTLYAFARIQTNFLSRPAKPPAEDGTAT

SEQ ID 7057

TTGGTATGTTTGCCTGCCGCAATATCAAAAGCTGAAAGTTCAAACGGTATTATACAAGACCTGTGGAAGATATGCCGCTGAAACCTTTTTCAGACGGCATATCTGTTAAACGGTT
TCGCTCAGCTTCGCGGCAACTCGATTCTTGTCTTTTGTTCACATTTCTTTGCAATTTTCAATTTCCATTTTAAACAAATCCAGCTTTACCGATGCATCC

SEQ ID 7058

LVCLPAALIKSLKVQTVLYKTCRRICRLKTFRRHICLNGFGQLAEQLDFVFCNSLQCFNSIPNKSFTDAS

SEQ ID 7059

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SEQ ID 7060

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SEQ ID 7061

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AA

SEQ ID 7062

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SEQ ID 7063

TTGAAAAAGAAATCCATATCGGTGTTTCCGCGCAGGAGGCATCGTGCCGCGGTGCGATGTTATGCTGTATCAGTCGAAAAATATCTTGTGATTGTATATAAAAAACGGCTGTTTGGCAAA
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SEQ ID 7064

LKESISVPRRRRAAVRCYAVSVENILLIVYKTAWQKAC

SEQ ID 7065

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SEQ ID 7066

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SEQ ID 7067

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SEQ ID 7081

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SEQ ID 7082

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SEQ ID 7083

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SEQ ID 7084

KNVFI*NPQPG*ILLYQLF*NGNSNFYPTVVRTPSALLQIQPEMLFGNAVKLAQ

SEQ ID 7085

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SEQ ID 7086

VMI LHPKGRAYLNGGLIAAVICGLIRLICVPCSPATGGVFGKCRKLVSDGILSCGSGFADGQDKQGRAGRYGIGVPHPAVVTELCHNDAADVRAESADLVGBHHQSEQSGEVARAE
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SEQ ID 7087

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SEQ ID 7088

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SEQ ID 7089

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SEQ ID 7090

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SEQ ID 7091

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SEQ ID 7092

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SEQ ID 7093

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TGTAATGGCGGATTTCGGT

SEQ ID 7094

LRCRRFDLFFPAFFLRADFFHAPFGSFDGQYRPMARAFFGNGRVPSGVVAVGIGAATVKQFVAVAGFALDEVAFALRALDAGIFGFRQLRDVFAFGVVGATDEFTAGAAVVFHQPASAA
FGAFATVEFLDFGRFGDAGSFPFGFVDVAGVTALGTTGRNETAHFELDLQFVFAAFRAGFVKFLRSEFGAFDALFFPHLFDERFPFVHGNPAAPAVGDFVKLVFEPGGEVVIDVL

GEVFGQEPIDDVACVGGHEAFLLKGNVFAVFERNNAGVGRGAADAVFFEGFNQCGFVARRRGGEVLFAVEFVDRQFVFAHFQGQFFAVPALFTVAAPFVNAKEACBGLHLSGYSEHAFADGNIDGGIVFEGGRHLTGNGTLPNHLIEFELVCTQBGFDAGRAVHGSRADRFMGFLGVFGFGFVLPGGTRQITFADFVFNVMADFC

SEQ ID 7095

GTGTTTATGGGGCGGGGGTTTTCTTTTTTTCACACCTCTTTTCATCAGGAATCTGCCCGTATGAAAAATCCGTATTAGCCGTTTGGCGCGCTGTCTCGGCAGCCTCGCGCGCAGCG
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CTTTAAAAAGCCAAACATCTGAAGCTGACTTACGACTTGTACGAAAAACAAGAAACGCTGGGAAGCCAAAATGCTGACCGGCAAAATCCGGTTACGATTGGTTGTGCGCGGCATCGCCTTC
CTGCGCGCCCAATTCGAGCGGGCGCGGTATCAAAAGCTCAACAAAGACCTTGATTTCCCAACTATTAATAAACATCTGATCCCGAATCTTGAATAATGCTGGAAGCGCGGACCGCGGCAACCACT
ATGCCCTCCCTATTTTCTCCGGCGTGAACACGGTTGCGATTACGGCGAAGGGCAAAGAGCTTTTGGCGCGCAAGCTGCCGAAAAACGGCTGGGATTGTGCTTTCAAACCCGAATACACCG
CAAGCTGAATTCCTGCGGCATCGCCTTGTGGGACACCCCGAGCAAAATGTTCCCGATTTTGTCTGAACTACTTTGGGCAAGACCCAAAGGCTTCGAATCTTGAAGATTGGAAGCGCGCGCG
GAAGTGTGGAAGCTATCCGCTCCGGACGTCAAACGTTTCAGCGCGCTTCATCATCAGCAGCAGCTGGCGCGCGGCACATCTGCTTGGCGGTCAGCAACCGCGCGGAATTTGAACTTGGCGGAAG
CGGTTTTCGAAGAAGTGA AAAACAACCTCGGCATCGAAGTGTGACACCGAAGAGTATGGGCTTTCTGGAATTGAGTCTTGGCTGATTCGCGCGATGCGCGAAACCTGCGCAACCGCCACAA
ATCATCACTACACGCTGCAGCCCGAAATTCGCGCGAAGAAACGCGCATTCGCGCTTAACCTTCGCGCCCCCGCAGCAACCGGCGCGCAAAAATGCTTCGCCAGTTGGTGAACACCGGTTTC
ATCTTCCCGAAGCAGCAGGATATGAAAGACGGTTTCGTCATCGCGCAATGAGCGCGGATGCGAAAAAATCTGTCGGTCAGCCTGTGGCGAATAACAAAGTCGCCACCAAC

SEQ ID 7096

VFMGRGVPTFNSLPHQSRAMKMSVLAVALAASLAACGSEKNVQPOAGSAPAANAEEAATDTLATYNWSNYVDESTVEDFKKANILKLTVDLYENNETLEAKLTKGSGYDLVWPGIAFL
LPRQLEAGAYQKVNKDLIPNYKNIDPELLKMLEADPGNQYAVPTFSGVNTVAITAKGKELLGGKLPENGWDLFKPEYTRKLSKSGIALWDTPEMFPTLLNYLKDKPKGSNPEDLKA
EVLKSTRPDVKRFPSPSIDELARGDICLAAGNGDNLAKARSEEVKNVGVIEVLTPKGMGFWIESWLI PADAKNVANAHKYINYTLDPETAAKNGIAVTPAPASKPAREKMPAEIWN
TFSPNEQMDKDGFMVPMQMSADAKLSVSLMOKIKVGTN

SEQ ID 7097

TTGGACGGGGATTTCGACGATTAAGAGGTTTTTCGCCATTTGTCGTTCTCTGGATGGTGGTTTTGACGGCGGTGTTTCAGACGGCATCGGGCGGGCCGGCGCGGTC

SEQ ID 7098

LDGDSTIKRFFAICRSLDGGFDAGVSDGIGRAGAV

SEQ ID 7099

TTGCGCGGACAGGCTGAAAATAACAATTTTACCGCATTATCATTTACCTTAATCGGAATAAAGCTCAAACAGACCCAGCAGCTCGACCGCGGGCTGCAACAATCTTTGCGCGTATTGCAGATGCGCGGTATCGAACTTGAACGCGAGGTGCGAAAATCGGCCGTGGACACACCCCTGCTCGAACGCAAGAAACGGATGAATTTTCCGATGCCGAATTCAGCCATTACACCGCGCCCGCGCTCAAATFCGCGCGAGACGAAGGCGAAGATATGCTGTGCAACATCGCCGGCGAAGAAGATTTCAAGCAATPACTCGACGCGCAGCGGTGCGAACACCECCCTTTCCGACCAAGAAGCGCGCTGCGTCCACATCCTTATFCGATTTCTCTTGACGAGCAGGGCTACCTGACCGACAGCATCGAAGACATCTTGAACATACGCCCTTGGAGTGGATGTTGGATGAAGCAATGCTGAAACAAGCCCTGACCGCATTGAAAAAATTCGATTCGCGCAGGCATGGCCCGCCGCGATGTGACAGCATCGTGTGATTCGCGCATAGAAAGATCGGGCGGAATFGTGTGCCAAACCCCGCGCCCTGCATATCGTCCGAAACGCCCTCGACAGCATCGCGCAACCGCGCGCAACCCCGCGCGGAATAAAGAAATCGTGCGCCAAACGAGCGACACTCGAAGCCGCACTCGGCTCATTTGCTTCCGCTCAACCTCTTTCGCGCGCGCGGTTTGCTGCTGCTCCACGCGCAAGTCTCTATTCTGACGAGGCACTCGCGAACCTGCTGGCTTTCCGCGGTA

SEQ ID 7100

LRRAQENNNFYRIITLIGIKLKQTOQLDQRQQSLRVLQMPGIELEREVENWPSDNPLLERKETDEFSDAEFSHYTAPARQIGGDEGEDMLSNIAEGEOPKOYLHAQACEHPLSDQEAAC
VHILIDFLDEBQYLTDSIEDILDHPTPLEWMLDEAMLQALITALKKFDPAGMAAADVTESLILQIERSGECAAKPAALHTVRNALDSIDGNRSQTPARIKNACPKPTAAHSPHSASILLRST
PFPFVLPFRPRPSPILTRHSPCHLSAV

SEQ ID 7101

ATGCCGTCGGAACGATGTCGACGGCATTTTATATTGGATTGAAATAGAAATATTTATACCGTCGCCCCACGGCCGGGATTTTCAGATTGCGGACATTTATAGCGGATTAACAAAAACCG
GTACGGCGTTGCCCGCCTTAGCTCAAGAGAAACGATTCTC

SEQ ID 7102

MPSEKSDGILYNIRIEIFIPSPPRPGFOIADIYSGLTKTGTALPRLSSKRTIL

SEQ ID 7103

CTCTTGCGGTGTCAGGCGGTTTCGATTGTGTTCTTCCAGCCGCAATTCCTTTTTCGGGGCAGACATTTTTCACGCCCCGGCGTTTGGTAGTTTGTATGGCCAGTACCGGCCAAATGGCAGTTTCGGC
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ACGGCCTCTTTGCCCTCGAGTTCTTTTCAACACATCGGCTTGAGCGGCTTCGTTTCGGCAGGTGCAATTTGTCGAGTTTCGCGCGCTGTGTTTGGGCGAGTTTGGCGGTGAACCTGCTGCGG
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CGCGCTTTTGGGAGAGGTTTCGCGAGCTGTCGCTGAGGACGCGAGGATTTCAAAATTCGCGCGCCCAA

SEQ ID 7104

LILCRRRDFFFAAFFLRADFFHAPAFGSGDGGYRPMAVRAFFGNGEVPSPVAVGIGAAVVKQFVAVAGFALDEVAFFALRALDAGIFGFFQRLDVFAGVGVATDEFTAGAANVVFHQPSA
 AFGAFATVEFDLFGFRGDAGSFFGGFVDVAGVTALGITGRNETAHFABLDLQVFFAARFAGVKFLRSEFGAFDALFFPHLDERFPEFVHHGNPAAPAVGDFVKLVFEPGGEVVVDV
 LGEVPGQEFIDDVACVGGHEAFLLLKGNVFAVFERRINAGVGRGAADVFFEGFNQCGFVVARRRGGEVLFAVEFVDRQFVAFAHFGQFFAVFALPIVAAPFVNAAEACECHLHLSGYSEHAF
 ADGNIIDGGLVEFGGRHLLTNGMTLPHNLIIEFLVCTQEGFADFAGRAVHSGRADRFMGFLGVFGFVLFGGTRQIFPADVFVNVNADPG*RFVPSIQHIVGTHIGNQDGTLPFYVYTFVKLLG
 GTHGAVGGEAQFTHGILHGGCGKRRRGVAAALFLFDGGNDGLFAFEFFQIHIGLSGFVRQVELFEPRAVVLGEGFGGELAAAFMAVEMHRRIFLRFKRADFVVALANQPGQGTHTARAQTA
 SDFFPQQRREVETDQIVQSAALRLIDQIHFDFARMGDGIEHGVGFGNLVEHDALRLDVFQTAQFEGDKQKMERNRFAFPVRVCGCEVDVPGFPGSGNNRLDFAVAADLVPFRKAVVGIDR
 AAFGEVDVDSVGGEDFKAALQ

SEQ ID 7105

ATGGTCAGATGGGTTACGGGGCATTGGAGGTAGTCATCGCTCTTGTTCCTTTTCTCAGGTGGTCAAATGGGGGGCAAACGGCTTACAGTACGATTTGGCGGAAAGCGTATTTCGTAACCG
GTTTCTTGATGTAAATAAATTCTGTAATCGACATTTTATTTTCCCTTTTGCAAAACTATGGATGCGATTATACGCCAAGATTTTCGTTATTAATAACTATGAAATTGATT

SEQ ID 7106

MVRWVTGHLLEVIALVPFLRLVKWGANGLYDLAESVFTGFLIVINFLNRHFIFLLQKLNMRLYAKIFVIKTKLI

SEQ ID 7107

ATGGATTCTCTTTTTCAAACCGGCAGTTTGGCGGCTTTGTGGCTGATGTTTGGCGTCCGCCCCGCCCTTGCAGCAGAGTTGACCAACCTGCTCAGCAGCGCGAGCAGATTCTCAGACAGT
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CCGAGCCCCCGCCCGCGGGCGGGCAATGCCGAGCAACTCATCGCAGCGCGATGGGGCTTTTGGGTATTGCCCTACCGCTACGCGCGCACATCGGTCTTCTACCGGTTTGTACTGCAAGCGGA
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GAGCGGCAAAATATCGGTTGCGCCCGCGGGTCAAGAAAAACGACCCGTCAAGCTTCTGAAC

SEQ ID 7108

NDSPFFKPAVWVAVLWLMFAVRPALADELTNLLSSRQIILRQFAEDBQPVLPVNRNAPARRAGNADELIGSAMGLNEQPVLPVNRNAPARRAGNADELIGSAMGLLGIAIYRYGGTSVSTGFDCSG
FMOHIFKRAMGINLPRTSABQARMGAPVARSELQPGDMVFFRTLGGSRISHVGLYIGNRPIHAPRTGKNTKITSLSHKYVSGKYAFARRVKKNDPSRLN

SEQ ID 7109

ATGTAATTTTTCGCGGCATGTGTCGGGACAAATCGCCGTTTGTGCTTTGTCAAGTTTGTGCATATCGGGAAACCAGAAATCGTCCGCACCTGTGCCGGTGTGATTCTGTCCTTGCCATCT
CGGGATATATCCAGCAAAATCGGCATATCCGGTATTTTGATTGTTGTGTGAGAAAA

SEQ ID 7110

MYFFGHCADKSPFCPLSGFVHIGKTEIVRTCAGVDSSLAISGYIQONRHIGILIGVLRK

SEQ ID 7111

ATGAACAACGCGCGGCCCGTTTGGCGACAATCAAAACAGCCTGACC GCGCGGCCCGCGCGGCCCTCTGTGACGCAAGATTTGTGGCTGAATGAAAACATCGCCGACTTCGTGCGCGAAGTCA
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CTTCATCAAAATACGCCCATATCCGCAACTGCTACCGTTGCGACCCGGCATACGCTGAAGCGTAGGCCAAGCCCTCGGACTGACCGTCGAAGACGCAAGCCGTCGCGCGACCGCATCC
CGACTGGGTTCAGGCGGATTTGCTG

SEQ ID 7112

MNNGAPVADNQNLSITAGPRGPLLTQDLWLNEKLADFVREVI PERRMHAKGSGAGFTTFTTDDITKYTRAKIFSEVGKKTETPARFTTVAGERGAADAERDIRGALKFYTEEGNWDVVGNN
TPVFFLRDRPRKFPDLNKAVKRDRPTNNMRSATNNWDFWLLPEALHQVTIVMSDRGTPASYRHMGGPSHTYSPFWNEAGERFWVKFHFRSQQGIKNLTNEEAAKI IADDRSHQRDLYEATE
RGEFFKWTMYTIQVMEADAEEKVPYHPFDLTKVWPKDYPLIEVGEFELNRRNPENFADVEGSAFAPSNNLVPGIGASPDKMLQARLFYNADARYLGVNFRQIIPVNRPRCFVPSHNSQDQSG
RDNGNYSGLPHYEPNSFGWQQQPDFAEPPLKINGDDAAHWYRQDDDDYPSQPRALFNLMDAQAQKALFDNTAAAGDAPDFIKYRHIRNCYRCDPAYGEGVAKALGLTFVEDAQAVRATDP
ALGOAGLL

SEQ ID 7113

GTTCATCGTGGGTTTGTGTGCAGTAAAAACGCGCTCATCAGCTCGTCGCCGACCAATACGGGCAGCTCGCTCTGTGTTGCCATAAAAGCAGCAGGGTCAGACACTTTGGCGGTATCTACG
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CGGTTTCTTCCTTGCTGTACACGCGCAATGCGCGCTGCCGGCGGGTTCGGCGGAAATTCGGAGCTGTTGAGCAATACTTCCATCATCATCAGGGTGTTGCCGATTCCATCGTATCGAA
ACCCGCTCTTCAAGCAGCATACCAAGTCTTCGGCGGGCGGCAGGTATCGAAATCTTGGAAATGTCGATGAGGTAGCGGATGACTTCGGTCACT

SEQ ID 7114

VHRGFFVE*KRAHQVLADQYQGLALVCP*KQQGQHFGGIYGNFVAGDVHERVDDDFPLFADGFFFNQILHQPHFLRQVVGFFFAVHAQCAAAGGFGGKFGAVEQYFHHQGVADPHRIE
 TRPFOHTOVFRRAGITELFMFDEVGDGFGH

SEQ ID 7115

TTGCGGAGTTGATTGTAAGTTGCAAAATCCCAACGGGCCGGATTCCCGCTGCGCGGAATGACGGCGGAAGGTTTTTTTGTCCTTCTCTGATTATAGTGGATTAACAAAAATCAGGACAAGCG
GAGGAAGCCGCAGACAGTACAAA

SEQ ID 7116

LRIDLKLNPNPDSRLRGNDGGRFFVFPDYSGLTKIRTRRGSRRQYK

SEQ ID 7117

TTGTTAACTCCACTATAATCAGGAAGACAAAAAACCCTCCGCCGTCAATCCCGCGCAGGCCGGGAATCCGGCCCGTTGGGATTTGCAACTTCAAATCAATCCGCAAAACGGGAATCCCGTCA
TCCCCCGCAGTCG

SEQ ID 7118

LLIHYNOEROKTFRRHSSRAGGNPARWDFATSNOSANRNPVIPAOS

SEQ ID 7119

ATGCCGCTCGAAACGGTCAACGACGCTTTTTCAGACGGCATTTTATGCCCGGTATTTCGCGTATCGGACGGCGCGGGACAGGATTCTTCAATTTCCATCCACATAAATGCCCCCTTACAGC
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TATGGCGGTATTGTGTAAGTCGGGCGCATCGCCCATGGCTGCGCGCGGTGTGTGCAACAAAGCCTGTTTCGCGCGTCGTCATCAGGTTGAACAAGGCGCGCGGTGGCTGAAGTAGTC
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CATTCGCGGAATCGCCGCGCTGATGGCTTGTGACAGGTCGCGCTGATGCTGTTTCGCGGTCGTGCGGATGATTTTTCGAGTTTCTGCTGTGGTCAGGTTTAAATCCCTTACATGCTGC
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[illegible]

SEQ ID 7120

MPSETVKRRFRHRFYARLFPVSDGAGQDFNFHFNHAPLQQTGLTQCGIGRADGLCLVFDQGSSEGGYAFVTCVRVATVAVADMAVDFDEVGRILAHGCGGVVKQSLFLRVVHVQVQEGARLAEVY
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NLVQGGQQRPEPVPVCGGTHIGARLAFDQVQVGFARVDEHGRVVDHIEPVAFFGLEFRKTAADVAFRI GCAALACHGEGTEHGLFGFADPAENFGAGMGTGDDVVCYKTERKTRATFG
VHTAPGDDFAHEVGEFFITQPQILRQGAARAGGQAVLIVGNRAVHVHQMGYGAFGGSHRSCFSQVQMGHGKRLTVRPGKRIIRNRPLDCNKFLESTFYFPFAKTMDAIIROQDFRY

SEQ ID 7121

TTGCAACTTCAAATCAATCCGCAACCGGAAATCCCGTCATTCCCGCGAGTCGTGAAATCGGAACGGCTCCGCACGGGAAATCCGCATCCCGTCATTCCACGAAAGTGGGAAATCTAGAATGT
CAAATCTCAAGAAACGGTTTTATCCGATAAGTTCCTATGCCGACGGACCTGGATTCCCGCTCGCGGGGAA

SEQ ID 7122

LOLOINPOTGIPSPRSRESERVTEIRIPSPFRKWE SRMSNLKKPFYPISSYADGPGFPARE

SEQ ID 7123

TTGTTAATCCACTATAAACGCAAAATATCCCGTCATTCCCGCACCATCCCCACCGGTTCAAACCGGCACGAAAACCTTTTCCCGGTCATTCCCGCGAAAGTGGGAATCCGGAAAG

SEQ ID 7124

LLIHYKRKISRHSRTIPTGSRHENFSASFPRKWESGT

SEQ ID 7125

ATGAACCGGGTCGAAGACCCATTTTATCCAGTATGCCCGGACGGCTGTGCCGCTGCCGCCCTTCAGACGGCATTTTTCGGCAGCGGGCGGGGGGTATGCCGTCTGAACGGGCGCGGG
CCCGTCTCGGGCGTATCTTTATTTATAGAATA

SEQ ID 7126

MNRVETHFIQYAADGCAACRPFRRHFCGRRRGVCRNLNGAAARVGRILTYRI

SEQ ID 7127

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CGGGGAATTGACGGAGGGGAACGGCGCAGCGACATTTGCCGAATCTTTTATGTTTCCATTATCATACTCTTTTCAATGCGCTATTCCAGGAAAAAGAAAATAGCTTGTGCGAGGCTGCTTTT
TGTTTTCAGACGACCTGTGAAT

SEQ ID 7128

MTETGNQARTFAGIFVYSIIILFSMRYSRKKKIIACAGCFLFFRRPVINGCLSNLLFKLPATAKSAATRSPLCGGFGFRGHFPSSCGNSPPPLKKFPNRPMTSLAAAYCPLNSLPRGERTMPA
GGILLIGTSESSFPKRWESRNPNAARIYRRNRNPDPDSRLSGMDGGERRTDICRNLICFYHYFLNALFOEKENSICRLLFVFOITCN

SEQ ID 7129

ATGACGGAGGGGAACGGCGCAGCGACATTTCGCGAATCTTTATGTTTCCAATTATCATACCTTTTCAATGCGCTATTCCAGGAAAAAGAAAATAGCTGTGTCAGGCTGCTTTTGTGTTT
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AGTTGCGGCAATCCCCCCCCCTCAAAAAATTCCTAACCGCCCCAATACAGGCTTGCGGCTTACTGCCCTCTCTCTAACTCTCTCCACAGGGAGAGAGGACTA

SEQ ID 7130

MTGNGARTFAGIFYVSIIILFSMYSRKKKLIACAGCFLFFRRPVINGCLSNLLFKLPATAKSAATRPSVGEGLGEGIFQVAIIPRKSNSLTAPIQALRLTALSUTLSHREGL

SEQ ID 7131

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GAAAAATGATGCGCGGAAGGGTTGTCGCCGAGGCGGAAGATGTGCCGGAAGCAAGCAAGGAAGCCATAGGATGACGGTTTTGACTGCTTTTGGAAACCAGTATTGATTCATGATGTCGCGG
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SEQ ID 7132

MSLYALLLVALGMSDAFAVALAKGAAVRMPRPKIAATLVFTGTVEAFMPLAGWVGGFYAKPFISEWDHWVAFVLLGGLGLKMMREGLSGEADVRESKQBSLMMITVLTAFGTSDSMIVG
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SEQ ID 7133

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GGCCCGTGTTCGGCGGTATCTTATTTATAGAAATATGACGAAGACCCCGTATTTTTCGCAATAGCCCCGGGCATTCGTCGTCAGGATGTCGTCCTCAAACTCCGTCAGTTTTCGCTCCGTTTAAAT
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CGCACGTTGCCGCGCAAAACAAACCGGCGCGGTCAGCCCTCGCTGCATCAGCAATTTCCGGGAAATCTTCATCTCGAAGCAGCATCAGCGCGCGCTCCGTCGCCGATTTCCCATTCCAACG
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SEQ ID 7134

SSDVLVSAAGCHGNAAVQFQFQQCGTQICGRHSLSGKHVGMNRVETHFIQYAADGCAACRPFRHFHCGRRRGVCLRLNGAAAFVGRILITYRI*RSTRILQ*PRAFVQDVQVTPFRFSVFN
QFVAAPAVGVVYRTGYRHHPAFPHCRQAGGNQRTFGQGLLDQORNLRQGNQAVAARKVAGIRPRADGELADNPFFGDFIGKVFVGRRLNAVYARPPHGDAAPCLQCALMGGGVDARSH
TRHGRNAPFTQRPAEIFGNPHRLRRGMAAADGGGRLVQQPHVAQKQNRRRRGQPIRQHFGEITLKQHQAAASVPHPFPQRRFCRLPRQSAFFRIAPSLKRVLMPHRRGNLFRRCQGILR
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SEQ ID 7135

SEQ ID 7135
ATGCCGCTCTGAAAGGCTTCAGACGGCGTTTTCCTACACAATCCCCACCGTTCCCATCTCTCCGATACACCGTAATCCCGAAACCGTCATTCGCCGCAGCGCGTCATCCGGGTCTGT
CGGGTTCCGGTTTCTCCGATAGATTCTCGCTCCGTTGGGGTTTC

SEQ ID 7136

MPSERLQTAFFLHNPHRFPSFPIHRNPETRHSRAGVHPGLSGPGFSDRFSLRWGF

SEQ ID 7137

SEQ ID 7137
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SEQ ID 7138

MMSENKMPSEALPVSDGILLNLILYRYYCVKLLKIKY

SEQ ID 7139

SEQ ID 7139

TTC TTCGGT TTTT TCCCCCGCCGCCGCGCAAAACGCCGATGCCGAGCTGTTTGAGTTTGCGGTAAAGTGC GTGCGTTCCAAAACGCACCTTCTGCGCCACTTTGCTCATATTTCTGACCTTCT
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SEQ ID 7140

SEQ ID 7140
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 RIVTECGRRDFLAFPHIAGNPLYQEGNVFMLHPTQGRNTDDRFKXKPGQPPFT*NAV*TCRVAARSNHPTDAAFCLADDKGNAGLDIAAVLGDVADIQNAALLRLQFPHRIDQIFDPCRTD
 PRRTVFMEIARHGFKRRTRLARQYKRGALCRRFDFAVHLLNRGTVAQFVEHRSRFDLRRTVFORVFDRRQQLLQGNRFQKIDRADFGFYGGIDAGMPAHHHHRHTELVPVFRPLILQKGD
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SEQ ID 7141

SEQ ID 7141

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SEQ ID 7142

SEQ ID 7142

MQQQHLLFRPFTLCLSLATPALPAYAENVQAGQAEKQLDITQWKAKKQKTRRDNEVTGLGLVKLTADTLSKEQVLDIRDLTRYDPGLIIVVEQGRGASSGYSIRGMDKNRVALTVDLGALQIQS
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SARITPGINILGKIDWNGVMDKLPBGWYSTFAYNRVVRVDIKKRADRTDIQSHLFDALQIPSRVYVSGSDYQDPEKGWGVNGLMITYSKAKRITELLGSRALLNGNSKDTKATARRTRPWIYIDV
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SEQ ID 7143

SEQ ID 7143
TTGCGGAAAAATCAATATTTTATTTTCAATAGCTTTACACAATAATACCGATAGAGAATCAAGTTTAACAAAATGCCGCTCTGAAACCGGTAAAGCTTCAGACGGCATTTTATTTTTCGACAT
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SEQ ID 7144

LRKINILFSLAHNNFTDRESSLTKCRLKPVKLQTAIFYFPTSLNQTQMR

SEQ ID 7145

SEQ ID 7145

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SEQ ID 7146

RISFYRFWQDDSDTRPTRILIAQADAAAVSNDFFPHYRQTQSRRLIRHIRLESIVQHLAESLAVVANRQDNPVSLPRFRFYDPFGHIGFFRRFPGGIFENIVQHLPHGGKIRRHHQRFA
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 AVAVVFGQYRRLAQDDPGIVRRGIFHLDRPVRTCRRTDGKHKFGKQGLLRNNAVPTVPAAPQGGERHQNLFRLVVEGFPQTAFVVKHHHTGSQPIQHALEVVTGGLAPAVAFVCFPGDG
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SEQ ID 7147

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SEQ ID 7148

LKDIVYSLNEVKIIVOTGRQTC SADYFFSVPIAPLAIFAENQYPIFNSFTQ

SEQ ID 7149

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CGCGAGCGTGTGGGACGTGGATAAGGCAGTTTACCATTCACTGGGTAAAGCGCAATTTGGTAAAGCAATTCGGAAGACATGTGGATAACATCTGCTGTAATCTCAAGCTCACTTTCCGCGCAAT
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SEQ ID 7150

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VDNMPTSQGHKGQPGGRNSPTALNAALIGSQFDGRAADVEEQAGGLVNVFEMANDSQEAAAAAKIAPVEYQEMFKAPPEDGAVSFKNITTAGPAPERTLTPTKWDEYLGKGVNALSE
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SEQ ID 7151

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SEQ ID 7152

FVPDDV*RFPTRI*HPVLRSQCVDLERLGQF*SGORQADFLRLGPCCFRTGQRAFVQDFPVGNRAGRAQCRIQSVVIGGKCADGNAVAVGORMET*FVVNTVVIANQLPQFKPIRSDCRGGK
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SEQ ID 7153

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SEQ ID 7154

MSRPVPAVFGSVFHSQMPVLAYREGKWQPTFWEQSSQDLTLAPGAHALHYGSECFEGLKAFQADQKIVLFRPTANTARMRQSADILHLPRPETOQAYLDALVELVKRAADEIPDAPAALYLR
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SEQ ID 7155

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SEQ ID 7156

LIFLSAVAFDSLNLPKFKPKSSGCIFSGIVRTNRRFVLCQVLCISGKPKSSAPVPVSIRPLPSRDISSKIGISVF

SEQ ID 7157

ATGACAATCCATTGGTGAATCAGGCTGCTATGGGTGTGCCGTGTGTTTTGTTGAGCGCTTGTCGGCGGAGGCGGCAGTTCGATCTTGATTCTGTGCATACCGAAGCCCCCGTCCGCGCCAAAGTATCAGAGTGTTCCTTCCAAAAAACCGGAAGCCCGAAAAAGACCAAGCGGATACGGTTTTCGGATGCGCTTCAAGCGGGCGCAATTGGTATCGCGCGTCAAAATCTTAAAGAAAA
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SEQ ID 7158

MNNPLVNVQAAAMVLVPVFLLSACLGGGGSPDLDSDVTEAPRPAPKYQDVPSKKPEARKDQGGYGAMRFKRRNWYPPSNPKNEIRLSEGDWEQGTGNGNIKNSPKQKNIIDALSGNGEAPLQD
SSQQGBGISKVYTDYHDPKYVWSGFFYKQIGNTIKKDDSSSKIIIEARNGPDGYIFYKGPDPSPKRLPVSGSVYEKGTWDFLITDYQANQKFTDLSGAFATSGSDRYSAFSGELDVIYVRKEEDKKD
GHVGLGLTTEITVNFKKKTLGSKLIKNMNVINNGDEPTTYQYSLEAQVTGNRPNFGKAMLLTDKPKNSKQHPFVSDSSSLSGGFFPGQGBELGFRFLSNDKNVAVVGSAAKTKDETASSGGT
SGGASVSANGATYSSGNSGNLTITVLDAVELTPDGKAEIKTLDFGNSAAQLVVDGIMILLSTESGNGVADLKGKNGGTDFTTYTITMPESDKDKTKAQGTAGGNGQTASDAAGVNGGQAGTKT
YKBZACCNSLNIKYGLLITRENSNSVMQTVKSSQAARLDAQSWMFLQEGRTDEKEIPKEQKVYDQYVHGIAANGTSWTGNASDDQSGNRAKFDVNFKDKKLTGTLTAANRQEAFTT
IDVIBDDNGFKGTAKTGNDFAPDONSSTGYIKVSHIANAEVGGGYFPGNAELGGWFYAPNGQOTKNAQENAAQSSGNGNSAVSATVVPYGAKRQOVL

SEQ ID 7159

TTGTCGTCATTTCCCGCGCAGGCGGGAAATCCAGACTTGTCCGCACAGAACTTATCGGGTAAAAATTCCTCAATTTTATGTTCCGGATTCCCGCTCGCGGGGATAACGATTCAGTA
TTTCTACATCGAATCCGCTTTTATATCAACC

SEQ ID 7160

LSSP^{PRRR}ESRLVGTET^{YR}VKRFLOFYVPDSRLRGDNDSGISTSNPLFIST

SEQ ID 7161

ATGCTTTTGAATAAGCGCGTAATAAAAGCCATCTTGGTGTTTGTTCGGTAAAGACCCCGGATTCGATCGGTCGCGCATCGGCATGGCGGTTGAGGAATTTTTCAGTTGCCCGTCGTTT
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SEQ ID 7162

MLLAKVKIKALIVFVR*KHPRFDRFGIGMAVEEFLQLPVVFFDEHGTGGKQHSAAFLQRLKPKCVQGGFLLAGGFEFVGRSAQPFVHGLAPRHAGSGARHVGDKDCVERLSIIPREQIPRIGT
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AQRHRRMGLQRGGDVVPVFRIMVFQVSHPPQRQVFRHIVFFAGSRQFFTFQAQKAQNRVKGRTVLPAPDFGYAFNSFVDHGVGRVARVMQLVQRQKQAFELRIVDGLFQHLREHMFQTA
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SEQ ID 7163

TTGGGAAGAGTAGTCCGCAACTTGGAAAGTGCCTCTCCCCAGCCCTCCGCCGCGCAGGGGAGGGAGCGGATTGCAGCAGGTTTGGCGGTTGCAGGCGGTTTAAAAAGCAGCGCGGAATGA
CGGTAATTGGTTTATTATC

SEQ ID 7164

LGKIAATWKVPSPOPSAAOGRERLAAGLAVAGGFKSSAGMTVFVFTY

SEQ ID 7165

CAGCTTCGCGCTCTGTTCAATAGACCGTCCGCCGCAACGCCGCAATATTCATACGCTGCCGCCGGCAGGCTGCAATTTCGGTAAATCTTCAGCGCGCTTCGCCCGAGGCAACGACCAAA
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SEQ ID 7166

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FALKLLQIGNNRRTDFHQRVDFVGGIGRLDGVAVFADHIAGVQTDVHLHNAHAGFGIAGLNRALNRRAAPTQQRSDVLEAAVFRRIQHFLRQNAVRGNHMYVRLDLFEHLQCFGVV
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SEQ ID 7167

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GTCGTATGAAAAATAAAAAACAGCCTGCACAAGCTGAT

SEQ ID 7168

LPQLGECPLPGPPFRGRERIAADFAVAGGLKSNLDLPLISGRMKNKKQPAQAD

SEQ ID 7169

ATGCCGCTGAAGCAACAACGCAAGAAACCATCTTATGATTGACACGCACTGCTCCACTTGGGCGAAGAACCCCGTTTAAATCAAATCAAACCGAAGACATCAAACCCGCCGTCC
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CTTCGCAACCGCGCT

SEQ ID 7170

MPSEAHAKETHLMIDNALLHLGEEPRFNQIKTEDIKPAVQTAIAEARGQIAAVKAQTHGTWANTVERLTGITERTVGRVGVVSHLNSVVDTPELRAVYNELMPEITVFFTEIGQDIELYN
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ELREQYIRAYVTRASELSNDGKFDNTANIDRTLENALKTAKLLGPKNYAELSLATKMDTPEQVNLFLDLARRAKPYAEKDLAEVKAFAREHLGLADPQFWDLSYAGEKLEAKYAFSET
EVKKYFPVGVKVLGAFQIKILYIGFAERTVPMHDKDVRYPELQNGKTTGGVYNDLYAREGKRGGAAMNDYKRRRFADGTLQLPTAYLVCFAPFVVGKEARLSHDEILLFHEHGHG
LHLLTQVDELGVSGINGVEWDAVELPSQPMENFVWEYNVLAQMSAHEETGEPLPELFDKMLAANKFORGHFLVRQMEFALFDMYISSEDECRILKNWQVLDVSRKEVAVIQPEYNRB
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SEQ ID 7171

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ATTAGTTTGCATAAACCTTAACCCCAACAGCCACCCCGTCTCTCTCCCTCGCGGAGAGGATTAGAGAGAGGGCAACAGCCGCAAGGTTTGTATTT

SEQ ID 7172

LPQLGECPLPGPPFRGRERIAADFAVAGGLKSNLDLPLISGRMKNKKQPAQAVLVCINLNPNSHPVLSPCGRELERGQQAVALVCINLNPNSHPVLSPCGRELERGQQAARFVF

SEQ ID 7173

AATCGTATGTTTTCGACGTTTTCAGTTTGGCTTAATCCGCCCCCTGTTGAGTTGGGAAAGCGGTCGACAAACAGATGCCCATCAGGTGATCTAATCGTGTGACGCAAAATCGCC
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SEQ ID 7174

NRMFLTFPQFGLNPLLELKGAPDKHDAHQVI*LVILHANRQOPVRLQREFFAFVQSLDLDAFGAGNGVNNARYGQAALFVSGFAVFNDDGVDEHARFAAVFGQIHHDAFVHIDLRERQ
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SEQ ID 7175

ATCGAGGTTCCGTATGGATGGATTGCTCAFTCCCGCGCAGCGGGAATCCGAACCTGTCGGAACAGAACTTATCGGATAAAACGTTTCTTGAGATT

SEQ ID 7176

HQSVWMDSSFPRRRESEFVGTETRIKRFLEI

SEQ ID 7177

ATGTTAAATGCGGAACATTTGTTATCACAGGCACATCCCGAGGGGCTGCCCGCGCTTTTTCACCAACCAATCAAGCAAGACAAACCGAAATTTATCAGATAAGGGGAACGGTTATGCAAC
GTCGTATTATAACCTGCTCTATATTACG

SEQ ID 7178

MLKCGTFVITHIRPGCRRFPQPNARQTEIYQIRGTVMQRRIITLYIQ

SEQ ID 7179

TTGCCGCGGTFACGGGCGCGGAATTTGCCGCAAGTGGCAAAAGCGTTCCTTTCGCACTAAATCTACACCTTATCTTTTCGACAGGCGCGCGGAAATGGAATATGGAATATGTTGA
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CGGACATGAAGCAAGCGCGGTTTTCGTTGCGCAGCGCAATATAACGCTGCTTTTGGTGTCTTTCGCTGCGCATTTATCTGTCGCGCAAAATCAAACGCTGGCTTTGTCGATGTTT
CGGTTGGCGCGCGGCTGCTGTCGCGGACAAAGAACTGATATGTCGTCGTCGCGCAGTATTTAAGGTCGTCACCCAGCAATACGCTGCGGACAGCTTCGCGGAACCGCTTTCCTTCCCAACAGCGCTGTTGTTGAGCCA
CGGCGCGCTGTCGATCAATCTGTTGAACACGCTGATGATGAGGTCGCTGCGCAACCGCTTCGCGGACAGCTTCGCGGAACCGCTTTCCTTCCCAACAGCGCTGTTGTTGAGCCA
CCCCGTCGCGCGGCAATATTTTGGCGGCTATGTCATCATACGCTGCAAAATCCCGGTTCCCATTCATTGGAATTCGATGAAGCGGTATGCGCTGCAAGCGGCTACTCGAGCCCTTG
TGCAGCGCTTACATCCCGCATTCAGCGGATTTGGAAGACGTGCGAGCGGAAACGTTTATCAACCGCGCGCGGCGGCTTACCGCGGTACGTCAGCAGCAAGCGCATAC

GCATCATCGTCCGCTTCGCTCCCCCGTTTCAAAAGCGGCTGGAAATCCAACAGGCGGTTATGGACGAATTTTTCGCGGTACAAATACCGCTGTTAAATCATCCCGCGGGCTCCGAAACACT

SEQ ID 7180

LRPVRARNLPAKWQKRFPAKTIYTLFSDRGEMETWMLNTWPDVPIRAEAEASVAVAAILLARALLNTHFRHPDFIGIESKRRFLVASRNTLLLVFLPSLAFIWSAQIQTLLSMF
AVAAAVVATKELDMLSGSILRSATQYVSVDYIEINGLRGRVVDINLIATLMMQVGNPLVGQLAGTTVSPFNSLLSHPVRRDNLGDYVHTVTEIVPPIHLSDEAVCRLLKAVLEPL
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SEQ ID 7181

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SEQ ID 7182

VAKKRCHFGAGKFRARTGRKCAARPRFRHFDADNAESGGEIYNTQLYAPSRPLFPQGADCFGGIAKSPQNPARNMTEQKHEEYGADSIQVLEGLAVRKRPGMYIGDTQDGSGLHHMVFE
VLDNAIDEALAGHCDKITYTTHADHSVSUADNGRGMPTGHPKEGRSAAEVIMTVLHAGGKFPDNNYSYKLSGGLHGVGVSVVNLSDWVTLITYTRDKGKHVPFVRGRTETEEPLKIVGDSKGI
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YIAPPLYKAKYQKQERYLKDBLEKDKQWLILGIALKEKATVSDGRITGEAELADTAQKPLLAKTIVYEQBSRFPVDBLVRAMLHASPIDLTSSENADKAVAEKLSGLLDRKEALERIIEGHEH
RFKIKRKLHGNMVMSYIEPKFLNSKAYQTLTQTAAALKGLVBEGAKLYKGENEYDASFETALDILMSVAGQMGSIOQRYKGLGEMNPQOLNETTMDPAVRLLKVRIEDIAADEVFPVTL
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SEQ ID 7183

AAATGCGGAACATTGGTTATCACACGGCACAATCCGAGGGGTGCCGCCGCTTTTTCCAACCAATAAGCAAGACAAAACCGAATTTATCAGATAAGGGGAACGGTTCATGCAACGTCGTA
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SEQ ID 7184

RCGTFVITRHLPRGCRRTFQPNQARQTEIYQIRGTVMMORRIITLLYIQ*SHNFLFPSADTPPVFH

SEQ ID 7185

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SEQ ID 7186

LLPINAAISNPVIPAQAGIRTFNAKATYRE

SEQ ID 7187

ATGACGGGATTTGAGATTGCGGCATTATTCGGGAGCAACAGAAGCCGCTCTGCCGTCATTCGCCGAAAAGTGGGAATCCGGTTTTTTTGAGTTTCAGTCATTCGGATAAAATTGCCTTAGCA
TTGAAGGTCGGGATTCGCCGCTCTCGCGGGAATGACGGGATT

SEQ ID 7188

MTGFEIAAFIGSNRSRSVIPAKVGIRFFEFQSPINCLSIEGPDSRLRGNDGI

SEQ ID 7189

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SEQ ID 7190

LGNDGSRRAAPVESAHRRCHCRRRSVRYPDGRRGRAPRLYRKQCADCAKYRISAVLKKETGSLPRLLLVQCTEMPSETAFRSKTMISIFDIKIGIGPSSSHTVGPMAAAAAAAGL
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QSETEKAVPYPPYNSCAGLLARCLNRLDISSEVLANEALAGCGEAEIRRRVAGVAIMEECIKRGLNAGGELPGGLNVRRRAPQLAAKLKVLRETEIVNTRLWPMVYANAVNEENAGGR
VVTAPTNGAAGIIPAVLHYFRKFNPHATQERVENFLLTAGAIGILYKTNASTISGADVCGQGEVGVACSMAGAYAEVIGGTPKQVENAEMAMEHHLGLTCDPWGGLVQIPCTIERNGLAAB
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SEQ ID 7191

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CCAA

SEQ ID 7192

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SEQ ID 7193

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SEQ ID 7194

LASHYIVIEIYFVLAIEVYARYTILHLKGNMGIVAGAI ECGQLYIYGFRRGGR

SEQ ID 7195

ATGCCCGAAAAATACATCCGAGGATTGAAATTTGAATTTGCGCAATTTAGCGAATCAAAAGCAACAGCCGATAAAAAATCAAAAGTTTATTTCAATGTTTCAACACACAGGACGACA
CA

SEQ ID 7196

MPKIHPEDLNINFGKFSKATADKKIKSLPQCFWTQDDT

SEQ ID 7197

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SEQ ID 7198

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SEQ ID 7199

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CCGATACGGCGTTGCCCGCCCGGCTCAAGGGAACGATTCCC

SEQ ID 7200

LMQNPDLVGQAFYPMESVSARTETIAAVSLADRYSELTKTGTALEPRPGSKGTIP

SEQ ID 7201

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CGAAATTT

SEQ ID 7202

HQIDFCGRFYRPIYKSIQIFKHSIYTRRKHILETSLNFPKF

SEQ ID 7203

TTGCGGGTTTACCGCTTCAACGCCAAGCTCAACAGCCCGCGGTAACAGCCCAAGCTATCCATCTCTGCGTGTTCGGGCGTTCGTCCAAGAAACACCGCCATCAGGAATGCAAAAC
GGCGTGTTTGCAGCATCCGGCAAGATTTTATAGTGGAT

SEQ ID 7204

LRVYRFMANVNTPAVTSPIHSCVFGRRSKRTTAIRNANRCLQHPARIFVD

SEQ ID 7205

ATGAGCAACTGGAACCCGATATCCCTATACGATTTACCACCCCTGCCGCCAAACAGGATATTGAAAGCAAAACCATCTGAAACGTTGTATAGCGCGCGTGCATCCCTTGCCTGCT
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SEQ ID 7206

MSNMKPDIPYNDLPLPKQDIESKTIILKRCIAARASLARLQAAELIPNQAMLINTLPVMEARASSEIENIVTTDKLFQSLQMDTERQDPATKEALQYRTALFAGYESLASRPLCTQTA
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NSPTSP

SEQ ID 7207

ATGGCTAAAATAAAATGTTTAATAAAACAAAATGTTGAAACTTAATTTGATAGAGCCTCTGCATATCGTATTGAGGCGTTAATGGAATTTGAGAAAGCTATTTTTTAA

SEQ ID 7208

MAKTKCLTNKMLKLNFDRASAYRIALMEFEKAIFK

SEQ ID 7209

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SEQ ID 7210

GFSGVFEISLNA*LSAPKSNVSRQASPKMFFIFRRQFYQYPERAPFQSRRLQENIGEHAFIGFARGDRVPRQCEHIHFQCLGNNARVVFVVGQHFRLPDLFRHAFVAVFDQOQGEHLRL
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SEQ ID 7211

ATGCCCGCTGAAAGGCTTCAGACGGCAATTTTTCACAAATCCCAACGGTTTCCCATCATCCCCGACAATACCGTAATCTTGAAATCCGTCATCCCGCGCAGGCGGGAATCCGGAACCGTTC

SEQ ID 7212

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SEQ ID 7213

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SEQ ID 7214

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SEQ ID 7215

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GAAAGCGGGAACTCAGAACG

SEQ ID 7216

NPSEAF0AAFAAFGLKIPSPRRRESEYIRTECIPSPRKRESR

SEQ ID 7217

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SEQ ID 7218

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SEQ ID 7219

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SEQ ID 7220

GFRHRI PVVGGFAVVA FOPRL PVVFLN I KPAFDRLAVAGA IGIRAAEHFGDFVGOGOMPLL YDLEIVDGDVHFRGGEQGEAVGGFTVQAHA FDFDDVFAALGFAGQVEAHGYRVAVVQ

SEQ ID 7221

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SEQ ID 7222

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SEQ ID 7223

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SEQ ID 7224

VADRRGRSSANRAPGGGIIVHYNSQIRILLSDGMVKKRRRVYNNRIVLCIGRIKGRMENIGRQRPIGVFDSSGIGGLTNVRALMERLPHENIYFGDARVPYGTASKATINFSMQIVDFL
LGHDKVAMVLIACNTLAAVAGRKIRQKTGNNPVLDIVSAGAKAALATTNNKIGIIATNTVNSAYARAHRDNPDTLVRTPQAAPLLVPLVEEGWLEHEVTRLTVCETLKPLADGIDTLV
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SEQ ID 7225

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SEQ ID 7226

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SEQ ID 7227

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SEQ ID 7228

NSVCLIEWPOOGGEFTPPADITATLTHGGGGRKCLLTAHTERGRESLEPL

SEQ ID 7229

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SEQ ID 7230

[illegible]

SEQ ID 7231

ATGTTAATCTGCAACCCCTACGAAGTCGTCACTCCAGCGCACAAAGAGTTCGCGCAAGATTTTCGCCCCGGCGACTGGGCGGAACGCCCTGTGCGGCATCTGTCTCGTTACCAAAAGACA
ACCGCCTCTCTTATTCGAAATGGGTGCGCCCCATGCTGGTGGACACATCCGTCGCTCGCGTCGATAAAAAACTGGAACCGGACAATCCGCAGATGTTTCGCGCTTCTCTGATGGACTTTG
CGCGCAACAGACTCGCGGTATCGACTGCAAAAGCCCTGCTCGAAGAACGGCAACAGGGCGGACAAAACGACCTGCCAACGAACGCGTCTCTGTGGCACAGGCAATCGAAGAAAACAC
GCCGCGAGAAAAACACAGGAACAGACCGCCTCGGGCGCATCTTACGTTTACGCGAAATCGGGCGGGACGACACGCCACCGCGCTTTTGACGCGCTTGAGCGCTTTGGCTTCTCCCTGACCG
ACATCGGCGCGCTTACCGAACAGATCAACAAAATACCAAGCCGCCAAGGCTACCGCTGCTGGGTATTTTGAAGAACTGCAACACACACCGCGTCGCGCTGTGCGCTTCCGGAACCGCTG
CACTCTCGCGCTGGCGGCCCATCCATCACTGACGACATCGTCTTACCTTCGCGCAAGCGCGCAAAAGCGCTACGCGCTTCGCGCTTTTGAAGAAAGTCCGCAAAATCGGCGCGGAACAGGG
GTTACCAAAATCCACCTTAAAGTCCAGTCAACCAGCAGCGTACCGACGCGCACCGCCTGTATTCAAACACGGTTTGAAGATCGCGCTTACCCTTCGCTGCGACCCCAAA

SEQ ID 7232

MLICNPYEVVHGTFTSSGKIFRPGDWAERLGILSSFTKDNRLSYKSWVRPLVDNIRCAVADKKLETNPQMFRFLMDFADNDLRVIDCKALLEERBQGGNDPANERVLLAQAIERKH
AAEKTEQETASGASYVLRIGADDATATAFALSVLRSSLFDIGRPTEQINKIQBPQGYRLLGIPBECKHNAVAVCGPREACT'LAGGRHITHIDIVTLPQSRKGYASRLLEEVKIGAEFG
VTKIHLNVHVNHDRTDAHRLYPKNGFEICAYHFRCDPK

SEQ ID 7233

ATGCCCTGCTGACCGCCCATACCGAAACGAGGACGCGAAAGCCTGCCGCTATGACCAAACCTGACACGAAGACAATCATCCGCCGACCGCCGGCACACTGTTGCGCCCTGAGCCCCATCGCAT
CCGCGCTGTCAAAAACGGTACCGCGCCCGCCAGTATTACCGCCGACGGATATGGCGCTGCGACACCTTACACCCGCTGACGCTGGAAAGACACCGCCGGCTCAAAATACAGACACTTCGGGCT
CGACAACCCCGGGCAGGTGGTCTGTCGATATACAAAACGCAAAACATCAATACCGTATTGACACGGGCTTTCCCAAAAAGTTATGGCGGACGACCCCTTTATCCGCAGCATACCGCGGGTAC
AACACCGCCGACACCGTCCGCTCTGTCATCGACTGGAACACGCCACCCACGCAAGTCTTCGGCTCTCCGCGCGTCCGCGGGCTTTAAGGACGCGCTCTGCTGTCGACTCTATTCGCGACG
GGATGGATGGCGGACGATTCGATATGATGGCTGCTCAACCGGACGCTGAAACAAAACCTTCGCGGGCTCTCCGGAAGCGCCGCCGCCCAAAACACGACCGCCCGCGGGCGGGGCAAAAA
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CGGCGTACCGACCAAGGCAACCCGCAACCTCGGATACCCCGCTGCTCGACATGACGCAACCCGCACTGCGCGACGCGCAACCTCGGCAAACTGGTGCTTGAAGAAATTGGGACGGCTC
AACCATCTGCACAAAGCGGGTGGACGAAGCCATTTCGCGCTATTTCGCGACCGCAACCATATGCGCTATCTCTGTTGGAAACCGCCTCTCTCTGTCCTCAATCTCGCGAAGAGAAATCTGCTGG
CGAGCGATCTCTTCCTGCGGCTGGCGCCCAATTCGCTCGGCTGGTCCCAACGCTACATCAATATCATCTGATATGAAGACGGGGT

SEQ ID 7234

MPADRPYRTRTRKPAAMTKLTRRQIIRRTAGTLFALSPIASAVAKTVRAQPTAARIWPSHTYTRLTLESTAALKYQHFALDNPGRLLVVDIQNANTINVLHGLSQKVMADDPFIRSTRAGQ
NPTPTVRLVIDLKQPTHAQVFLPVVGGFKDRLVDLYPHGMADDPMALLNGSLNKTLRGSPADPAQNTTPRPGRGKNGRRPVTMLDPHGEGEDPGAVSPGGLEKHHVLSIARETKK
QLEALGVNVFTMRNEDVFILGVRVAKGRARRADVFSIHADAFTSPSARGTGVYMLNTKGATSSAAKFLBQTPQNNADAVGGVPTSGNRNVDALLNTQTATLRDSRKLGKLVLEELGRL
NHLHKGRVDEANFAVLRAIDMPSILVETAPLSNPAEKKLIGSESFRQCAQSIASGVORYINTSVLKRQ

SEQ ID 7235

ATGACCGCCACACCGCCGCGATTTAGACCGBACTCCTCCCCCAAAACCAATGCCGCGAATGCGGGTATGAAGGTCCTGCCCTACGCCCGCGCGATGCTGCGGGGCGAGGCGCAACACTCT
GCGCCCCGGGGCGGCGCAACCGTCGTCGCGGACCTTGCGGCCCTGCTCGGCAAAACCCCTTGTCGACCTGCCAAAACCAAGCCAAAGCACTCGCCCGGATAGACGAAACCGCTGTATCG
CTGCACCGCTGCAATCCGCGCTCGCCCTGCCGATGCCATATATGGGCGGGGCAAACTTATGCACACCGTCATACACGAGCAATGCACCGGCTGCGGACTCTCGCTCGCCCCCTGCCCCGCTG
GACTGCATCCATATGACAGCCCGTTGCCGACACCGTCTCGCCGCGCGCGCGCTTTCAGCCTGTCCGACGACAGCGGTTTTCGCCGCGCGCGAACACGCGCGTGCAGCTACCTCAAAGCGA
ACGAAGCGAAACACGCGGAGCGAAGCCAAACGCAAGCCATGCTTGCCAAAGCGAAGCCCGCTGCGGACGCGCGCTGCGCAACGCGCCGACACGCGGAAACACCGCGCTTCAACCCCGC
CGACTCTATCGCCGAAGCATGGCAAGACGCAAAACCAACAGGATGCGCTGCGCGCGCGCGCAACCGCAAGGCTATFACGAGCAACACAGATAGCGCAAGCCCGCGCGACGCGCGGAATTG
CGCGCGCGCCCAACGCGATATGAAATACGCGACGACAGCGAAAAAGCGCGCGCTCGAATACCTCAAACAATACAAAGCCAAACAGGAAGCCGACAGAAATACCGCCATCC

SEQ ID 7236

MTATAADLRRLPOTQCREGEGCLPYARAMLRGAEHNLCAPGGATVVRDLAALIGKPLVAPAKTQAKALARIDETACIGCTACTIRACPADIMGAGKLMHTVITDTECTGGLCVAPCFV
DCIHMQPVADTVLPRARRFSLSDSRFAAAEHARARYLKRNERKQREADERKAMLAEREAAVRNARPOTPDTPKPAFNPADLIKAMAKAQTOQDRLAAADNRQGYQAKQIAERERAEI
RRAORDMKYGSDEKAAALEYLKQYKAKQEAQNTAS

SEQ ID 7237

TTGGTATCTCAAATTATCCATACCTTTTCATCATAAAAACCGCGGTTTGGGGCGGAAGTAGGTTTATGCTTGCCTTCATCCGACAACATATATTTTGAACAACCGCCCTTTTCAATCAACCCCGC
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SEQ ID 7238

LVSQFIHTTHHKNAVWGSRRFPAPIRQLYFETPPFPSTPLQYGCIDVALDTRGNGLGALPTEGFAAQQLPFRIGQEGGGDQDRRHIGCAQYGEIGFVHPAPVQMVEPAQFPFKHQFAEFA
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LQATARADGAGVPTAVSRIEHDGDSAPVFPAPPGSGRGVLGGVGFRRAAQGFVQAAVEQGRHHRIVGITHPVRIEVDDEAVLKAADGRKREDLCVGGFLQVDDDEADGGRVILTRAYAADKGVRH
NFLGKPVQYQIDVCLVYIDDQPARVVEREVLFERGGAPFORQAGVGVRPRYPCGGKLGCAYRFGNGCCDGAQGSQCCAGGAADLSSCQFGHSGRLSRFSRVMAVSRHFLPPPCPNVAVMS
AGGVNSPFCGCHSRITDPLAANSSSSPSSSHSSGAKFR

SEQ ID 7239

ATGATATATGGGGTATAATTTTTCCTAAACGTTCCAAATTTGGGATTATTTCGCGTCAGCAATAATTATTTATTATTATAAATTTAAACTTCCAAAATACATGGCGTATTACTCC
CATCATATACATATTTATTCAATATTTATTCATGCAATAAAATGCGATATGATTTTATTTTTATGTTTCATGCGTTTATTTCCGCGTATACATATTATGATAAAAAATCTTA

SEQ ID 7240

MDMGVLIFFFLIVPTILGFICATINYFIINKFKLPKYMAYLLPSLSILFIFTHAIKLEHMLFFYVSCVYSAYTTYDCKSL

SEQ ID 7241

ATGTCATTCGCTAAGCGGATTACCGACATCCAGTACGGTTTGGCGGAAGACAATAACGGCTGGCTGGTTCGAAGTGTGCTGATGCTTTAAATAAAAAATGCGCTCTGAACCCCGTTTGGCGT
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CCCAAGAGTTTGCAGAAATCGCGGATGCCCGAGGCGCGCAGCGCTTTGATCGGGCGCGGAAATGCCGTTGCAGCGGATGCCCTCTTTACCAGACAGGCGCGGTTAAGCGGATGCCGT
CCTCAAGGCTGGCTTTTGCCATACCCATCAAGTTGTAATTCGGAATCGCGCTACCGCGCCCAAGTAGCTAAGGGCGACGATGGCGGAGTTCTGCCGCGCATATCGGACGGCGCGCTT
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AAACGCTCCCAAGCATCCCAATTTGTTGCC

SEQ ID 7242

MPSEVRLPTSSVWRKNTYAGNSKADALNKKMPSETRLAFTAPSRSDRFRRTCSKSVQRQSVKTSVRISHPACRKSGLSLEIRFKQTAARNRYSARTAHGFENGGLSLGAQGINAVTA
VNI.SDFAGNAGRGVQQEGGSI.PDFDGNVAAQRVVGGDVQSQEFARIGDAGGGERFRDRAGNVAADALPTQTGGGKADACLKAGFCHTHVIVIRNAYRAQVAKGDDGGVPAABHRTGGF
CQCGQAVCGNFVCGVERFAADAVEVAQGFRRREADGMHQTVQAI.PMFA

SEQ ID 7243

GTGCGCGCTTCGGCTTTTCAGACGGCATATTTGACGTTATGATTAAACAGTTAACAAGATTATCACACCGCGTCAAAAGACAGACACAACA

SEQ ID 7244

VRGFGFSDGIFDVHIKQLFRFITTTPSKDRHTT

SEQ ID 7245

TTGAATGTGTGCCAAGTCTACAAAGGAGAAGTAGAGGAGAAAAATCAAGCTGCATCAAGCAACTCAACGGCGGTAATTATCCGCCGTTCTTATCTGCTGTCAATTATTTTGGAAATTT
ACCCGACCGGATTCAAATTTTGCAAAAACCTTGCCCGATGGCTATCCGGTAAACAAATTCCTCAAAAACCCGTCATCCGATTTATCAAAAATCATATGCTTTTCATCGGTTCCTTTTCG
GTTGAAACCCCTGCCCTTTAGGCGCG

SEQ ID 7246

LNVCPVYKGEVEERKQAASSNSTAVIIRRF.LSAVNYFLKIYPTDSNFARNL.PDGYPTVNSLKNPSIRLF.KKSTAF.IVFPFLKPCPLGR

SEQ ID 7247

ATGTTTGTGACCCCGCTTCTTACCAAAACATCCATGTACGGAGTTGGAAGACAGCGGAGATTCCGGCATAGTAAACAAGATTGGATTTCCTTTCGGCGCGCGCTTCGATGCCACG
TTACTGAA

SEQ ID 7248

MFVDPRLFKHPCTELESTARFRHSKTRFGFFLRGFDCHVTE

SEQ ID 7249

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ATATTTTCCGAAATTTCTCCATT

SEQ ID 7250

LSDEGRHKPT.SAPNRVFMKGMKLYQRDLNIRPIFTABGEYL.TELSDRLPLSVLTVDSNRNIEIGIDFVYSPAKLEGNTYNYQDVALKLQTAGGKLYSDAVMLINLRESYRHL
SGLDSPKPF.DLWDLFKTTHSLISENLEKSGGVRRDSVPTISGDTYPLSNPQLDTELKWLQ.EAPKLENPF.DRAVYLHNNLAYLRYFKDCNKR.TARNCM.TLSLMRS.GFFPCVPS.PDSY
PAYAEAVVAYIYETGDYGLPKKYFI.SAYENTVKNYGPQ.DVDIDIFRNF.SI

SEQ ID 7251

ATGCCGCTCGAAGCCGCTTCAGACGGCATTTTATCAAGCTCTCCGTCGCGCGTACCCGTCGCGTATCTTACGCCCAACCCCTCCGCGCGTCCGCTTTTCAA

SEQ ID 7252

NPSEASDGI.LSSSPVAPVPSVSYRPPFRPCRQ

SEQ ID 7253

TTGCTTGGCTATGTTGTGACCCCGCTTCTTACCAAAACATCCATGTACGGAGTTGGAAGACAGCGCGAGATTCCGGCATAGTAAACAAGATTGGATTTCCTTTCGCGCGCGGCTT
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AACCGGAAACCTGTTTTCGCTGCTGATCCATCGCTGGGGCACGCTCAACGAGCAAAATCACAAATTCCTGAGCGCATGGAAGAACGCTGATGGCGAATGGAAGGAAAAATTTAGGACATG
TGCCAAAAATACTGATTTTGTAGAAATCAGATGTTTTTAAATAAAATCCCGTTCGTCAACACGTTTACGCTAGAACAAATCCAAATCGCGCAAAACGA

SEQ ID 7254

LLGLCLILTPASYQNIHVRSWKARRDSGIVKQDLDFSCGAASIALTLNNFYGRHYSEALDKMDKTQMRSTFDDMRIMPGLFPAQGYALPFEQLVLQKIPVTVYLKYRKNHFSVLNGI
NGETVLLADPSLGHVSTSKSQPLSAWKTRDGEHEGKILAI.VPKNTDFVRNQMF.FNKNPVQRTRFTVBEQIQMRQR

SEQ ID 7255

ATGGGCATCAAAAGTCGCCATCAACGGCTACGGACGATCGGCCCGCAGGTTTTCGCGCCATCTACGACTATCAGATTCAAGACCAACTCCAAATCGTCCGCTCAACGCCAGCGCGAGCC
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CAACCTTCGCCAATCGCGTGGAAAGAACTCGGTGTCGATTGGTCATGGAATGCAACGGCGCGCTTACCAGCAAGAAAGCCAAATCCACCTCGAAGCGCGCGGAAAAAGTCTCTC
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CGGTTGCCAAAGTGTGAGCGAAAGCGTCCGATCGTCAAGCGCAATGACCACTCCACGCACTGACCAACGACCAACCGTTTACCGACGTGCGCCCAAGACCTGCGCGCGCGCGCG
CAGCGCGTGGAAACATGATTCGACCAAAACCGCGCGCGCAAAAGCCGTCGGTTTGGCTTTCGCCGAATTGAAGGCGAGACTCGACGGGTTGCCATCCGCGTCCGCGCGGACCGCTCAACGTA
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CATTTGGTTTCCATGACCTTCAACCAACCCAGGCGAGCCACTTCGACGCAACCGTGACCAAGTCTGCGACGCAACATGGTCAAGTGTTCGCGTGTATGACCAACGAATGGGCGCTT
CAGCTGCAAAATGCTGAACACCGCACGCGCTATGTTCCGACTTGAAGTGGCGCGCTCAAA

SEQ ID 7256

MGIKVAINGYGRIGQVLRAIYDYQIQDLQIVAVNASGSLETNAHLTKFDTVHGRFEADVSHDGGNLI.VNGDKIPPFSTRNPAELPWKELGVDLVMECTGAPTSEKAKIHLESGAKVL
ISAPGGDVDAITVYGVNDSVLTADMTFVSNASCTTNCLSPVAKVLSVSVIVKAMGTHAL.TNDQTVTDVVRHKDLRRARSQGVENMIPKTGAARKAVGLVLP.LKGLRDLGLAIRVPTVNV
SLVLDL.FQARDTTVEEINALMKAVSEAGALKGVLYNTLP.LVSMDFNHTEASHFDATLTKVVDGNMVKVFAMVDNEMG.FSQMLNTARRMFGLEVRPLK

SEQ ID 7257

ATGAATACCTTTATATACACTTTTCGCCACCTGCCCGCGCGCTTGGAAACCGTTTATCTCAAGAACTCGGAAGCCTCGGCTGTACCGATGTCCAAGCGTTTTCGCGCGCGGCTTCTGCG
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CAGCGCGCAGATTGCTATCGAAGCGCTTGGATTGCCGCGCGCGCGCGCGGATGATGCGCGCTTCGCTTTGAAAACTGCAAAATTCGATAAAACGCTGTGGCGGATTTGCGC
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SEQ ID 7258

SEQ ID 7258

MNTLYTLFATCPRGLETVLSQELGSLGCTDVQAFDGGVSCRGGLEQAYAAANLHSRTAGRIILLRLTKGTYRTERDIYKLAKNLNMFNMTLQQTFKVKIEAKRANVKSLOFAGLTVKDAVCD
AFRDIYDARPSVDKAAPDVRIHAFILDERNVEIFTDTSGEALFKRGYRLDTGEAPLRENLAAGLLLSAGYDGTQPPQDPDFCGSGSTIATEAAWIAAGRAPGMRRRPFGEKLNQFDKTLMDLRL
RRAEAQTRVPVRAPIAGSDNGRRIRVQTALDNAHAGADDIVSFSVAGAQSVRPNGENGIMVSNPPYGVRLLEEVRALQALYPQLGTWLKHHYAGWRVGMPTGDRMPKFMRLLPKKIPLYNG
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SEQ ID 7259

SEQ ID: 7259

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SEQ ID 7260

SEQ ID 7260

LTVCLLFRHAFKSEHTACGVQLHAAEAPFVVVPREHFDHVAVDGQRCVEVAGSGGVVVEVHGNQWQGVVAQNAFERACFDGFGHCQVDFFDCGVARGLEAQTYQGYVDGRHADGKPVES
AFQFGQDQTGFCRAGFGRNHVPHAAAGAAQVFAHVHNGNLVVGQCVDGGHCAPDDADAFQAHFGRNRRREAVGGAGSVNGDHVGGQDAVVVHAVHDGCDITVAARCGNEDFFRAAPEVDGFGF
GQVGGGAGAFPHDIDTEFFPRQPRVAGREEGDPAVAVDDEVAAVVGVGFKASVYGVGFQMGVGFKAAGVDGDDLELVNLITVVDGAQNLAADASVAVDGFDAHGLPLC

SEQ ID 7261

SEQ ID 7281
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SEQ ID 7262

MFSSFRRHFSFLTAILPGCRHFOFYSGNLNRYGVASPCRTICTVCGFAALS

SEQ ID 7263

SEQ ID 7263

TCCGCCCGCCTTGACCGCACCCCTGCTTTGCCACCTGCGCGATGCCGTCTGAAGCCCTGAACCGCCCTACCAGCCCGATGATGCACGACACGCGCGGAAGGGGCATACACAAAGCCGTCAGCACATAACGCGCATTTCCCGGTATTGACCAAGTCGCGGCCCTTCAGCAGCAGCGGCGAGCGGTTCGCCACTTCCACAGCGAAGCGCGCTGAAGCCCAATACCGGCCACAGCCCCAACATCCGGAACACCCCGATTTCAGAGACCTGCCCGCGCGACCGGAACGGTTGAGCAAAACACAAACCGCCACCCGAAACAGACCAACGCGGCCATACCGCGGTTGGCGACAATCTGCAAACTGTGAACAGCGAATATCGGGCGTAACCGCCACACAGCCTTCCGAATCCGGCAGCGGCACTGCAAACTCAAACTCCAACTGCAAAACACCCAGCCTTATCCGCAAAAGCATCAAAACCGCCCAATCTTCTATTCAGCCACCGCTTCAAAACCTTCAT

SEQ ID 7264

SEQ ID 1264

SARLDETCLCHPACRLKPEFFYPQDDARHRRKGHTQSRQHI TRIPRIDHVRALQQQQRVRPLPQRREARQYRHQPQHPEHPDFQDLPPPHRTVEQKHNRPQETDHRRTAVGDNLOL
VERNIENRNOHAFRI RHGTQLOIOTLQIHQHTVDOIKKHAYRQSTONPPLHPI*PTVONLH

SEQ ID 7265

SEQ ID 7265

ATGCGGTATTCGCGTGCCTGCCCTGCACAAATTAAGCCTTTCCCGACTCTGCCTATGCTTTGGCCCGGTGCGACGGGCTGGTCGGCTGAGCAGGGATTGGACGCGGGGCGGCTGCTCGAGG
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GCTGCGTAACGGCAGCTATCGGGTTCCGGTCAACGGCTGTTTTTCGGGAAGTGTGCGCGCATTTGCGCGACGGCGCGCCCGGAATCAGGATGGGACATGGATTTCGCGCCCGAGTTTCTCAGACG
GCATATTTTGAAGCTGCACGAAATGGGACACGCGCATCTCTTCGATGCCAATTAATCCCGAGTAAACCGGTAAACAGAGGTTGGCGGCGCGCTTTACGGCGTCTCAGATCGGCACGGTGTGTTT
ATGGCGAATCAGATGTTTCTGCTTGCACCCGATGCGTGCAGAAATCGCGTTTTCCTCGCGCGCTGGCGGTTTGGCGGATTTGGGCGGTGGAAGTAGATAGCAGTGCACAGGATGACGGAACATAT
CGCGCTCTTCGGTTTCGGAGCTGCTGCGCTTTTCGGGATTTTCGGCAACGCTCTCGCGATGTTGAACGCGCTGCCGTTTGAAGAGGAAATCGGGCGCGCGAAGTGGCGTGCACAGGGCGTT

SEQ ID 7266

SEQ ID 7266

MRIPLLAPDNYAFDPDPAYALARCDGLGVGSRDLDAGRLLLAYRNGVFPWF SRDGWFFWYAVGPRAVIVPERLHVPRSLAKTLKNGSYTRVAVNGCFAEVAHCAAAARPNQDGTWIAPEFQT
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SEQ ID 7267

SEQ ID 7267

ATATGGTTTTCGTCGTCGCAAAATGTGTCTGTGTGATTGATACGAAAACGAAGTTTCAGCGAAGCTAAATATGGCTCAATTCGCTCACATCTAATACATCATAGCTACGATAACAATCGTA
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CTTTACCGGCAGCACCGCGACCGCGTTTGCCCTTTCGCTTTCGCGCAAAATAACTTTCATCTGCTTCTACTTCCCATCAAAAT

SEQ ID 7268

SEQ ID 7268
IWECSAKCVI*Y.IRKRSFSEAKMAKFAHT*YLIATITIRINNTVRFHLFTDNRK*SSGLSIRYCNRLNLTISLQKTEYGDFTGSTATAFAPALSAKITFCFYFAIKH

SEQ ID 7269

SEQ ID 7269
ATGAATAAAAAACCGCAAATTACTGCTTGGCCGCACTGCTGCTGACTGCCCTTTGGCCGCTTCAAGCTCGTTTGTGTGCAATGGTGGCAGGCGCAGCAGCCGCAAGCCGTGGGGCGCGAATGG
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CAGCTTCAGTATGAAAAATATGGATATGGGTTTCAACCGCTATATGTTTCGAGCGCAACCGTCGGGGACTTTGGCAGGCAGCAGCATCCGCTGCCCGTCTGTTGTGCAAGGCAGGCGCGAT
TTTACGCCGGGACATTCAATCGGCAGCCGGACATTTCAGACGGCATTTACCGCGGAA

SEQ ID 7270

MNKNRKLILLALLLTAFAAFKLVLVLQWQAQOPQAVAAQCDLTGEGCTLPDGSRRVAAAVSTKKPFDIYIEHAPAGTEQVSI SF SSKMMDMGFNKYMFERQPSGTWQAARIRLPVCVEGRD
 FTADITIGSRSTPOTAFTRAE

SEQ ID 7271

SEQ ID NO: 7271
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CCGGCCCGCGTTTGAAGATTTTGGATTGTTCGAGAAGCAGCGCGAAGAGCAATTGAGTGCGGAAGATGTGTACCCATTCTGCTGGAAGAGGGCGGTGAAATCGGTGTGGCGACGATTTA
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GGCGAGGTAAACGGAATCCCAAAATCCCGAAATCGAAGCCCTGCAAGACA AAATCGCGAGGAAAACGGCTACCGCATCTGTGATCAACGCGCTTTATATTGACGGCGGTGTCAGCGACATGTC
AGGCCAAGGCCAAACGT

SEQ ID 7272

SEQ ID 7272
VIVGQAEIAYSYVYPTGILNIMEKPSNIAQLKDSGLKVTGPRLKILDLFEKHAEHLSDAEVYRILLLESGVEIGVATYIRVLTQFEQAGILQRHHFETGKAVYELDKGDHHDHIVCVCK
GEVTFEHNPRTRALODKIAEENGYRIVDHALYMYGVCSDCOAKGKR

SEQ ID 7273

TTGACGGTAAATATCAAAACCATTAATTTTAAATCATATTTTACAGAATATCCGCCGCGTTCAACAAATGGACATCAAACCGGTTCCAAATTTCTGTAATTTTGCAACAAAATACCGCAA
AACACCCGATTTGACAGCCGAAAGGACTTTCATA

SEQ ID 7274

LQVKYQTLNLNHIFFTEYSAAFTKWTSNRFQISVILQONTAKHPIETERTFI

SEQ ID 7275

GTGATCGCAGCATGTCGGTAGCCGTTTTCCTCGGCGATTTGTCTTCGAGGGCTTCGATTTCGGGGATTGTGGAATTCGCTTACCTGCGCGCACTTCAACGACAGGATATGGTCGTGGTGGTGG
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CGGACGGGCGTTCGGACACAGACAGGGTAAATACCGCTTAAGCGTA

SEQ ID 7276

VDDAVAVPLGDFVLQGFDFGIVEFRYLALHADDVVVVVALVOLINRLARFKMVALQARLLELRQHAVNRRTDFHALFQONAVHIFRTQHLFRVLLBQIQNLQTRAGNLQTAVFQLRH
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SEQ ID 7277

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SEQ ID 7278

MIQDTRPLIRVVAGILLSDGNYLLGSRPEGKPYAGYWEFAGGKVEAGETDFOALQREFGEELGIRILAATPWLTKIHSYEHARVCLKFLVWNPQWEGGQPSREGQEWSHQKAGDFTVAP
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VARYGKMLGLGAHAVRDETIGKNHE

SEQ ID 7279

ATGAACACGACAAAGCCGCGATCTGAACCCGCATCAGCCACAACACCAAAATCTGTGCGACCCCTTGGGCGGGGCAGCAACAACGCTGGAAGCTGTTGGGAAGACATGATCCGGTCCGGCGCCCTGA
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CCCGAAATCCCGGCTGAGCAAAATCGCCGCGCGCGGATCGAAATTCAGCAAAAGGCGCGCTCATTTGGTACTCGATGCGCGCTCGAAGCGCGAAGGCGACCGCGAGGCGCGTCTGGTTTGGACATC
CGAGACTCGCCGACAGCTGTGCGCAGGCGCATGTCTTGTGGCTGGACGAGCGGCTGACTGACCTGACCGCTGGAATCCGTCTGAAGGACAGCAGGATATATCAACAGGGTGGAAACAGCCACA
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CGACACGGCGGTGAACAGAGTCGAAACGATGCTGTGGAACACAACATCTCTGATCTCGGCGACCATGATCATCACCAGCGGCTCGCAAAATGCGCGAATCCGGTTTCGACCAATACCGCTG
GAAGTCTCGCGCTCAAA

SEQ ID 7280

MNQTSRDLTRISHNTKIVATLPGSGNNVLELDMIRVGGLNVVRPNFSHGTFEPHQENARIVREAAKRAQGGKIAIADLQGPKIRVGKIAAGGIEINRGSTVLVLDAALEGEGTREAAGLWY
 RDLPPDVAAGDVLMLDUGLLTITVESVEGSRIITRVENSHILKSNKGINRKRGGLSAGALFEKDFRDLKTAIAIGCDYLAISFVKSAEDLHIAARAKVEEENKSGSTAVRPLGVSKIERVBAI
 ENLDEIILAGDGINVARGDLAVEVGHAAVPAVKQRMIRRARERLRFSTITATQMMESMITNFPVPTRAEVSVDVANAVLDGTDVAMCSAETA VGAYPFPETVSQMAIICAAAEKEQDSLNGVAEQ
 TEYPEAVSTNLAIAGGAVSVARAVHAKAIVALTESGSTAFEISRHNTLPIFALTPSVSAQRMMYRGVRPLILATSTDHDTALNEVETMLVEHNILLEGSDQYITITSGSQMRESGSTNTL
 EYLEVK

SEQ ID 7281

GTGAACAAACCCCTCATCTCGCCCTTTCGCGCCCTGTTTCAGCCTGACCGCGTGACGCGTGAACGCGTCTCGCTGTTTCCCTCTACAACTCAAAATCATCCAAGGCAACGAACTCGAAC
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CCGCAACGCGATCATCAAGAACGCAGCAACCTGACCGTCTATTTTGAAAACGGCGTACTCGTCCGACCGAAGGCAGCGCCCTCCAAAATGCCGCGGAACCCCTCCGCGCGAAACAAAC
GCAGACAAACA

SEQ ID 7282

VNKTLLIALSALFSLTACSVVERVSLFPSYKLKIQQNELEPRVAALRPCHTKDQVLLLLGSPILRDAPFTDRWDYTFNTSRNGIIKERSNLTVYFENGVLVRTEGDALQNAAELRAQK
ADQK

SEQ ID 7283

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CGCATTTGGCGAAGCCGAATTTTCTACGGCCCCGCCCTGTCGAATGGCTGGAAGAACAAGGCATCAGCCGCGTCAAGCTGAGTATGGCGGACGAAGCGATACCGTGTTCGCGCTTTCGC
CTTCCGCAAAAA

SEQ ID 7284

MTYTGIGTDIVSLKRIIRLAKKFGQAFAGRIITPERLLLEFPQAGKPVNYLAKRFAAKEAFKAVGTGIRGAVSFCNIGTIGHDALGKPEFFYGPALSENLEEQGISRVSLSMADEGDTVLAF
VAK

SEQ ID 7285

GTGTGTTCTCTTATGTTTGTCTCGCTTTTGTATTCGCGCGGAGGGCTTCGCGCGCATTTTGGAGGGCGTCGCCCTTCGCTGCGGACGAGTACGCCGTTTTCAAAATAGACGGTCAGGTGCTG
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GGCGAGGATGAGGGTTTCTTCACGGGAGAACCCTTCTGTGCAATCGGGATGCTCTAGTG

SEQ ID 7286

SEQ ID 7286
VCSILLFVCLFRAEFGGILBGVAFGADEYAVFKIDGQVAAFDDAVAGGVEGIVPAVGMESVAQYGAEEQBDLVFGHAGAQQGNGARFEFVALDDFEFVGKKQDADFDAARGQAEQGGK
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SEQ ID 7287

SEQ ID 7287
GAATTTTTCCTTCGAGAAAACCAATTTTGTATCCTTCAAAATAGTGTTCGGTTCGTCTAAACCGTTGATTATAGCAAATTGTCCCTGTTTCTGTGTTTTCAAGTTGCAGCGTCGACAC
GGCAA

SEQ ID 7288

EFFCLAENPFCILQIVFGSP*TVDYSKLSLFLCFHVAACRRQ

SEQ ID 7289

SEQ ID 7289
GTGCCAAGTCTACAAAGGAGAAGTAGAGGAGAAAAATCAAGCTGCATCAAGCAACTCAACGGCGGTAATTATCGCGCGTTCTTATCTGCTGTCAATTATTTTTGAAAAATTACCCGAC
GATTCAAAATTTTGCAAAAAACTTGGCCCGATGGCTATCGGTAACAAATTCCTCAAAAACCGGTCAATCCGATTATTCAAAAAATCATATGCTTTCATCGTGTTCCTTTTCGGTTGAAC
CCTGCCCTTTAGGGCGGTAGAATCAGACTTTATAGTGGAT

SEQ ID 7290

SEQ ID 7280
VPSLORRSGRGKSSCICKQLNGGNYPPFLICCCQLFFENLPDRFKFCKKLARMLSGNKFPQKPVNPIIQKICFHRVSPSVETLPFRAVESDFIVD

SEQ ID 7291

SEQ ID 7291

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TGAAAACTCCGGCCAAATCGTTATTGTGCGATGAGGCGCAAGACGTATGGCCCGCAGCTCCGCGAGGTTGCAAAATCCCCGAAACGTCCTAATGGCTGAACACACAGGCGATCAGGGCATA
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CGGCGCAACAGAACAGCAGGCGACTACTTCGGGATAAAACAGAAAGGAATCGGTGAATATCGCTTACCAATTCATCCGCGAGCTGTATAGAACGGCGGAGAACCCGAGTGACCTGCTATTTCGCATCAAGGGACGGCATTGAAAGAAGTGACCGAGTT
TATTATACCGGTGAAGGCACTGAAGCACTTTGAATATATGACGAGGCTGTATAGAACGGCGGAGAACCCGAGTGACCTGCTATTTCGCATCAAGGGACGGCATTGAAAGAAGTGACCGAGTT
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SEQ ID 7292

SEQ ID 7292
MAEICLIITGTPGGSKTLKVMVMANDENFKPDENGVRVRKVPNTNIGLKIPHTHIIETDAKKLPKSTDEQLSAHMIYEWIKKPNENVAITVDEAQDWWPARSAGSKIENVQNLNTHRHQGI
DIPVLVTQGPKILLDQNLRLTIVKRHHYHIAANKMGLRTILEWKVCADDPYKMASSAFSSIIYTLDDKKVVDLYESAETHFVNKVRKSKWFLPVLPIILILIPLVGLSYMKLGSYGGKKQEEPAQES
AATEQGAVLPLDKTPEGESVINGNLTDAMFVPTLPEKPESKPTIYNGVRQVRTFEYIAGCIEGGRTGCTCYSHQGTALKEVTELMCKDYVINGLPPNFPYKESQGGQEVQQAQQHSDRAQVATL
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SEQ ID 7293

SEQ ID 7293
ATGCCCGCTTACTTCATCACCCCTCTTAACGATGGAAAAATACAAAAAGCGCGCGGAAACGCCCACTACAAATCCAACCGGCTTCATACCGCTCCGCTTTTGGCGCTTCCAAGCGTTTTTTG
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SEQ ID 7294

SEQ ID 7294
MPPYFITLITMENWTKSAAKTPTTIQPASIPSAFAASKAFFAVSGNAAFACAASGAAVTTASFAPYLRQVLNFMIPSKKCLAVMDGEFFRRPNIRKSVFQKSEYDKFALVADFFQTC
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SEQ ID 7295

SEQ ID 7295
TGTGTGATATATATCGAATGTTAGAAAAGGAGAAAAACATGCTCGAAGAAAAAATTGAAATGAGTTTCGAGCCAAACCGTAAATCGAACATTTGGGTGTAAAGATGPAATTCGCACACTGTTCTCTG
CGAATGCCGAGTATGATAGCGAATGCTACGATGATGCTGCTACGGAAGTGGGAAGTTAGGTTTATTCGATAAACCGGAGCATAAAATCGTTATTAAAGATAATGGCATAGGAATGAGCTTCGA
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TATCTTCAAATTCGAACAGTATGAATACAGCGGATTAATACAAGGTAAGTTTATTACAACGGA AAAACCTTTAAAGAATAATATGAAAGGTATTACCTTGTTTGCCAACGGCAGAAATGG
TAAATATGACCGGAGTTTTTCACTGATAGCGAATCCAGCCATTTC

SEQ ID 7296

SEQ ID 7296
 LLGISNVRKGEWMSSEELKMSFEPTVIEHLGVKMYSHTPAIAELIANAYDACATEVEVRLFDKPEHKIVIKONGIGMSFDEINDPYLRIGRNRREEKQASPCGRIPTEGKGLGKLALFEL
 GNKLEISTIQGNERNVFTPLDYABIKKSERIQPEFQKESVKPHTENGTTITLPELTKKQGYPLDNTVGHLSRLFDPPAQDFKIKVSLNGSEPRIIDGNLKYNLVTPQFEWEYQDLATNISS
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SEQ ID 7297

SEQ ID 7297
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GGCTGGACCATCTTCTACAATCCCGCCGGC

SEQ ID 7298

SEQ ID 7298
VOIROHRIKSSAYTRAKOGISDCLFYLSTVRLPTETETPTFLKKPSCCSALPLPPHLSTHPATTSANRSRSTRKARQMPPTRRPSTIIPA

SEQ ID 7299

SEQ ID 7299
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SEQ ID 7300

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DKQGHAYARVQDQDFGEFGDFLLRQYVQTAFGDRDLPFFPRHDAHVFRHHFKRVFEHFFRQRHFKVQARADGVFDGKYIRVFDVAAVFAQVHGNQVCTVRFGNQCRLHGAGISRAARVADGG
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SEQ ID 7301

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SEQ ID 7302

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GAVRAAVVWNGKTLGYMDVLGLMNR

SEQ ID 7303

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SEQ ID 7304

VLPSTHYEADSATDFTGLPVQGSKNGKITKTTPVAPHIYGAYKVNNDLVLGLGVYVFGSATFEYKDSVLRHNINKLGLTSLAVEPVAAMKLNHRHSFGAGIIAQHNSAELRKYAD

SEQ ID 7305

ATGCTTCTGGGTGTCAACATCGACCATCGCCACCGTCCGCAACCGCGCGGCGCAGCTTATCCACGCCCCGTGGAGCGGCGACTGGTTGCCGCAAGCGACCGGTGCGAGCTGATTACCA
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SEQ ID 7306

MLLGVNIDHIAITVRNAGRTTYPSPVEAALVAETHGADLITMHLREDRRHIKDADVFAVKNAIIRTRINLEMAITREMLENALKVMPEDVCIPEKQEIITTEGGLOVLAQQEKIAEFKILP
DAGIRVSLFDADRIQIQAARDVGAAPVVELHTGAYADAQSHABQIRQFERIQNGAHFAGDGLGVNAGHGLTIHNVTPVAQILAIRELNIGHSLIAQALFLGLPEAVRQMKERHAFRLLP

SEQ ID 7307

TTTGTCCACCGTCCGCTTTTACGGAACCGAATGACCCCTTTACACTGAAAAACCGCTCTGCTGCTCGGCACTGCTTTGCCGCGCGCATCTGCCACGATCCGCGTACCACTTCG
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GCTGCCAGCACTTATTATGAAGCAGATTCCGCCACCGACTTTACCGGCTTCCGCTCAAGGTTCTAAAAACCGCAAAATCACCAAAACCGGTCGACCCCACTTTACGGCGCATAC
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GCAAAATGCTGCAAGCAACCTTCTAATCTACTGCGCGCTGCA

SEQ ID 7308

FVHRPPFYGNRNDPFTTEKTVLLGTAFAAASVHAGYHFGTQSVNAQSTANAADASTIFYNPAGLTKLDSSQISVNANIVLPSIHYEADSATDFTGLPVQGSKNGKITKTTPVAPHIYGAY
KVNNDLVLGLGVYVFGSATFEYKDSVLRHNINKLGLTSLAVEPVAAMKLNHRHSFGAGIIAQHNSAELRKYAD*GIPKKAQHLQATPSNPTAAQ

SEQ ID 7309

TTGTCATGCTGCACAAGCAACTTTATTGATATGCCGATACGAAGCTGTCCGCAAAATGCCGTGGAACAATATCTTTTCAGACGGCACTTTTGTATGGGGT

SEQ ID 7310

LSCCTSNFIDHPIRSLSAKRLNIFSDGILYGG

SEQ ID 7311

ATGCTGCAAGCAACACCTTCTAATCTACTGCCGCTGCTCAAAATCAAGGCCGACGGACCGCGGATGTCAAAGGCAGCGATTGGGGCGTGGCTACCACTGGCGTGGATGTGGACATCA
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SEQ ID 7312

MLQATPSNPTAAQIKADGHADVKGSDWGVGYQLAWMDINDRVRGVNYSKVSHTLKGDAEWAADGAAKQVNDMLTPLGYTANAKASVKIVTPESLSVHGMKVSADKDLFGDVTW
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SEQ ID 7313

TTGTTTCATTTGTTCTTCGTAATTTCTATTTTAGGCAATTGTGCCCTACACCAATTACACAGACTGGGTAAAAATTAATTCAGCAGTTTCACTATCTGAAATTTATCTATGGATACG
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GACCACTTTATCATAGATATAGTTTCCCGGGAATAGAGTTGAATTTTATGATCAGGAGGTTTCAAT

SEQ ID 7314

LFHLFPVNFYRQLCTPNYTTDWVKIKPKQPSYLYGYATERNQDKIDNTLELGLQDDDEILDYGGALALIGRRYNLPSTFIIDIVCREIEFLDQESFN

SEQ ID 7315

TTGCGCAGCTTCAAAACACCGCGGACATCATCGGCTGCAATACACCTACAAATTCAAATAAACGTTACACCGCTTGAATATAAAATGCCGTC

SEQ ID 7316

LRTFQKPRRHRAPIHLQIQINVTPEYKNAV

SEQ ID 7317

ATGGATTATTTTCCCGAAGCAGCAGCTATTACAAAAAGGGGGAGAAATTGTGATTATGGCAGATCAAAACATAAGTATTTAAGAGGAATTCCAAATGAACAGAACTGGCCCGAATGG
GATTAAGGTTAAATATAATGGTTCGTTAACTGAT

SEQ ID 7318

MDYFPEAARIITKKGKIVNGTSNNKYLRGIPNETELARMGLRLKYNGSLFD

SEQ ID 7319

ATGTCGAATACCGAGTCAACACGAAACCCGTTTATGCTGGCATCTTCGCCCTTGGCGCGAAGCAGCCTGCGGGTTGAAGCAFTTACGCCGCCGTTACGGGCGTGTGGCTTTGCTGGCGC
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GACCGCAATACCGCG

SEQ ID 7320

MSEYRVNHEPVMFLASSPWRESSLRVEAFRRYGRVALLARSARKRQSELRGVLVFPVPASVSWYGSQELKTLHRAEWMGWRQPGRALFSGLYVNLVLKLTAREDPMSSELYDALAKVM
EAVCREANHLADLRFPFWKLNLALGVAPDLHADGTGGDILADKTYRLMPEAVMPVCRDTGALSHEAGATVEGQSLIDLREGSFRTAESLQALIKITRLLIGTLLPEGLKSRQVLEQIRQF
DRNTA

SEQ ID 7321

TCTCGGTATTCGGGAGAATATATACAGAACCTCCTTCATATCAAAATGGTAGGAGCCTCGGCGAACAGGACGGCGGCGAGGACGCTTGGTGATGCCGTTCAAACCGCGCGGGAACAGCGCA
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GTTTCGCAACACGTAATCTGCTGTTCGAGCTTTCGCTTGGCTTTCATCAGCCTGTTGAAGAAGCAGCGTTGCTCCTGCACTTTGGCGGTACAGGCTTCGATACTTTCCGATACCGGCC
GAATCTGTCGAGGATATTTTCCAGACAGTTTTCAGTCGCTCAGGACGCGGCCATCTTCGCGGAAATCTTCTTCAGGCTTCCCTGCCGAATGGACAA

SEQ ID 7322

SRYSGEYIQNLHLIKMVGTLGGQDGGRLGDVQTAREQRNPLFALFRIICFVVDGNYFAMAVQRVHFHDIGFVVDGCRFLQHVNLVPELVVGFHQPVERRLLQFGGTGDFTFYRYP
ELFEVFFQTVFQVQQAAGHLAGKFFFRLSLPLNGQ

SEQ ID 7323

TTGTATATCCACTATATGTGGGGACAGACGAATATGGTTGATAAAAAAGCCCTTTGATTGCCGTCAGTGTGCGCGAAGCGTCGGCGGACCTGTTGGGCGGCGACCTGATACGCGCCATCC
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GGCGCTCCCGGAAATTTTACGATACGAGGAGCTGCTACGGGATTTGCTGTGCTTGAACCTGATGCTTTTGTGCGTATCGATGCGCGCGATTATATCTGGGTGGCGGAAAGCTG
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TGTGCGGCTGCCGAATATCTGTTGGGTAAGGAGGCGGTGCCGAATTTATGCAATCGAAGCAAAACCGGAAACCTGGCGCGCATTTGGCGGACTGTTACGAACACCCCGATAAGGTT
GCCGCGTGAACAGGATTTCGGGCGTTCACCTGCTGTTGAAAAAGATACGGCGGATTTCGCGCGCGCGCGGTTTTGGAAGAGCGGGATGT

SEQ ID 7324

LLIHYMWGQTNMVKKSPLIASVGEASDILLGAHLIRAIRKRCQARLTGIGGELMKABGFESLYDQERLAVRGFVEVVRRLPEILIRIRRELVRDLSLKPDPVVGIDAPDFNLGVAEKL
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AATEATKRRRLAEVLQRPEFAGLALTVDROSETVCRADAVALVTSGTATLEVALCKRPHVISYKISPLTYAYVKKIKVPHVGLPNTLLGKEAVPELLOSEAKPEKLAALADWYEHDPKV
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SEQ ID 7325

ATGGTAGGAGCGCTCGGGCAACAGGACGGCGGCGAGGAGCTTGGTGATGCCGTTCAAACCGCGCGGGAACAGCGCAATCCGCTCTTTGCCCTTTTCCGATAATCTGCTTTGCGGTTGTGG
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TCATCAGCCTGTTGAAGAACGAGCGTTGCTCTGAGTTTGGCGGTACAGGCTTCGATATCCGAGGCGCGGAACTGTTGAGGATTTTTCAGACAGTTTTCAGTCGCTCAG
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SEQ ID 7326

MVGTGGQDGGRLGDVQTAREQRNPLFALFRIICFVVDGNYFAMAVQRVHFHDIGFVVDGCRFLQHVNLVPELVVGFHQPVERRLLQFGGTGDFTFYRYPLEFEVFFQTVFQVQ
AAGHLAGKFFFRLSLPLNGQYSLFKIRTRRRSRQYR

SEQ ID 7327

GGACGGCACATAGGGCGACGCTTATGTGCCGCTCTGTGTTGAAACATCAGCATAGGAAACACAGGAAAGCGCGCTGTTTTCGCGCTGCGTACCGTATTTGGTCAAAATGCCGCTGAA
ACCGACAACAGGCTTTCAGACGGCATTTCGCTCAA

SEQ ID 7328

GRHIGRRFMCRRPVC*NISIGNTGKAGCFAPAYRIGQNAV*NRQGFRRHFRQ

SEQ ID 7329

TTGATGTTAGAAATGACCGCAAAATTACCGTTTCAGGCGAAATATGTTCCCAACTATCGACGAACCTCTCATCCCGCACCGCAACCGCATCGACACCATCGATGCCGAAATCTGCGGCTGC
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SEQ ID 7330

IMLECTANYRSGEIMSQTIDELIIPHRNAIDTIDAEILRLNRAQHAIHAGELKGTGAVYRPEREVAVLRIQDLNKGPLPDESVARLFRVNMSECLAVERPLTIAYLGPQGTFTQAAI
KHFHGAHTMACPTIDDCFRQVETROADYLVAPVENSTEGSVGRTLDLAVTALQACGEVVLRIHNLRLRNNGSTEGIAKVP SHAQALAQCNOWLGRRLPHARLIVASNABEARLVAES

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SEQ ID 7331

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GCAGATGTTTCCCTTATCGGCATCATTTGATGGTTGTGCGCTGGCCGACCCATGCTGGCGCATTTGTTCAGGAGATTGGCGCGATGGCGGGGATTTTCGTTTTCGGCGCGGTAT
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SEQ ID 7332

LFMFATFAGQVAGGAVSDIKGRKPVALTGLIVYCLAVAAIVFASSTEQLLNLRVAFAGAGMAVVIVGAMVRDYYSGRKAQMFAFIGIILMVVPLAAMPVALLQGLGGWRAIFVFLAAY
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PSQLAAVLPFGLPPFPLVACVMPFVGTTQGLVADTQACFMSYFKEBGGANAVSGVFRSLIGAGVMAATVMAATMTASASCGIALLMLCSHRAWKENEKRLILVNRCPKPLQTAFFDVR
MHGKLPFRNRYVFNRYRTPHPAPQRHHRHRCNSAPAQRTRATCPRHRAERHGRGVPRTRGCRVAFHSGFQRPAARRIGSTPVSIGSDERVPRRRSTADHRLSAGAGHVYPTGGHAPR
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SEQ ID 7333

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SEQ ID 7334

MKTHEISKGSVSLIGVAZHEAQRLDNYLIKILKGVPKYIHRITRAGEVRLNKKRCKPDSRIABGDTVRIPPVRAEKEMPSSERRAAVPARAFEVVYEDALLVNVKPSGVAVHGGSGVS
PGVLEQLRRARPEAKYLELVRHLKDTPSGLLMVAKRSALVVKLHEAIRNDHPKITYLALGVGLPDPNHFVKLPLFKYTGAGGKEMVRVSEDGQSAHTVFRVLSRPSDGLLHGVLGSLTL
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SEQ ID 7335

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SEQ ID 7336

LAHILLNVICIFYLKQASVRDVVMFHLVVKPHTRSEIFNPNPKPDFL

SEQ ID 7337

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SEQ ID 7338

MNITRALLIILGCLAAGETAVLAGIKLPGSIVGMVLFALLQAGVKTSLWQLTALMANLTLFVPPCVAVISYLDLIADWFSILVSASASTLCVLLVTKVHRHRSII

SEQ ID 7339

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SEQ ID 7340

SLGAQGINAVTAVNISDPAGNAGRVGQDEGSIPTDFDGNVAAQRVVGDDVSQFAEIGDAGGGERFDRAGGNVAAADALPTQTGGGKADACLKAGFCHTHVIRNRAYRAQVAKGDDG
GVPAAHRTGGFCQCGQAVCGNFVCGVERFAADAVEVAAQGFFRREADGMHQTVQALPMFA*VGEHLVDFVWAGDIAAEYFPGI*FRHFADALPQFVHNVKRPFRALFAAGFGDAVSD
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SEQ ID 7341

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SEQ ID 7342

SAEQVGDIFHLFPKTFVPAQSGGNCFFARQTVVRTELPPFFDFGCGGTFQRPDGNPAPGDGIH

SEQ ID 7343

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TAATA

SEQ ID 7344

LGLRCRLTSAPKRQNFKLDYVLRLPAGNRRRENALRSAFLI

SEQ ID 7345

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SEQ ID 7346

IDGIAAKILYLPFARHPRVALELEVGVFLPVLCLRGGLSAVADFFLRPLALFADQLFLHVGIESPFGKGNFGFRTLVLVYARLFHFAP*YNGIGTLDVVGNQDFGPGCAFPGGLGYARIAAGG
 IVGQNVFPGYGGFRFFFTGFAAQNPDVRVFFCHRLAVYHHDALHAVRQQRGRQLRRHRTDRVVDKCRPSVFGQGEADGCRQYAVFKLDIAARLLHHDVQQRFPFIQQGAVCLGIGKRFRHGN
 VOIGDTRFAPAFILRFRSVFORKROTGVGGDNFVGIDKLPVTFARERTFLRLERFLMTAAYVLQHGCVGAFORLGRFFPAARCKQQGKRQNEFFTH

SEQ ID 7347

ATGCCGTCGTAAGACGGGTTCGGGCGGCATATCCTTCGGTTTTGCCCCCGCTCCGATATGTAAACTTGCGCCCGTGCCGACCGTCGTTTGCGACGGTTTCCTTTATTGTGATTGAACGGAA
AAACCATGTCTCCGCCCTTCCTCCGATGAGCGGAAAACTGATGGCGGTTTGTATGGCGGTACTGGTCGCGTGATGCCGTTTTCATCGATGCCCTACCTGCCCGCGATTCCCGAAATGGC
GCAGCGCTGAACCGCGGATATCCACCGTATCGAA

SEQ ID 7348

MPSEAVSGGI SFGFAPP S DMLNL RPCRPSFATVSLFDLNGKTMSPPLPPMSGKLN AVLNAVLVALMPFSIDAYLPAIPEMAQPLNADIHRIE

SEQ ID 7349

TTGAAAAATCCGACGGGATGCACGTTCCGGGGAAACCGTGTCCGGGAAGGTCGGATAAAGAAGGCTATAAAGATCGATCGCGCGGTCTGCCTGCCGCGTTCGGAACGCTCGGGTCGGAAAAAT
GGCGCGCGGCTTCTTCCTCTGTATTATCGTGATGCCCTGTGTTTTCCGGCGGTTTTCGCTTCGGGGCTTGGGGCTCCGCTGCCGCTCTTACTTCCGCGCGAAACGGCAAANTCAATTCAAACCTTGAC
TACGCTTCTCGCGCTCCGCGCTGGGAACAGGCGCAGGGAATAATGCTTTGCGGAATGCGCTTTT

SEQ ID 7350

1.KTPRDAPSGEPFCARGSDKEGYKDRCGGLPAAFRITLRSEKNAPASSCYRDACVFGRFAGANGSAAVLLPRRNGKINSNLTTFCACRLGTGAGKMLGVRF

SEQ ID 7351

SEQ ID 7351
TTGAATAACATTCCTTTTCATGATCACCTCGTGACGGGCGGCATTCCGGCGCGCCGGTCCGGTTCGGCATTCCGTAAGGCTGGGTTTCCGATGCTCTCCGGATAAAACCGGTAATCAGTTT
TGAGT

SEQ ID 7352

LNNILFMITSWTGGIRARRSGSAFRKAGFPMSSDKTGNQFLS

SEQ ID 7353

[illegible]

SEQ ID 7354

SEQ ID: 7334

VTHKRLFNATQAEELVAIVDGNLLDLDETFLGKEQRKGNITYKGIITRIEPSLEACFVDYDTRHGFLPFKEVSRSYFLGYEGGRARIQDVLEKGMETVQVEKDERGNKGAALTTFIS
LAGRYLVLMPPNNPGGGVSRRIEGERQELKAAMAQLDIPNGMSTIARTAGIGRSAELEWDLNLYLKQLWQAEIAGKAMHDPYLLFMESLLIRAIRDYPRPDIGETLVDNQVEYDQVAB
FMSYVMPGNAGRLKLYEDHTPLFSRQPIEQHIESAFSRVSLPSGGAIVIDHTALVSLIDVNSARATRGADIEDTAPKTMEEAAEVARQMLRDLGGGVVDFIIMENPKHQDVENVLR
DALKKDRARVQMGKLSRFGLLIETSRQRLKPALGESSHAACPRCAGTGVTIRGETALHVLNRVQEEAMKINTGEVRAQVPVDVATFLINEKRAELFAMEERLDVNVLLIPNTHLKNPHYET
NRIRTDDEVEDGEPSYKRVAEPEEDESAPKFGGEKAKAARPEPAVKGRVHTSPAPTAAPKEKTSNWDSPKAMLRIPGGSETQVAPAAETSEKRSSTANRSGSRNANPNFRSKRSGSKI
EVREAAGKTAGQKARADAKETRNNGNRRNRNREGDRATERANEASTQRNVQPAAPVADAAPPETEGTQKRRNGNSRNGQTAPETAFAAVQTAQAEITAPPEPTTAEQKSGKSPSRNR
REDRSDAKERRERNQDRRRQKGNKRNIPSAAKIBQYILNIHDPADKVRSAADHVFGETTANAPITVSIADPLIATPQTASSAVSNGDALITYDAEKTIRRAAADILPEGAAPKAAQENP
SETAPTPAAABQARETAQTGGLVLIETDPAALKAWAAQPEVQAGRLLRSBQPKPSEAAVTPAEMIQVETROG

SEQ ID 7355

[illegible]

SEQ ID 7356

LYDHLPLPLTMFYQILALITWSSFTIAKYVYGGIDPALMVGVRLLIALPALPACRRHVGIKPREWKPLILIVSPVNYVLTLLQFVGLKYTSAASASVTIGLEPLLMVVFVGHFFNDKA
RAYHWTCGAAAFAGVALLMAGGAEBEGVEVGFCLLVLLAGAGPCAAMRPTQRLIARIGAPAPTSVSLAASLMCLPFSLALAQSYTVD#SVGMVLSLLYLGLGCGHYAYWL#NKKGH#SRVP
ANASGHLISLEFVVGVLAVLILGEHLSPVLSALGVVFVVIATTAAGRLSRDDAQNGAV

SEQ ID 7357

ATGGTCATACAAAAGTATAGCGGATTAAACAAAAATCAGGACAAGAAGGAATGCCGACCGTCATTCGCGGCATTTTCGTCAATCCGCGGAAAGCGGGAATCTAGGACGCAGGGTTAAGA
AAACCTACATCCCGTCATTTCCCTCAAAAAACAGAAACCAAATCAGAAACCTAAAAATCCCGTCATTCGCGCGAAAGCGGGAATCTAGAATCTCGGCATTTTCAGA

SEQ ID 7358

MVIQYSGLTKIRTRRNARTVIPATFRHSRESGNLGRRVKKTYIPSPQKQTKIRNLKSRHSRESGNLSRTFR

SEQ ID 7359

GCCTTTAAAGAAATTCACAAAAACGGTGAGAAATCGCGGCATTAAATCAAATCGACAAAGAACGCCGCCACCATAGGCACAATCAAAAAACGCCCTTATGTGACGCGCGGAAAGATGCGTGAAC
GACTGCAATATTGCCACCGCCGTGGCGGTTGCGCCAAACCGAAACCGCAGTGGCCGCGAGCCAAATCTCGCGCATCATAGTTCGCGCCCAATAAGACATAGGTAAACAAAAGTCGCGTACA
AAACCATCATCGCGGTTGTATCGCAAGAATCAGCGTTACAGACCCCGCCAAACCGGTTCAGCTCCCAACAGTTTCAAATTCAGCAACGCCCATTGCCAAAGAAAGCGAAAGCGAAGCATTTGCC
GAACACATCATGATGGCACCGTGCAACATATTGACCTTGTAATGTCGGCGGTGAAGGATGTGCGGATAACACCGCCGCAAACAGACACCAACAGAAITTTGGCGACCGTGAACAGGATTTCTTTG
TGAAACCGCTGCAATAATCTTCGCGAAACCGCCAGACACGCGGCAACCAAGCAAGCGCTTTTCAACCGGCAATTCGCGCGATCATCAGCGGGGTGTGCTGCTGCTGCAACAGCTGCTGCGCGT
TGTGCTCTGATCTCTGTTTGTGTTTCAACCGGTTTGGCGGCAATTTTGTGTGATCAGCGCGCGCGCAACCGGCCCTCCGATCAGGCGCGCGCAACACAGCCCCGAAAGTAACCGAAGCAAT
ACCCAAACCGTTGCGCGGACCAAGCCGATTTGCGTTTCAAATTAGGTCCCAACGCACTTGACGTGCGGTGTCCGCGCTGTCAGCGACACCGAACCAGGTAATCAGACCGATGAGCGGGTCC
AAACCCAAAGCCGTAGCCAGTCCGACCCCGACAAAGTTTTCGACCAAGATAAATCGGCCACAATCGCGGTAAAAAACCAACAGCGCAACACCGCCGCCCTTCAAACGGGAAAAATTCGCGC
TCAAGCCGATGGAGCTGAAGAAATCAGCATAAACGCATTTTTCAGCGGTTTCTCAAATTTGAAGCTCACGCCCTACGCCCTGCTGACGCGCAACACAGGATAATTCGCGGCATCAGCCGCC
CGCCACGGTTTCGGGATGTAAATCAGCGAAGATTTGATTTTCTTAACCAAAACCTTGCGACCAACCAAAAGTCGGGCAATCAAGGTGTATTAATCTGTTAAACGCCCATTTCC
ATATCTTTGACCTCCATAAATGTTTTCTTTATATCCGCCGAAGGGAGCGCACAGCGCAAGATATAGGGGAATAGTTTAAGCGTTGTCAA

SEQ ID 7360

AFKEIHTKTENGRGINQIDKERADHRHNQKRLM*RAESMRDGLHICHRRRCAQTETAVAGSQYCGITVAPHKDIGNKSrvQNHHCGLYCKNHGYPRTQTQLPQFQIQORHCQEKRRKSIA
EHIDGTVEHIDLECGGKVDADNHAAKQTPHEFGQVEQVFPVETVHNLGKQRTGKHGKFRNGFRNRQAGAFCLLEHVVRVVVLLIFCVFNRAAHFVQDAARNRPSDQAAEHQEPESNRSN
TQTGCADQAVLRFKIRSPRT*RAVSARQHRHTGNQTDERVDQTSRSQSDPKVLHQDKSAHNRGKNHQRTARLQTGKITRAQADGREENQHKRILQFLKFEAHAVRLVQRKQDNRGVQPA
RHGPGDKVITQDFDLNQLADQONSGNGVITVKRPFHIV*PPKMPFFISARRGKREDIRGIVKACQ

SEQ ID 7361

TTGACTCGCCTTGCCGTA

SEQ ID 7362

LTRLAVLSVSVASSPCPDNLHYTTIFYKQNAV

SEQ ID 7363

TTGACCTTCGGCCAAAGGATGGCTTCGGAAACTTGC GCGGGCGGGAATCCGGACCTTGGAAACAACGGCAATATTCAAAGAATTATCTGAAAGTCGAGATTCTAGATTCCCGCTTTCGCGGGAA

SEQ ID 7364

LTFGOKDGFGLRAGGNPDLGTTAIFKDYLVKVRDSRFPLSRE

SEQ ID 7365

TTGTTTGGAGCAAAACAGATGAAACAGCGCTGTTTPTGCGGTACTTTCGCGGAGCCTGCCGGCATCGGCCCGATATTGTGTTGGACATTGGCGTTTGCAGCGCTGCCCTGCCGCTGCGCG
TATTGGGCGACAAACAGCTGTTTTCGCGCGCGCGCGCGAGCGCTTGGGCAAAAGCGTCGTCTGCGCGACATTCGATTCGGAATCAGGCGGCGCGCACGAGAGGCGGGCTGGAAAGTCTGTCA
CATCCCTGCGCGCGCAAGCGGTTTGGAGCAGGCTGGCTCAATCCGCGCAACCGCGCTCTATGTGCTGCAAACTTTTGGAGCGCGCGCTCCGACGAGCATTTTCASACGGCATTTTTCAGCGGCATCTGCT
ACCGGCGCGCTGCACAAAGGACATCATCAACGCGCGCGCGAGCAAGCTTTTATGACGACACACCGAATATTCGCGGAAAAGCGCGACGCGGCGAGGTGATGATGATGCTTTCGCG
GCAAAAGGCTGCGCGTCGCGCTCTGTAAACGACCCACCTGCGCGTGAAAGAGTTTGGCGCGCGCATCACGCAACCGCTGATTGAAAGCGCTGCACAGCATTTTGTATCATCAGATCTTAAACACAA
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GAAGGATATAACCTCGCGGCGCGCTATCGCGGAGACATATGTTTCCACCGCTTATGCTCGAAGGTCGGATGCGCTATTGCGGATGTACACAGACCAAGGCTGCCGCTGTTGAAATACC
ACAGCTTCGGCGAGGCGGATGAAACATCAAGCTGGGCTGCCCTTTATCCGCACTTCGCTGATACCGGACCGCGCTCGATTGCGCGCAACCGGAGGCGGAGATCCGCGAGCCTGATAAC
TTCGCTGGAACCGCGCTCGGACATGCGCGCGCGGACGCTT

SEQ ID 7366

LFGANTKQPVFAVTSGEPEGAGIDPICLDLAFARLPCCRAVLGDKHLIRARAEALGKSVLRDFDPESGGAHGEGLVLIHTPAABAEVAGWLNPAANAAYVILQLDAAALAGISDGFIDGIV
TAPLHKGIINAARASTGFGSGHTEYLAESGTGQVMMLAGKGLRVALVTTHLPKDVAAATQPLIESVARILHDLKHKFGIKNPKILVAGLNPHAGEGGLHGHESTDTIIPALENLR
EGINLAGPYPADTLFOPFMLEGADAVLAHYHDOGLPVLKYHSGGQVNTILGLPIRTSDVHGTAALDAAATGRADSGSLITAVETA VEMARGSL

SEQ ID 7367

ATGGGAAATACATATTTTGAAATAACAGAAAAAGCGGGGCAAAAACCGCCGCTGCATCTGTGCTGTACATCCCTGCTGTGCGACTTTACCGCTTCAACTTCGCAAAACGCATCCGCCATCG
CCGAATTGGTTGGGACACGCTCGTTGCGTTGTGGTTTTCGCGCCGCGCTGTCCGTTTCGCGGCTGCGGTTTTCACAGCTCGGACAGAATGTCCAGAAATGTCGGCAGTCCGAAGTGTTCGTTCG
TGAAGTCGGACGCTTTGATTTCCTTCACGCGCTCGCGGTTAACTGCCATAAATATGAAATTCCTTGGTCTCTCTTG

SEQ ID 7368

MGTHIFRTEKAGAKPAAASVAVHPCRTYRFNFANASALAEVLGTRSLRCGLRPAVRSRLRFFOLGONVONGROSEV FVGEVGRFDLLHALAVNCLNKKFLVFL

SEQ ID 7369

TTGGCGAGGTCAA AAAATCAGCGCTACCGAGTATTACTGTAATCAGGCACATGGCCGGA AAAACAACACTTCTGCGCGCGTGGCATCTCCGCCACGCATCAAAGGCAAAATATGTCTC
AAAGCGTTACGGTCGCAAAAGCGGCTCGTTACCGCGGAAATGAATCAGACGGCGTAAACAAAGAAATCCAAGGCAAAAGACTCTCCCTGTGGGCGAGCGCTGAAGCCGGTTCGGTAAATATG

GTTCGCGGCAGCCGGTTACGCCGCCAAAGCCAAAGACGCCGACGCTTACCGACGAGCGCGCACCGCGGCGCAAAGGCGAAATCGACACCAAGCAOCTGCCGTCAAOCTGC
CGCGATAAATCAACTGCCAAA

SEQ ID 7370

EQ ID 7370
LAEGQKSAVTEYYLNHGTWPEINTSAGVASSATDIKGKYVQSVTVANGVVTAEKMSDGVNKEIQGKRLSLWARREAGSVKNFCGQPVTRAKAKADDDVTDAGTONGGKGKIDTKHLPTC
RDKSTAK

SEQ ID 7371

SEQ ID 7371

AATATGAAATCTTGGTCTCTCTGTAGCATAAGTCTCTGATGATATGCCAAGTAAGATTTACGTTTGTGCTGAGCAGATGTTATCTAGCTTCACATCACACCAACGTCGCCAAACATCA
TCTGATCAACCGCTTAGATTTTCACCAATATTTCCTTCATCATCAAAAGGAAATATATTTCAAATCAAAATAGGCTATCCAAAGTACGACTTAAATAGCAAGCCGTTATTTGGGTCGTATGCTTCGG
TATCATCCGACAGGATGAAAGGCTTAATATGACTGGCAATCAATACAGGATAGGCAAGTTTTCGACATACATTTTCACATACCGGTAATGTTCTCACTTCTCTGTAAGATTGGTTTT
GTATAGGCGATGTAAATAAGGGTCGCGTTTCTTCACAGTAATTTTCATCCAAATTACCAAATAACGTTGGGCATCTCTCAGCAAAATATAAGTCATCACCTACTCGTTTTAAGTCGCTTAAT
TTGTCATAATAGGTCCATAATAAATTAATTTGATGTGATTTTCGTTCAATAAATCTGATTTCTATCCCTGTTGAAAAATAATCATTAATCTGTTTCGGTTAGATAATCTTGTTGAAAAG
TTTTTAAGCTCTACTAACATCATGGCGCAATTTCTTTTTATTAGCTTCGCTTCGCTGACACCGTTTAAATCAGGAAATTTATTGTCGAATATTAGAGTTTTCAGTTACTGA
ACGCTGAAAGCCAGAGTGCATATACGATTTTGGAAAGTAGGGTTTGTGCTTTTCGGTTAGTACGAGCTGTACATAATCTCGTGATAAAGGTGTATAGCTTGATAAAAAAGGTTCTATA
AATCCCAT

SEQ ID 7372

SEQ ID 7372

NMKPLVFL*HKFSMICQVRFTFVVEQIVL*LHITPTSPNII**PLRFPHHSFIKRNIFQIK*AIQOTT**QAVIWWVFCGIIRODERLNMTGNQYRIGKPFQHTFHITVMFFTFFLKLIVF
V*AM*IRVAFPYFSNFIQITKNITGLLSKI*VITYSP*VV*FV**VP*ITYLIVFSPNKS*FYSLLKIIQFCFG*ILLKGF*VY*HGGNFFPI*LALWMLDQRFNQEIYLSNIRVFSY*
TLKARVRIYDFGK*GLSFVSUSTSLYIIS**RCIA**KRFYKSH

SEQ ID 7373

EQ ID 7373

TTGGCTGATTATTACTCATCTCTGTCTCCAGAATATTTCGATACCAATATTCTGTTTTGTATTAAAGTAATATCTATCATTCATGTATTTTCTAC

SEQ ID 7374

LADYYSSLSPRIFDTNILFLYLSNIYHSCIFY

SEQ ID 7375

SEQ ID 7375
ATGAACAGAGAATTATTACCGAATGGCTGCACGGCTGGGTGCGGCCCATCAACGATCCGATGTGGTCATATCTGGTTTATATGCTTTTGGGTACGGGGCTTTCTTCACCGTAACCAACGGGCT
TGTTCCAATTCCGGCTGTTTCGGGGCGCAGCATCAAAAGAAATGCTCGGGCGGGCGCAAACAGGGGGACGACCTCACGGCATCACCGCGTTTCAGGCATTGTGAACCGGCTTGCCACGCCGGT
GGGCTGGGCAATATCGCGGGCGTGGCAATGCCATCAAAGTCGGCGGGCGGGCGCGGTGTTTGGATGTGGGTAAACGGCTTAATACGGCATAGATTGGCGGTTTGTGCGAATCTTCGGTG
CGCGAGCTCTTTAAAGTCCGGACTCGGACAACCACCATTTCCGGGGCGGGCTGCTTACTACATACAGCAACGGTCTGGGGCAGAAATGGCTGGGCGTGTGTGTCGCCCTGAGCGCTGATT
TCTGTTTCGGTTTGTGTGTTGAAGCGGTTCAGACCAATGACCATCGCCGATACCGTCAAAGCGGCTGGGGCTGGGAGCTCATTTATGTCCGCTGCGCTGATTTTAAACCGCGCGAT
TATCTTCGGCGGCATCAGGCGCATATCCAAAGCGGGCGGAAATCGTGTGCCCTGATGGCGGTTTGTACTCTTTATCGGCTTTTCATCATCTTGAACCATTAATTCGATGATTTCGGAC
GTGTTTCGGTCAGATTTTTTCGGCGCGTTCAAATTCGACGCGGTCAGCGGCTACTCTCGGCGGTCTGATTTCGAAACGATGATGATGGGCATCAACCGCGGCTGTATTTCACACGAGG
CGGATATGGTTTCGGCGCGGACGACGCCGCCGCCGCGGCGGAGTGAACACCCCTGTTTCGCAAGGTATGATTCAAATGCTGGGCGTGTGTTGTCGATACCATCATCGTTTGTCTTCGACCGC
CTTCATCATCTTGATTTTACCAACAGCCTTATGGCGATTGAGCGGTGCGGCGCTGACGACGGCGGGGATTGTACAGCAAGTGGGGCAATGGGCGCGGGTTTCCTCGCCGTCATCTCTGTT
ATGTTTGGCTTTTCCACCGTATACGGCAATATGCTATCGCGAGTCAACGTCCTCAATTCATCAAAAGCCATTGGCTGATTAGCCCGCTTTCCGCTATGCTGTTTGGCGTGGGTCTATT
TCGGCGGGTTGCCAATGTGCACTTGGTCTGGGATGGCGGATGGCGATGGCGATGCGGCTGGATCAACCTGCGGCTCTGCTGCTCTCGCCATTTATCGCTATGGGTTTTCGCTGCTGCG
CGGATTCGCGGCAAGTGGGCTGCAAGCATCCGATCTTCAAATCTCCGAACATCGGAACCGCGCATCAATTCGATGTTTGG

SEQ ID 7376

SEQ ID 7376

MNENFTWMLHGVGAINDPMNSYLVMLLGGYLPFTVTGTFVQFRLPGRSKEIMLGGRRKGDDPHGITPQAFVTVGLASRVGVGNIAGVALAIKVGPGGAVFMMVTLIGNSSAFVSSSL
AQLFKVRCDCNHRFRGGPAYIITHLGQKMLGVLFALSLIPCQGFVPEAVQVTFPIADTVKAAWGNEPHYVGVVALVILTAPIIFGGIRIKSAAEIVVPLMAVLYLFIALFILIATNIEMIPD
VFGQIFSGAFKPFDAAGGLLGILLGSLQMKMLIKRGLYSNEAGMSGAPNAAAAAEVKHPVSQGHQIMLGVFVDTIIVCSCTAFILITVQQPYGDLGSAALTQAATVSVQVQMGACGLAVILF
WQAFSTVIGNIYAYAESNVQPIKSHWLITAVFRMLVLAWVYFQAVANVPLVWLMDMAMGIMAWINLVAIILLISPLAFMLLRDYTKLKWGKDPFELKSEHPGLKRRIKSDVV

SEQ ID 7377

SEQ ID 7377
GTGTTTAAACGGGTGGCAATGAGGCACATGCAGGGCCTTGAAGCGCAATCGATATATTATTTCCACGGGAACGGACGACCCCGCCCGCCTTGCAAAACCTTTAAAGACAAGCCGCCCGGT
TGATCCGGCGCGCCGTGGGAAATCACTTACCCTTTGATTATTTAAATTT

SEQ ID 7378

SEQ ID 7378
VFKEVAMRHMQGLEAQSIYYFHRNGRPRPCKPLKDKPPGLIRAAVGNHLPFDLFKI

SEQ ID 7379

SEQ ID 7379
ATGACGCGAAATCCTCAGGCAGCCAGCGGTTCTGCTTTTCTCAGCGTTGCCGTGTACGCGCTTGCAGATTATCGTGCGCACGCGCACGGGCAATATCTTCTGCAACCCGCTACTCGTCAGCA
CTATCGTGCCTGATTGCGCTACTCTGAAATCCTCGGTATCGATTATGCGGTGTACCCACAACGCCCGGCAATTCATTGATTTTCGGCTGAAACCGCGCGCTCGTCTGCTTGCCTGCGCCCTCA
CCAAAACCGCCGTAATAATCTTCAACCACTGCGTCCCGTCATCGTTTTCGACAGCTTTCGCGGACAGCGTACGGGCAATGTATACCGGGATGTATTTGCCAAGTGCTGGCGCGGACGCGAA
GTGCTGCTTCGCCGTTCGCGTCCAAATCTGTTACCAACCCCATCGCCATCGAAATCACC CGCTCCATCGCGGCACTTCGCGGCATTCGCGGCATTCACGCGCCACCGCTATCATCTGCTTGGTTCGCGAC
AGATTGCGCGGTACAAATATGTTGAAGAACCGCTGTCATGCCCTCGCTCCGTGGGTATGTCGCTCGGCACAGCGCTTCGACCGCATGCGCATGCGGCATTCGCCGCTCGCTCGAACGACGCGCGCAT
GGCGGCTATCATCGGATGCGGCTGACGTTCAACGCGCGTGTGACCGCGCTGATTGCGCGCGTCTTATCCCGCTTTTGGGGTTC

SEQ ID 7380

SEQ ID 7380
MSBILQPSVLLFLTLAVYALAIIVTRTGNIFCNPVLVSTIVLLIAYLKILGIDYAVYHNAQFIDFRLKPAVVVLAVPLYQNRKIFWQNLPVIVSQLAGSVTGIIVTGMYFAKWLGAERE
VVLPLASKSVTNPIATEIETRSIGGIPAITAATVIIAGLCGCIAGYKMLKNTVVPSPVSGHSLGTASHAMGLAASLERSRRNAAYAGMGLTFNGVLTALIAPIILIPVLGF

SEQ ID 7381

SEQ ID 7381
GTGCGCTCATTGCCACCCGTTTAAACACGGTTTTTATCTGACAGGCGCGCAATCCGCCCCCTCATTTGTTAATCGCGCATATTTGTTAATGAAACACCGGCCCGGAACCCGATATAATCCGCGCTT
TCACATCAGTGAAAAATCTTTTTTAAACCGGT

SEQ ID 7382

SEQ ID 7382
VPHCHPFK HGFYLTGAQSAPSVNPPYCIETPPGTRYNPPFNISENLFLTG

SEQ ID 7383

SEQ ID 7383
CAAAATGATTAAATAGCTTACGAACCGAGGCCAAATTCATGGCCTTGCTTGTCTCTCGGAAGCCATAACGGAATCTTGGGCAATGTTTGGCTGCAATGCTTCATATAGTTGCTGCTGTAT
GGCTGGTCTTGATTGCGATCAATAAAGTCAAGACAAATATTGAGTGCAGTACAAAAATTTTGTATCGTTATAAATTTGTAAGGCAPTGGTAAACGCCCAATAATCTTCATAAAATTTGGCTGT
TTGGCTGATTATTACTCAT

SEQ ID 7384

SEQ ID 7384
QID**LTNRGQIHGLACSLRSHNGILGNVLLQCFI*FVAVWLVLIRINKVKTNIECSTKFLIVIIICKGIGKRPIIFINLAVWLLITH

SEQ ID 7385

[illegible]

SEQ ID. 7386

MNPARKKPSLLFSSLLFSSLLFSSLLFSSAAQAASEGNGRGPYVQADLAAEAERTHDYPTAPGKNKISTVSDYFRNIRTHSIHPRVSVGYDFGGWRLAADYARYRKHNKNKYSVNKE
 LERKNNKTFGGNQLATIKYQKTEHQENGTFHVSLLGLSAVDYDFKLNDRKFKPYIGARVAYGHVRHSIDSTKKITGTLTATPSDADAAVTVYPDGHFPQNTYQKSNSSRRLGFGANAGVGIDV
 APGLTLDAGYRYHNWGRLENTFRFKTHEASLGMRYRF

SEQ ID 7387

TGTAATTTTCTACTAAAAACAGAATTCCPTATGGCTTGGCTCTTTCTCTTTCCCTGTAACCTTATAAAACGTGAGGCGTTTCCAAGATTTGTACATTTTCGCCCACTTTTAACTAACATTTCTCTCAATTCATCTCGGTTTGGATATGAAGACATTTGTGTAGCTTAACAGCCCAATATTTAAATGGTTTCAAATGATTTGATTAACCTTTTAAATAATTCGACAGCCCTGCTTTTATFCCATGAAATGATTGGCAAATGGTTTGGTATGTGATGATGTAAATGTAAGTCTCAATATCCGTAAGAGCCAAATATGTTTCATCGTCCCTGTGTAAAGTGGCTTAATAGACGGCATCAGCTGTGATATAGTAGGATAAAATCAAATATCTTTGATTAAGCGGTATGATGCGCCAGCCATTTGTAAACAGCTTGGTTTATGTCACTCAAATTTTTCGAGAAATGAGCTTTGAAACCTTTCTATTGTGGTAGGCGCGCTCGACGGCCATAATTTAGCATAACTGTATTCTTCATCAGCGAGTTGTTTAACTTTTTCCCAAGGAATTTGTGAATCGTGAATAGGGCATTTTACGSTATCATGGCGGACGCACTTAAGTAAACGCCAAAGCAGCTTTATACCTGGTTATTTACAGCTTCCCTATATTTTACCGGTACAAATCAGTTTGTGGCATTCATCTGTGAAATAGAAATTTTTCGGAATTAACGCTGACTCATAAACCGGCATCGCGGCTGCTTGAAAAAAATTCATTCGCAATCATCTCCTCATTTAATGTTTCATGGTTGTTTTCTATTAAATGCTAAAGCAATTTGGTAAATTAATTGCCAAAATATCTGTTAGTAATCACACGATAGCCGCTTTTTTGGCTTCGTAGGCAAGGACAGCCCTCCACTAAATCTGCAATCTGATCTACGACGGAAGCTGGTCAAAATCCAGGAAGCTATTTTCCTCTTATTACCGATATAGTTAAATTTTCGATATTTCTTATTCATTTCAC

SEQ ID 7388

CIFY**KQNFIMALLFFSCNLINVRFFQDLYISPIFT*HFF*PISVWT*STVVA*QPIKPMQMDYPPK*FDSLIFTHEMIGKWFYGY*CNVTVQ*SVRAKIVHRACVRW*IDGISLY
IR**IKYILFKMGVMPAIIENSLVIVIQLOKMTLKTPIVVGASTAIFSITVFFITQLFNFFRNCS*IGHFTYHGATH*SKRQSTFVLIVQLPYIFTVQIKLAFIVKLEFFGITLTHK
TGMRAA*KNHCDIIVI*CFMVVFF*CSNLVINCONTVNSHTLAAFFGFVGKGTASTKYICNICYIRKLVNTPGSYFLPITDIVNFRILPH

SEQ ID 7389

ATGTGGGTCATGTGTGTATTCGCTATCGGTTTTCAGACGGCATTCCAAGCAGGATGCCGTCTGAAAAACGAAACGGATTCAAAAGTAAAGGGTTGGATTGTACGCTGTTCGCCCTGTT

SEQ ID 7390

MMVNCVLPFGPSDGI PSRMPSEKRNFGFKSKGLGLYACSPCFYSARKGKSRFAGKRLR

SEQ ID 7391

TTTCAATTTTCACTCATTTTTTAAAAACTTTTTCAGCAATAGCTTTTGGCCAATAAAGCGGGCAGCGCGTTTACCAACCTGCTGCTGCTGGGCAATTTTGTGCGCCGCAAAAAATAAAATATACAGG
AAAGATTTGTAAGGCGAGCTAATTCAGGAACGGTTAAAGCCCGATTTCTGTTTCATAGTGAAAAATCTTTGGCGATATCTCTGTAATACAAACGGCTGGTTTGTGTGCTGTGTACAGCGGTATT
TACGGATATCACTGCTTTTTTCGGAGCGAATGGTTTCAGGAATACTGTTACGTTTATCTCCATTTTTTAACAATAAGCCATTTTTTCTAACATTTGTGCGCCGAAATGATTCATAGTATCATGATTTGC
AAGCTGTGAGTATGTTTTTCGCGACGAGCCAGTTTTCGAAAAATGTCCTATTGCTGATCCCAACAGTCTGAGTGGAAATATTCGAAAGGTTCGGGAAGGAAATTTTGCCTTTATCCCTCTCCCG
ATAAATATCACTCGGCTACGTATCTGAGGAACACCGAAATCGGCTGCACTCAGTATCTTACATTTCCACCGAATAACCGATATTTCTGAAATGCTTGAATAATCTCAATACGTGTTTTACCTG
AATTGTGTGTATAGAGTGCAGCTACATTTTCCATAACAAAAAATATGGTTGGACAAATTTTAACTATTTCGGAACAACTCTTTTAAATAAATGGTTGCGTGGGTCACTGTGAAATGTCCTCGGTC
AATCTTTCTCGCCATATCAAAACCTTGACAGAGTGTCTCCCAATAACCAAATCAACTGATTGTCCGTTAAGACAAATGGTTAAATCTTGTTCGGTTAGTGTGGTTAAATCTTTTTGCAAT
AATTGATGACGGGGAGGTTGGTACGTTAGCTTGACAATAATCAGATCCATTTCAACGAAAGCAATTTGTTGGAATCCGCGCTGTGTCAAAACCCAAAGGATAGCCCTCTGCTCTCTGAGA
AAAGGCTCAATATAGGTAAGTGGTGTGTGTCAT

SEQ ID 7392

PFTPTNFTNSNSFCQRRHGVTNLLLLGNFAAAKNKIIRERI*GS*FTNG*SPILFIVKFNFAHSCNTNGFVAVVTDVFTDITCFRT*WFRNIVTVTSIFNKHCF*HLCRMHSHFHC
 NVWIAFASSQFWKMSYC*SNLSMGNLQRFQKGNFAFIPPPDKYHSATYLRNTEIGCTQYLTFHRITDILKCLNNLNTCTP*IVCIESRYTFHNKKIWLNFNYSDRLP*MVAVVICRCP
 NLSCHTKTLTRWSSNNQIN*LSVKTIG*ILFG*CG*IFLQ*LTGEGVTIVSLTIIRLHFNKQJLLESGLFKTQC*ASCS*EKNVIGKNCVH

SEQ ID 7393

GTGCGGGACGTCGGGATTCCCGCCTGCGCGGAATGACGAATTCGAGATTGGCGGTGTGTCTCGGAATGACGGTTCGGGTATTTTACTGCGGCCCGCCCCGCGCTGTAAACGGCGGGCGA
TTAAAAATGCGCGTC

SEQ ID 7394

VERTGPD SRLRGNDEF RDCGVVGNDGSGILLRPPRACKRRRAIKNAV

SEQ ID 7395

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SEQ ID 7396

SEQ ID 7396
MTHMYTYPKTYDIVIVVGGGHAGTEAALAAARMCAQTLLLTHTNITELGQMSCNPSIGGIGKGHLVRELDALGGAMALATDKSGIQFRLNASKGAAVRATRAQADRILYKASTREMLNQNENL
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VSCWHTHTNTQTHDIRSGFDRSPMFTGKIEGVGPXYCPSEIDKINLPADKKSHQIFLEPEGLTTHEYYPNGISYSLPFDIQIALVSMCKGLENAHLRPGYALEYDYFDPNKLASLETK
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SRISGVTPAAVALMLNHLKRGFGD

SEQ ID 7397

SEQ ID 7397
TTTGGACGCGAAGCAATCGCGTGGGGCTTCAGTCCGGGCAATCCCATCAATCCAACATTTCCTACCGTTTTTCATCGAATCCATCGAATCCGCGCTCTTTTCGACCACCCGGCCCTATGCAAC

SEQ ID 7398

LESMNRWASVRHSHQSNISTVFIESIRASFDHPALCN

SEQ ID 7399

SEQ ID 7399

ATGCAACTGAACCGTCATCCCAACGGAAGTGGGAATCTAGGACGCGGGGTTTGGGCAACCGGTTTATCCGATAAGTTTCCGTGCGGACAGGTCGGGATCCCGCTCGCGGGGAATGACGA
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SEQ ID 7400

SEQ ID 7400
 MJLNRHSHSGNLRGVRWATVLSDKPCGVRI PACAGMTNFEIAVLSGMTVVRVFCARPAVPGVNGRLKMPSESGDIGIGESEAVAHQGRGVFGFEAGVQASPVVVAVAGVQGAQRDV
 YAHARHRAEAQAAAFAFLRQVFLRMSVRINRNCVSTIRVGGKSTCYFFSRIDA VSDVSVGDARTDIGFEFVVEFEIVNGGQAERRNGVECAVFMFLRLVTVKLVAAKSFIIISFQLF
 VYHGIFTVVFPVPTGIIRGDAPAAEVVADRHPGVDGMRTDVS EIIATRAYFVFANSWGFR IIVGNAPGGVG

SEQ ID 7401

SEQ ID 7401

TTGAAATTCGTCAATCCCGGATAACACCGCAATCTCGAAACCCGTCATCCCGCGCAGGCGGGAATCCAGACCCCCGACGCGCGGGAATCTATCGGAA

SEQ ID 7402

LK F V I P D N T A I S K P V I P A Q A G I Q T P D A A G I Y R K

SEQ ID 7403

SEQ ID 7403
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SEQ ID 7404

SEQ ID 7404
MPSETIFRRHRTIPTGNIMHILTAGVDEAGRGLPVGSVFAAAILPETFDLPGLTDSKKISEKKRDALAEIMKEQAVAMHVAASTPEETIASINILHATMLAMKRAVYGLAARPEKIFIDGN
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SEQ ID 7405

SEQ ID 7405

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SEQ ID 7406

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GFGVGDVFPVVALRGGFHVLRLFGKHVRQRLQTVFVRDLRFGAAGFPGVQVQVQFQRGFVVGFDLRPEVV*KLALLFNAP*HNGIALFQLAQVLQPLKLAQLRIVQPARGFPTVTRDKG
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SEQ ID 7407

TTGTTTATGACCGTCTGATTACCGGGCGGACCGCGTTTATCGGTTCCGACACCGCGCTCGCTCGTCCAATCCGGTTACGATGCCGTGATTTGGATAATCTGTGCAACTCGTCTCGCG
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SEQ ID 7408

LPFTVTLTGCGTGFIGSHTAVSLVQSGYDAVILDNLCNSSAAVLPRLRQITGRNIPFYQGDIRDQCILRQIFSEHIESVTHFAGLKAUGVESVAEPTKYGNVYVGSVLAKEMARAGVLKI
VFSSSATVYUGDAEKVPYTEDMRPGDTANPYGASKAMVERMLTDIQADPRWSVILLRYFNPIGAHESGLIGEQPGVGNPNLLPYTCQVASGRLLPOLSVFGGDDYPTPDGTGMRDYTHVNDLA
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SEQ ID 7409

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SEQ ID 7410

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SEQ ID 7411

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SEQ ID 7412

LRHIPPIYGHGGTLRKPFTQMPILNHTALIGVGLIGGSPVLDLKRQGLVVRTVGIDTRDNLERALERGVIDRASVWIDADSIGGADLVLIATPVATVPVAVLTALRPVLPHEHTWISDVGST
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SEQ ID 7413

ATGGCGGTTTGGAAGTTACCTGAATTCAAAAAAAAAACGGAAACGGACGGATTGGATTCCCGCCTGGCGGGAATGACGGATTTTAGGTTTTTT

SEQ ID 7414

MAVWKLPEIQKNGNRTDWIPACAGMTDFRFF

SEQ ID 7415

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SEQ ID 7416

TYAGNLESLTDIADNPYAEQVQIDCRAELQVRFQYRPDAVMHLAAESEVDRAIGSAGEFIRTNVTGTDLLEAARAYWQMPSEKREAFRHHISTDEVYDGLHGTDLFTETPTTAP
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SEQ ID 7417

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SEQ ID 7418

LLIRYIVIPAKTKLIKNRKLYRHSRAGGNLGLSVRKLI GKNGFSNPETPDSCFRGNPVFLSPSH

SEQ ID 7419

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ACCGTTC

SEQ ID 7420

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SEQ ID 7421

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GACGCTTGGCGGTATGTTTCAGACGGCATGGCGGTGGAACAAACGCTGCTATGTCGATACAAACGCCCGCGCTCAGCGCGCGCGAGCTTCCGAGTCCGCGCTTTCGGAATCGG
CGGCGCGCAGGCATATGCTTTTTCGCGCGCGCAATCAATACAGAAAGCGCGGTACTTTTATGCGCGACCGCGCTTTCAGACGCGCAT

SEQ ID 7422

DAAQRFVHAGFGAGLVHAFDDGTVKAVAVPGRQAAGHDDRTCRYAALVDFACGTVEFPGTLDEHAHRNHAAPFDNRAFDFGTRADEAVVFNDDGGGLQGFYAADADTAQVDFVA
DLRARADGRPSIDHRAFVDVADVDVRRHQHGVFNKAASGHRTRNCAEACVFEVFPVKGPRHFVFEVFAVVEVDFVFLDABEQQHGFPFPFVDFPLAHQAQFDAQFA*IELADGF
QHGFFDFGNGGRSDVRAVFKGGFDNVLQRHNVSILRDLISGRLEFVLRFRHGWKNRAIVPYKRPVPSRAAGLPDAGVSESGRQAYVFFRFRINTERRYFAAPPFFRRH

SEQ ID 7423

TTGCTTTCCCAAATTTACTCTATTTGTTAAAATCAATAAATACAAAGTAAATCCAAATGAAGAAGTATAGATAAAATCGATTTCGCGCATCTCAAATTTCTTCAGCAAAATGCCGTA
TCCCGATGACGAGCTTGCCTGAGAGAGGTAGGTTTCCAGCACGCCGTTTACAGAGAGGATGCGCTTTGGAGCGGGAACATTATATTTCCGGCTATCAGCTCCATCTCAATCCCATCT
GTTGGGCAAAACCCCATTTGTTTGTGAGCTGAAGCTGCAATCCAAATCGGCAATATTTTCGAAGATTCAAAAAAGAGTCTGAAATTTCCGCAATATGAGGATGCCATCTGCTG
TCGGGCGAATACGACTACCTGATTAAGTACGTTTCCCGGATATGCTGCTATCGGATATGCTCGGCAATATCTTATGCAACTGCTGCCGCTTCGAGAGTATGAGTATGTTGTA
TGGAGGAAGTCAAGAAAAATCCGGTTTGGATTGGAT

SEQ ID 7424

LISQIYTLFVKINKYVIMKELDKIDFRILKIQONARIPTMTELAEKVGLSTPVTVERCREREHYISGYHVLNPHLLGKPLVFLVELKIQSKSNIFEDFKKEVLKIPQIMECHLV
SGEYDYLKVRLLPMSAYRDMNLNILLQPAASESRSYVMEVEKNPVLDD

SEQ ID 7425

ATGCAAAACCGCAGGCAAAAAAATCCTCGTTACCGCGCGCGCGGTTTATCGGCTCGGCGATGCTCGCGCATATATCCAAAAACCCCGAGATTCCGTCGTCACCTCGACAAGTAA
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CAGGCTGTTACCGAAGGTGTTGTCGCGGAACCTTACAATATCGCGGACCAATGAAAAACCAATCTCGAAGTGATCAAAACCATCTGCCGCTCTTGAAGAACTCGCCCCGAAAAAC
CGCGCGCGGTGGCAGGTATGAAGATTAAATACCTTTCGTACAAGACCGCGCGCATGATGCCGCTACCGCGTTCGATGCGCGCAAAATCAGCGGAGATTGGCGTGGCTGCTTTGGA
AACTTTGAATCCGCGCTCCGCAAAACCGTGCAATGGTATTTGGACAAACAAACCGCGCGCAAAACGCA

SEQ ID 7426

MQTAGKKNILVTGGAGFIGSAVVRHIIQNTDRSDVNLDKLTAGNLESLETDIADNPYAFQVQDIDRAELDRVFAQYRPDAVHMLAESHVDRAIGSAGEFIRTNIVGTFDLLEAARAYW
QMPSEKREAFRPHISIDEVYDGLHGTDDLPTETTPYAPSSPYASAKAAADHLVRWQRTYRLPSIVSNCSNNGYPRQFPEKLIPLMLNLALSGKPLPVYGDGAQIRDLWLFVEDHARALY
QVVTBGVVGTEYINIGHNEKTNLEVIKTIALLLELAPKPAVARYEDLITFVQDRPHGDARYAVDAAKIRDLGWLPLETFESGLRKTQVWYLDINKTRQNA

SEQ ID 7427

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GACCGCGCTGCCACTTGGACGGGACAGCGGCCACGAGGGCGGCTTCTGTCGCTGACCGCTTTTGGCTGGCTGCGCGGATTCGCGCTTTATCCCGGTTGGGTCGCGCGGCA
AGCGGCATATCGGTACGCTGTTTCTGTTACGCGCGGCTGTCATGCTTTCGCGCTTATCCGTTTCGCAAAACCGCGCAACTATGTCGCGCTATTCGCAATATTTGCTGCGCGGTA
CGCATGCGCGCTTCCACGCTCCAGCTGCACAACGGCAACCTAGGCGGACTCTTGAGCGGATTCAGTGGCGCTGTTATGTTGTCGCGCTTATCGGCTGATTGGGATGAGGATTATTTT
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CGCGCTCGCTCATCGGCAATTCGATTATCCGCGGCCAAAGCGCTTCCGCTGCGCTTTGGCTGATGATGCGCGCAACCGCGCTCGGTATGCTGCGGTATTTCTTCCGCGACTGCC
TACACGACAGCATCGCACGCTTTCGCTTTCGCTACGCTGCTGCTGATGCTGCGAATACATTCGCTGCTGATCCGCTCGCGCTTCGAGCGGACGCGCGGT

SEQ ID 7428

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SGILGLTFWYGAVALPVLIRSONRRNYVAVPALFVLGTHAAPHVQLHNGNLGLLSGLQSLVMSGFIGLIGMRIISFFTSKRLNVQIPSPKVAQASLWPLMLTALMAHGVMPW
LSAFAFAAGVIFTPVQVYRWYKPVLEKPMWILFAGYLTGLGLLAVGASYKPAFLNLGVHLIGVGGIGVLTLGMARTALGHTGNSIYPPKAVPVAFWLMMAATAVRMVAVPSSGTA
YTHSIRTSVLFALALLVYANKYIPWLRPRSDGRPG

SEQ ID 7429

ATGAGTGGCAACATCTTCCATCGCCAAATCAGAAGGCGGTGTGGGCAAAACGACGACGACGGTAAATTTGGCGGCTTCCGTCGCGATCGCGCGCAACCGGCTGCTGGTGGTGGATTGG
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CGGATACGCGCTGTTGGGTGCGCAACCGCGCTTCCGCGCGGAAATCGAGCTGGTGCAGGAAATCGCCGGGAAGTGCCTTTGAAAAACGCGCTCAAGCAGTGGCGGAAGATTACGAC
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TGATTGCGACCGTGCAGAAATCCGTCAGCGGTCAATCCGATTGGACATCAGCGCATCTGCTGATGATGACGACGCGCAGCAGGCTGGTTCGCGAAGTACGCGCAAGTTCGCT

CAGCCATTTTCGGGGATTGCTTTTGAACCGCCATCCGCGCAATATCCGCCCTTGC GGAAGCGCGAGCCACGGTATGCCGGTGATGGCTTACGACGCGCAGGCCAAAGGGTGCCAAAGCG
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SEQ ID 7430

PSANILAIANQKGGVKTMTTNNLNASLASRQKRVLVVDLPQGNATPGSGIDKAGLQSGVYQVLGDAVQSAAVRSKEGGYGVLGANRALAGARTELVQKTIAREVRLKNALKAVAEDYD
FILIDCPPSITLLTLNGLVAAGGVIVPMLCEFYALEGISDLIATVRKIRQAVNPDLDTGIVRTMYDSRSLVAEVSEQLRSHPGDLLFETAIPNNIRLAEAPSHGMPVMAYDAQKAKA
YLALADELAARVSGK

SEQ ID 7431

ATGGAACCTTAAGAAACGCTTCGCTGCAGGCATTCGCCGATGGGCGCGATATTTTCGAAACGGCGCAGGACAGGCTTTTGGCCATATGTGGATTTGTGAAAAAGTGGAAACAAACCTACA
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ACTGGCGGGCATGAGGCGGTATATCCGAGGGGAAATCGCGCGCTGCCCGCATGTGTGTCGAAAAAGTCCAAAGGCTGCAGCTGCCGGCTTGGATGCGGAACGCCATATCTGT
CATCCTTGAGCTAAGCGT

SEQ ID 7432

SEC ID: 1502
MERKEKLRLAGIAAMGPDISETAQDRLILAYVDLLKKWKNKTYNLTALEDEEKIMVHLLLSLTLLPYIEGAQTHLLDVSGGGGPGIPAAVCRPDVQITLLDANTKKTAFILRQAATIELGLDNVR
VYSGRVEAVSDVRADVVTSRAFAELADFVSTAHLLKDDGGYWAAMKGVYPOGEIGRLPDQVCEVKVQRLDVPGLDAERHIVILSKR

SEQ ID 7433

ATGCGCTCTGAGCGCGCTCAACGCTTGCCTCAGGATGACGATATGGCGTTCCGCACTCAAGCCCGGCACGCTCGAGCCTTTGGAGCTTTTCGACGCACACATCTCGGGCAGGCGGCGGATT
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CGGCAATGCTCTGACGAGGCGTCTTTGACGCTTCACATATCTGCTCTGCTCATATTACGGCGTAATGTTAGCGGAAAAACATGCCGCTGTCGAAACCGCGTATCGGGTTTCAGACGCGCATTT
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SEQ ID 7434

[illegible]

SEQ ID 7435

SEQ ID 7435
ATGGTGATTATGGACAAACAAACCCGGCGCAAAACGCATAAAACGGCAACTGCCGTTCGGAAACGCTTAGGTTACGGGCAAAATAGTTTTCAGACAGCATCCCGACGCAATGCCGCTGTGAAAACCATGTCGCAAAAGGAAAGAAAGAAAGATGAAGAGCATCATACTGGCAGGCGGCAGCGGTACGCGCCTATATCCGATTAGCGCGCGGCTATCCAAACAACTGTCGCCCGGTACGACAAACCGGATGATTIATTACCCTTGTGCGGTTTGTATGCTGGCGGGAATCCGCGATATTTTGGTAATTACCGCACCCGAAGACAAAGCTGCGCTTCCAACGGCTACTCGCGACAGCGCTCCGACTTCGGCATCCGCTGCAATAATGCCGTTCACACCAGCCCCGACGGCTTGGCGCAGGCATTTATCATCGGGCAGAATTTATCGGCAACGGGCAATGCTCGCTGATTTTGGGCGACAATATTTTCTACGGTCAATCATTTACGCAAACTATTGAAACAGGCCGCGCGCAAGACCCACGGCGCAACCGTATTCCGTTATCGGGTTAAAGACCCCGAGCGTTTCGGCGTGTTGAATTTGACGAAAATCTCAACGCTTATCCATCGAAGAAACCCGAACAGCCCAAATCCGATTGGGCGGTAAACCGGCTTGACTTCCACGACAAACCGCGCGCTCGAGTTTCGCCAAACAGCTCAAAACGCTCCGACAGCGCGGAAATGGAAATTTTCGACCTCAACCGGATGTATCTGGAAGACGGCTCGCTGTCCGTTCAAATATTGGGACCGGCTTTCGCGGTGTGACACACGACGCAAGAAGCTGCAACGAGGCGGCTCCTTCGTCCAAACCGGTGCAAAATATCCAAACCTGCATCGCGCTGCTCGAAGAAATCGCCTGGCGTAACGGCTGGCTGACGAAAAAAGATGTGGAACACGGGCAAGACCTTTTGAAAAA
AACCGCCTACGGGCAATACCTGCTGCGCCTGATCGGCAAA

SEQ ID 7436

SEQ ID 7436

MVFQGNPAAKRIKRLQPLPGTILRYGQIVFRQHPDAMPSENPSQRKKEKMGII LAGSGSTRILYPIITRGVSKQLLEPVYDKPMIYYPLSVLMLAGIRDILVITAPEDNAAPORLLCDGSDFGI
RLQYAVQPSPDGLAQAFII GEEFINGNVCLILGDNIFYGGSPTQLKQAAKTHGATVFGYRVKDPERFGVVEFDENFNALSI EEKPOQPKSDMAVGTGLYPHDNRAVEFAKQLKPSARGE
LEISDIANRMYLEDGSLSVOLILGRGPAWLDGTQOESLHAA SFVOTVONIQNLHIA CLBEIAWRNGMLTKKDVE TRAKPLEKTAYGQYLLRLIGK

SEQ ID 7437

SEQ ID 7437
ATGCCGCTCGAACC CGGTATCGGGTTTCAGACGGCAITTCGGTCCGTCCTATTTTTTCCTGTGGAAACACCACAGGCTGCACCGGCGCGCGCTCAGGCGTTTCGGCAGCGTCAGCATAG
ACACGACGCCACACGCGAAACGCATATTCGACACCGCCTCCCGGCTCAGCCCGCCCAAGCGCACTGCCCAACAACAGCGTTGAAAATCCAAAGCCACGCGCGCAAGCGCCACGCGCGCA
CAGAAACAGGCGCG

SEQ ID 7438

MPSETAYRVSDGIVPSYFFLANITGCTGARVRRFGSVSISDTSETANAYSDTASPLSPPKAALPNNSLKIQATAAQATPDNSA

SEQ ID 7439

SEQ ID 7439
ATGAAACCGTTGAAACGACATTCGCGCCCTGTGCGGCTTTGCGCGCAACACCACTCGCTTTCCCTGTGCGTGCATGTTGCGGACGCCCGGGGAGAACATCGTGCCGAACCTGGAGC
TGCATTTTGCCGAACCTGGAACCCATTTTCGCGAAGGAAGACCAAGTTTGCCCAATTTGGCAGAATGTCGCGCTGAGTTGAAAAACCGGTTTTGAAGCGCATCAGCCCAAACCTGGGCA
GATGATGGCAAGCCCCGAATGCGGTAAACGCGGCTGGAAATACCGCTTTTGCCACAACCTGCGCGACACCGCGCGCTTTGAAGAACGCGAGCTGTTTCCCGCGCTGAAACCGCTTTTTCGCG
GCA

SEQ ID 7440

SEKID 17440
MKPLKRHSALVGLSREHHHSLSLCVRMLRTPGADHRAELHLEHFALETHFREEEAKFAPINQWVAPELKTRFEGDHAKLRQMHASPECGNAWNTAFATTLRDHARFEERELFPAVEPFLP
A

SEQ ID 7441

SEQ ID 1/441

ATGATPATATAAACAGCGTTGTTTGTGCAACCTTTTCGGCGCGGCGGCAAGCGCGTGCOCGGTATAATGCGGCCCTGCTTCGGAAGAGGGGGGACGGCGATGTTTGTGAACGAGAAATATCCTT
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CGCGCGGCGTGGCGGTGGGACGGCACTGTTGGTTTGTTGTTTCGGTGTGTTTGCCCTTTTGAAATGCGGTTTCGCGCGGGGCTGACGAAACTGGCGGTACAAAAGATGATGTCGGCGGCAT
TCGCGTTACCGCTGTTTCTGCTCGGCGTCGGCGGCTTCGCGCGCGCTGCGCTTGGAATTTCAAGCTGTGTTTGGGCACTGCGCCCTTGCGCGGGCTGACGCGGGAGCGCGTGTGCGAATATG
CGTTTCGCGCTGTGGCTGGTGCTGATCTGCTGACGCTGCCAAAGCGCTTGACGCGCGCGCGCTGTCGAGCCCTGTGGTGTTTCCACAGGAAAAAA

SEQ ID 7442

MIYINGCLCNFSGRGQGARYNAACFGRGGTAHFVNEKYPIATLPAGLVFLTLPPALAVHDACAFACFRAGLLVSVSDGGFGRRGWDGTWVFWVFVGFAPLNVVVVSAGLTKLAYKKMMRRH
 SRVALFLSGVAACAATAHIFKLLLGSAALGGLSGEAVSEYAFVFLVSMILPKRIITRAPVQPVVFRKK

SEQ ID 7443

SEQ ID / 7443

ATGGGACATCATCGACACGCGCCTCCCGACGTAAAACTTTTAAAAACCGCAAGTCTTCACAGACGGGCGCGGTTTTTTTATGGAAAACATTCGCGCAGCGTAGTGTCAAAGAAAAATTGCGG
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CGTGGCCGTGATATGCGCGAAGGTTCCGCGACTTTCGGCAAAATGGGCGGGCGCAACCTTGTGGCGCAAAACCGATACAGCTTTGGATACCCGAAGGCTTCGCACACGGTTTTTGGCGTT
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TACTTTCCGCGCAAGACCTTGCCTGGCAAAACGTCGGCACAAGCCGAAAGCTCCGCTTACGCTTTCCCGA

SEQ ID 7444

MDIIDLTPDLVLLKPVQVTFDGRGPFMETFRDGFKNIAIDRTFVQENHNSKGLVRLGLHYQTENTQGLVRIIVGVEFVAVDMREGSPTFGKNAGATLSAQNRYQLMIPEGPAHGFCV
LGDAAEVVKCTDYNNFETBQVLIWMDPAIGWPLQATAPLLSPKDLAGKTWAQAKRLRLTLR

SEQ ID 7445

ATGTATCTGACCCAAATACCGACTACGGGCTGCGGCTCTCATCTACACCGCGCTCAACGACGACGCGCTGGTCAATATCGCCACCATCGCTCGACCTACGGCATTTCCAAAGCCATT
TGATGAAAGTGGTTACCGCGCTGGTCAAAGCGGGTTCTTGACAGCGTACGCGGGAAGGCGCGGGCTGAGGCTGGCCGCGCGCCGGAACGCATCAATATCGCGCGGGTCTCGGCCA
CCTCGAACCGATGACGCTGGTGTATGAGTGTATGGGCCGAACAAAGATGCTGATTACGCGCTCTGCGCGCTGACGGGCATCTCGCGGTGCAATGAAGTGGTTTTTACGCTATCTGGAC
GGTTTACGCTGCAAGACCTGCTCAACAGCGGACCTACGACCTGCTTTATGAATCGAAAAATCCGATTCGGGTGCGA

SEQ ID 7446

MYLTQHTDYGLRVLIYTAVNDDALVNLIATSTYGISKSHLAKVVTALVKGGLFSVRGKGGLRLAAPPERRINIGAVVRHLEPMQLVECMGPNNECLITPSCRLTGILGGAMKSFPTYLID
GPTLQDLNKPFTDLYESKIPIAIVR

SEQ ID 7447

TTGCACAAACACCGTTTATATATATATACGAAAAACCGCGGTGTAGCTCAGTCGGTAGAGCAGCGCATTCGTAACCGGAATGTCGGGGTTTCGATTCCCTTCTCCGGCACCAATACCA
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GGCAACCTCCTCTTCTACCTGACCATCGGCACGCAAGCGCACTGGCGCGCTGGCGCGCGGTGCGCAAAACCGGCTACGTCCTTATGCTGGCGGGCTGACGATGTGCATGCTCATCGGG
ACAACGGCAGGAATGGCTGACAGCGGGCTGATGCGCGGATGAACGTCTCATCGCGCGGCAATGCGCAATTCGCCCGCCAACTGCTGCGGCTGAAATCCACACTGATGTGGCGTTT
CATGCTTGGCGCAACCTGGCGGCTGACGCAAAATGATTGCGGAATCAGCAACGGCAGGCGTATGACGCGCGGAACGTTTGGAGCAGAATATGGTCAAAATGCGCCAAATCAACGCAAGC
ATGGTCAAAAGCGCGACGCTGCGCGCAATCGCGGCAAGCGCATGACGCGCTTCCATGATGAGAGCATGACGACGCGCCACCGCAAAATCGTCAACACCGAGCTGCTCTGA
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CGCGCGCGCATCGCATGACACCGCATCAACCGCACTGGAAGCGCTCGCGCAACCTCCACTACCAATGCGAGGGCTTCTCTGGCTCAGACCAATATGCGGTGAGGAATTTCC
GCCCTGCTATCTGCTGCAACGCAACCGCGCAAAATGGCTGGATGCCGCAAGCGCAACACCTGCGCGCAAGCGCTGCT

SEQ ID 7448

LHKQFFIYITKNAGVAQSVQRIRNANVGGSIFFSGTWNKRPISLGPVLFHISASDGIRYELLATQTFPRPLAQLRLTLPPTTCHRAARRNRVRRHRTPATPPPTRRHRRDRDLRR
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HACRQPRGLQQNDRNQRQAYDARTFGAEYQNAAPNORTHGQKPPRRHIGRKHPOPLHDGSHAARPPQNRQHRAAPDHRRAAISQTRQRNPAARPLHTAPNRPATNRRPHQRQT
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SEQ ID 7449

ATGTGCGGGGTTTCGATTCCCTTCTCCGGCACCAATACCAAGCAGACCGCTCCCTCGGGAAGGCTGTGCTTTTTCACATTTCCGCTTCAGACGGCATTCGATATGAACCTCCGCAACGCA
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AAACACGGGAACACGGC

SEQ ID 7450

MSGVRFPSPAPIPSTDPSSGLCPFTTFLQATSDMNSSQRKRLSGRWLNSYERYRHRILIAHVLRGTVLFATALRLLHLQGEWIGMTVVFVLMQLQFGAIYSKAVERMLGTVIGLGA
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BQNMVVMRQINARMVRSRSLAATSGESRISPSMMEAMQHAHRKIVNTPPELLITAAKLQSPKNGSEIRLLDRHFTLLQTLQDTAALINGRARRIRIDTAINPELEALEHLHYQWQ
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SEQ ID 7451

ATGCGCGCGGTATCGCGCGCGTGGGAATATCCGTTTGAAACGGCAACAAATGCCGTCCGAACCGCGGTTTGGCGCGCATTTGATGCGTTATCGCACCGCAATCGGGATTTCGATT
CA

SEQ ID 7452

MPARIAPGRNIRLKRQTKCRPNAGLGGILMRYRTAIGIFDS

SEQ ID 7453

CCTACCGCGCTTCAGTACGCGCTGTGCAAGAAAAACATCCCGGTAAACGAAGAACGCGCAAGCCCAACCAAGAACGCGCGCATCCAGTTTTCGAGATTCAACGCGAGCGCGCATCCGAG
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CGCGGTTTTCCGCTTCTTGCCAAATGATGTGTTTCAACACCGCGCGCAACACCGCGCTGCCAGATAGCGGCGGATTAATGCGGATACCGACCGCAAGGACGGG
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GTGATCAATGCGCGAGTATCAT

SEQ ID 7454

PTRLQYALCKEHPNEERQAQPRSGGIPVLQIQERRIRAAVGHREGNNKRHNYTNQAFDQACREKRTDVGVPQTAFVFRLLANDVQHRHQHACHDGHIDGRRQINAHTRDKQG
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DYCRSAKKRQRO*EFVGLIRQOTSGFAYQQNQ**NNDGDHDAHAGNRAGRRADQCHITAGGGDQKADDGSKRANRHOKEPRHAARNVRIADKVVKRHA*NKHHRHQHPENHGFRRQILFG
APCSGRTAARTLERHLHAFHHWLEQHQRPNRRDTYGSRTDKTHFFLPQLHRKRRHFHIGRLRN*GEIRHGNTPSNRNAQDGDAAARQSDQITRAQQGQ*KAYRQLENCRATFKPITRAI
GNHTQTSGARAHQSRQRAAGRQLFDTAAALTVIPFMTAHPQNFSSRHTFRIRQLAPHHHRVTPQRNGENHPQNPAGAT*KRRLPKRETAFAVHQBQTDDEDDG*KRTSRGLGLHVVFPQ
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SEQ ID 7455

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SEQ ID 7456

MPSEASVQTASRALPAAARNAGAYRARSEYFETANKMPSEGFGRHFDALSHNRDPRFIKQVVGRLVEQVLRQVIREKRLHCTAEYARQPAQRNQAQVVRRAHLDQLHRFEVAD
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SEQ ID 7457

ATGCCTCGAGCGCTAGTTTCGCGGTATTTTCTACCGAACCGGATAAGATTATTCATTATTTCTTCTTTCGACACAGAGCTTCACATATTTGTTGGCATCAGCGCATGATGTCAAGTTT

SEQ ID 7458

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SEQ ID 7459

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SEQ ID 7460

LGRQLYQEKQTAFLPENCCSLKLTQSLIF

SEQ ID 7461

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SEQ ID 7462

LFPGFTGQVDSHNSPCECVGQTAWVEMPSETGSEPQNGDKRRNRQGHQHAVERQPHPRVCRHAAAFERGGNAHRVRSRAERETHGRGHDDRVLQHFVTGNLSQDGTGNDGGGGNGNA
ADGAGDFDGDGVGNRFRGEREDFAFRAQPLGKHPRNARNARLKNDDGQPLVEDFTAVLVERHGKDDGGFQPKINELRGVVHRIIDTDFQVGNQHSDEYGAEDIAARAHD
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SEQ ID 7463

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CATCGAAGTAAGAAATTTGAAAGTAAAGATTCGCACTGGCGCTGAATAGCAGCCACCAAAATCAAAGCTCTCTGTTGATGACAGCATGCTTCAAAGGCTGCAAGATGCGGAAATA
TGGGAAGAGAAAGACATTATCTATAATTTGTCGCGCTCGT

SEQ ID 7464

MNIIDAIINLANNPVVGNWSHQSNNRANQAGDALEETVKDLFGSPFNLNBTQRIARHAKVFSYLGNNSPDAMLNGDAIEVKIESKDSALALNSSHPKSLSVDDSMILAKCKDAEK
WEEKDIIYNCRR

SEQ ID 7465

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SEQ ID 7466

IKQIAQLV*KRFLARRLVQARRNPLKFFQKLFITVGGIDRRFDNNMAVQIAGRAAA*RFDTLTFHAHPAGLGFPGDGLDFAVQGRH*LPQSSHGKTNRQFAMQIQTIALENLMRPN
ADGYIQVAGRAVHTRPAPTAQTDITLVIDTGNIDFHLRLIPPHATAFDARFNNMARTAGRTSLHTENRLLDVHRTTFASRAGFRGCPFRFAAAVADITFISRNIDAFLHFFC
GFFKRDPDITLHVLTLIRLGAPRTTSKHLAENIPKVTLLRTAKSAKPSAPLSAAPKREMTILVHGTFLVQGSFIRLLYFFKILLRLEFIVRIAVGMVFRQVTFVGFNLIIGSCSCT
QRRIKLITHPFI*K*NI

SEQ ID 7467

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SEQ ID 7468

MTIRKQMAQFFAVHPDNPQERLIKQAVEIINQGGVVVPTDSCYALGCKLGDKAAMERILSIRKIDLKHHLFLMCADLSELGTAKIDNVQFRQLKAATPGPYTTFILQATKDAPARALEP
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SEQ ID 7469

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SEQ ID 7470

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SEQ ID 7471

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SEQ ID 7472

LAMVYIDYCADAEYLKIKNQIKBGIGNIGGIQFAETKELGRVNRIDPLNITLYLRVGMWGIENPWFVNYIYQRNMEKSFNFMALINEDKWNFPNMTDKLLAIQOSKLAISDIKIKPN
NPARLENAKLITPYL

SEQ ID 7473

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CACGACACAAAACCTTAGATAGGTATAAAACCAACCGCAT

SEQ ID 7474

LGRKQLKTCVWVSABGRAFLQRSQATAYKLKRNFLFRYARHKNLDKRYKTRH

SEQ ID 7475

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SEQ ID 7476

MQNSSTTYNPMKIIISLFGCGGLDLGFEKAGPEI PAANEYDKTIWATFKANHPKTHLIEGDIRKIKEDFPERIDGIIIGPPCQSWSEAGALRGIDDAAGQLFDFYIRILKSKQPKFFLA
ENVSGMLANRHGAVQNLKMFDCGYDVTLTANAKDYGVQERKRVPYIFGFKDLEIKFSPFKGSTVEDKIKITLEDVITDLDQTPAVSPQNKTPDVAINNNEYPTGSPSIPMSNR
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SEQ ID 7477

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SEQ ID 7478

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NPANISGLIAAQEHFPGIPNVGVMDTSFQZTPERAYTAVPRELRKYAFRRYGHGTGMRYVAPEAARILGKPLEDIRMI LAHLNGASITAVKNGKSVDTGNGPTPIEGLVMGTROGD
TDPGVVSYPTPHAGMDVAVQVDEMLNEKSGFPGISELPNDCRTLEKLADEBREGARLAEVMTCLRAKYIASMAVACGSVDALVFTGGIGENSRNIRAKTVSYLDFGLHIDTKANMEKRYG
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SEQ ID 7479

TTCATCGATTTCATTCGCCGATATAGCGAGGCTTCTTCCAGCATTTCCTTCCAAACAAAGAACAAAAAGCGCGCGCGCAGCGATGCCCTTCTTACAGGTTCCCTTATTTT
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SEQ ID 7480

LHRFIPRYSAGLSFPAISLPNKEBQKSAGGSRCPFLYRFPYFLTAGSTGLAGPPGAGAPTEAMSFSPASTAGPMPTFLIKSSTDLNAPFCARYSAMAFAGMPGSSSSCCEAALMPTAAREK
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SEQ ID 7481

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SEQ ID 7482

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SEQ ID 7483

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SEQ ID 7484

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SEQ ID 7485

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SEQ ID 7486

FFNRQRHFGGAFWCGRADGSLVPQLRQHRRTDALHLDDQIVHRLERAVLRAVFRNGLRRAYARQLQLLLRSRIDVYRRKGEGAGBQHTQYKHPFHGSPFKGCKQQTASCDMDAD*QKPV
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SEQ ID 7487

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SEQ ID 7488

LNAEPKADMSSTQTLIEHTAI PRHIAVIMDGNRWAKRFLPRIMGHKRLDALENMVKHCALGVQYLTVFAPSTENWRRPEDEVSLMGLFLQALQKQVERLHENMRLKILGSRER
FNRQILQIGIEEAREALFANNFTGLTSLAADYGGRWDLQAANKLIAEGVSEITEDTLAKHMLGDAPEPDLFIRTGGETRISNLLMQMAYAEIYFTDILHFPDFDETALDAVASFPKRRER
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SEQ ID 7489

AAATGAATATCCAAAGTTTCAAGCGTCTCCCGCAACCCGACCGGACACCGTACAGATGCGGTCGCCCATCCCGACATTTTTCGCGGCAAGCAAAACCCCGGATATCCGGGG
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SEQ ID 7490

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SEQ ID 7491

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SEQ ID 7492

MLSALISSELSYPANQALQPVHQRVHSGPLVLGAAPVKLPPTADRDQTVSRFPKPSRTTLNGBQPYPNDRLOPQDVMSRHRGAKLRRRYELIGISLISPEYLLSVERWPFHTPEPD
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SEQ ID 7493

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SEQ ID 7494

MLKQVITAMLLPLMLGMLFYAPQMLAAFCGLIALTALWEYARMAGLCKFTNHYLAATLVFGVYVAGGWMLENLVVYVVLAFWLAVMPLMLRFLKRLNGWQVYAVGWLILMPFWFA
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VFDRTSLIAVSVYAAIESVLN

SEQ ID 7495

ATGTTCCCAACCGCAATTTGGTGCAGGAAATGATGTGCCGAATATAGGTGCTGTAAGCCACGCTCATCAACCGCGGCATTCCGACCGTTTCTGAAACGCGCGGACTTGGGCTACA
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GTACGCTGCGTGTGCGGTGCTGCCGCGAATGTCAGGACGGAATGAGACGCGCCGCAAGCGGTATGAGCGCGACGCGACGCTGATTATGGAAGTGGGTGCGCGTTCGCCGATGATTG
TTT

SEQ ID 7496

MFPTGNLVEIDVFNIGRLKATLINAGIPTVFLNAADLGYTGKELQDDINNDAALEKFFETIRAYGALKMGLISDVSEAAARARTPKPAFVAPAADYTASSGKTVNADIDLVRALSMGK
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SEQ ID 7497

TCCTGCCCACTGTGTCGGTTTGGGTACGGTTCGATTCAAACCTGAAGCTTAGTGCTTTCTCGGAAGCGTGTATCGGTGCTGCTGTCGCTAGACACTCGTCATCAC

SEQ ID 7498

SCPVSVCCTVRFKLKSFGSWKRGIGCFVSVDRH

SEQ ID 7499

ATGCTTGACATCTTCAATTAACCTTCGGCACCGGCGAGGCGTACACACCTATACCTCACTTTCGTGTGGCAGAGTCTGTGTTTTAATAACAGTCGACGCCACCTATCTCTGCG
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AGAAAACCGGATTTCGC

SEQ ID 7500

MLAHLQLTFRHAGVTPTSTFVLAECVFNKQSQPILCDPPGLTEQVLNLRHGTFSRSGINLPSFSRVLSSALEFSSCPVSVCCTVRFKLKSFGSWKRGIGCFVSVDRHFSVL
RKPFA

SEQ ID 7501

ATGCCGCTGAAAAACGCTTCAGACGGCATCCGATATAAGTTATCTCATTATGACACCAGATCTGACCATATTAGGCAGTACCGGCGAGCATAGGCGAAAGCAGCTGGAGTTGTCT
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GGCATTTATCGGCACACTGCGC

SEQ ID 7502

MPSENADGIRYKVLIMTQVLITLSTGSGIGESTLDVSRHPEKFRVVALAGHKQVEKLAACQCTFRPEYAVVADAHAARLEALLKRDGTATQVLHGAQALVDVASDEVSGVMCAIV
GAAGLPSALAAAGKGTIYLANKETLVVSGALFMETARANGAAVLVDSEHNAIFQVLPDRYTDRLNEHIDISIITASGGPFLITDLSTFDSITPEQAVKHFMNRMRKI SVDSATHANK
GLELIEAHWLFNCPDKLEVVIHPSVHSMVRYRDSVLAQLGNPDMRTPLAYCLGLPERIDSGVGLKDFGALSALTQKPDFGRFPCLKPAYETINAGGAAPCVLNAANETAVAAFLDG
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SEQ ID 7503

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SEQ ID 7504

MPQIKIPAVYYRGSTSGKIFPKRTDLPAAQEAAGGARDKILLRVLGSPDPYKQIDGLGNASSSTSKAVISDKSERADHDVDYLPQVVSIDKPFVDMGNGNHLTAAVGTFAIEQGLVDKS
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SEQ ID 7505

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TCGCACTTCTGATACCTCCAGCACATTTACAATGCCACTTCATCAGCTACAGAACGCTCCCTTACCATGCGGTAACCGGCACTCGCAGCTTCGTTATAGATTGTAGCCCGCTTACA
TCTTCCGCGCAGGACGACTCGACCATGAGCTATTACGCTTTCTT

SEQ ID 7506

LPKSSTYRLKQAIPTACQFNLLRPHIAPESSTGILTCFPSTTHPCLALGADSPYADERCVGNLGLSAGLPTFRFIATHVNIRTSSTLYNAPSSAYRTLPYHAGKPASAAVSDILSPVT
SSAQDSTSELLRFL

SEQ ID 7507

TTGCCGCTGGATTATAATTCCTCAATTTGCTAATAAACACTTGTTTGGTAAGGAATGAATTTATGCGGCTTTGAACGTGCGAGTACAGTTGGGCAACCTTAGGCACA
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CGGCACTCGGAACCAATGCGAGCTTGAAGCTTTGCTTTCCCGCAATTGGAAACCACTGTCAAGGCTGCTGTTGAAGATGAGTTGCGGAATGCAACGCTACCGGATTTTTCCTCATGATT
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TTGATGTCAATATAACAGTCAAAATTCACCTATATCGAG

SEQ ID 7508

LPLDYNSPIDFLILLINTCLVRNEFMRLNVQIRLGNLRHNYRIILKEMHGKLLAVVKADAYGHGAURCAALADLADGFAVATIDEGIRLRESGITHPIVLEGVFEASEYEAVEQYSLW
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PFGGSDRLRLKPVMLSTRIPGGERVLQPHSPIGYGATFYTSKSTRVGLIACGYADGYPRAPRSPVAVDGLTRVIGRISHDMMTELDASQOGLGHEVELWGDVTNINVTVAEAAGTIPYE
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SEQ ID 7509

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ACAA

SEQ ID 7510

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RGRVEKMAVHRVRP*QFAETPRANRHHQGTDRPDGLASAPHVVRHKHAAPRABNTLRRFRIGRHKAMVRPFGFREPTAIPRLDRICI EQGFRCFKGLAGNAKHCCFCVGQTA*DLIQ
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SEQ ID 7511

AGTAAGCAAAC TTGAAATCCCTACTTTGATAAAGCTTACTGCTTGGTTGTGCTTAATCCCGCCTTTTGTGTTTCAGGATTAAGTCGATACAA

SEQ ID 7512

SKQT*NPYFDKAYCFVVS*SCLLCFRIKSIQ

SEQ ID 7513

GTGGGCGGTTTGGGAAGCGAAACCGTGATGCTGGGACGCGCTCCATGATGCGCCTGCCGATATTGTGCGCGTGGAGCTGACGGGCAAAACGGCAGCGGGCATTACTGCCACAGACATCG
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SEQ ID 7514

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SEQ ID 7515

TTGTGTCCTTAATCCTGCCCTTTGTGTTTCAGGATTAAAGTCGATACAATCATCACCCAAATACATGTTTGTGTTTCTTTTCTCTTGCAGAAAGGTTTTATCCTTTGCAAAGAATAAAAAATC
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SEQ ID 7516

LCLNPAPFCVSGLSRYNHHPNTMFVFFSLAKGFYPLORIKNONKLIVFVC

SEQ ID 7517

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SEQ ID 7518

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SEQ ID 7519

TTGTGTTTCAGGATTAAGTCGATACAATCATACCCAAATACTATGTTTGGTTTCCTTTTCCTTGGCAAAGGTTTTATCCTTTGCCAAAGAATAAAAAATCAAAACAAACTCATTTGCTTTT
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SEQ ID 7520

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SEQ ID 7521

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SEQ ID 7522

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VTHSLAVECGGYDPAFRKNREIEDRNEDRPHFDWTKTAPENVOVIPAGNGIMHOINLEKMSPVVVKNGVAFPDTCVGTDSHTPHVDALGVISVAMAVWKRKP

SEQ ID 7523

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SEQ ID 7524

VRMRVRDAGIGESHAVFLDDGRFFQDLVDLHDAVARRNHVHFICGCGFVDEVEVTVFTSVDFDFAVFAEGIRJVTALHRQRVDDKRLRLHRIHFGRIAAFPGNRIAQACQIHORGL
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SEQ ID 7525

TTGTCCTTTGTTTGTGTGATTTCCGGCTTCCAATTGTGTTAAAGATCGATGCGTCGTTAATCTACTTCGCAAAATCAAAAATAGCTGCTAAAAACAGCAAACTTGCTTTTCATTTGTAAAGTTTTG
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SEQ ID 7526

LSLFVDFGFPIC*RSMRRYSTSQIKISC*KQQTCFHL*SFGGGKRDRTDDPLLAKQVLYQ

SEQ ID 7527

ATGAAACTGAAACAGATTGCCCTCCGACATGATGATGTGGGCATATCGCCCTTTGGCAATTTGCCGACTTCACCATCCAAGACATCCGTGTGCAAGGCTTGCAGGTTACCGAGCCGAGCACCG
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GACATCCAAACCAAGAGACAAAACCGAGGACACATCAAATCACCGTCCACGAAGCGGACGTTTCCGCTGGGCGAAAGTGTGATTTGAAGCGCAGACCAACGAAGTCCCCAAGGCCG
AACTGGA AAAATCTGCTGACCATGAAGCCCGGCAAAATGGTAGAACGCCAGCAGATGACCGCCGTTTGGGTGAGATTTCAGAACCGCATGGGCTCGGCAGGCTACGCATATCAGCGAAATCAG
CGTACAGCCGCTGCCGAACCGCGGAACCAAACCCGTGATTTGTCCTGACATTCGAACCCGGGCGCGAAAATCTTACGTCAACGAAATCCACATCACCGGCCAACCAAAAACCCGCGACGAA
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SEQ ID 7528

MEKIQIASALNMLGISPLAFADFTIQDIRVEGLQRTPESTVFNLYPVKVGDTYNDTHGSAIKSLYATGFFDDVRVETADGQLLTVIERPTTIGSLNTGAKMLQDAIKKNLESFGLAQS
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 DIQTNEKTRQTIKITVHEGGRFRWGWKVSIEBGTNEVPKABLEKLLTMKPKWYERQMTAVLGEIQNRMSGAGYAYSEISVQPLPNAGTKTYDVFVLIIEPGEKTYVNEIHTIGNNKTRDE
 VVRRLRQMSAPYDTSKLQRSKERVELLGYFDNVQFDAVPLAGTPDKVDLNMSLPERSTGSLDLSAGNVQDTGLVMSAGVSQDNLPGTGKSAALRASRKTTLNGSLSFPTDYPYFADGVS
 LGYDIYKAFDPRKASTSVQYKQYTTAGGVRMGIPTVEYDRVNFGLAAEHLTVYNTYNAKPKRYADFIRKYGKTGDAGDSFGKGLLYKQTVGWRGNKTDASWMPFGYLTGVNAEIALPGSK
 LQYYSATHNQYFWFPLSKTPTMLLGEVGIAGGYBTRKEIPFENYFGGGLGSVRYGESGLTVGPKDYBDEYGEKISYGGNKKANVAYSAELLFMPGAKDARTVRLSLFDADGSLVGDGRYVTAA
 ENGNKLSYVSEAHKSTPTNELRYSAGGAVTWLSPGLGMPKFSYAPLKKKPEDEIRQFQFOLGTTF

SEQ ID 7530

SEQ ID 7531

SEQ ID 7532

SEQ ID 7533

SEQ ID 7534

SEQ ID 7535

SEQ ID 7536

SEQ ID 7537

SEQ ID 7538

SEQ ID 7539

SEQ ID 7540

SEQ ID 7541

SEQ ID 7542

SEQ ID 7543

SEQ ID 7544

SEQ ID 7545

SEQ ID 7546

LFCOLYHNVCP LGSPOKKNKALQSGFIPLIFIRLIA

SEQ ID 7547

ATGATTCCGGCCACCTGCACCTGTGCCAAATCACCGCGGGCTCGCGGGGGAATGGCGGGCGAGGACATTTCCGTTACCGCGGTGCGCCCGCTCGCAGACCGCGCAGGCGGAACACATCA
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SEQ ID 7548

MIPATCTLSQITARLGGEWRGDISVTAVRPLADAQAEHISFLANPKYAEVHDSSAGAIIVSAAADGFEGRNLIVADDPYLYPAKVARLPSFVVKARGGIHPTAVVEPGATVPASCEIG
ANAYIGANTVILGEGCRILANAVVQHDCKLGDEVVLPNAVYYGCTLGRHVEIHSAGVIGADGFLAFAGDSWFKIPQTAGVTLGDDVEIGSNTNIDRGMSDITVGNKTIDNQVQIGHN
CKIGSHFVIAARTIGSSVTIGSYCIIGGVGTGHIETADKTTIGGTSVTHSTIESGKHLAGIFPMSEHKEMARNNAVYTHRLSEMNRKLTLEQQLSDSKDTQ

SEQ ID 7549

ATGACGCTACAACTCCCATCGAAGCCAAAGACATCCAAAACATCATCCCCACCGCTACCCGTTTCTCCAGCTCGACCGCATTAACCGCTTCGAGCGGATGAAAACCCCTGACCGCATCA
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AGCGCGCGCAAGGAAACGAATTTTCTTCTTCCCGCATAGACGAGCCGCTTCAAACGCAAGTCATCCCGCGCAACACTCGTCTTTGAAGTCGAATCCTGACAGCGCGCGC
GGCATCGGCAAAATCAACGCGCTTGCCAAAGTGACGACAGTCCCGCTCGAAGCGGTGATTATGTGCGCAAAACCGGTGGTT

SEQ ID 7550

MDVQLPIEAKDIQKLIPHRYPFLQLDRIAFEPMKTLTAIKNVTINEPQFGHFPDLVPMFVGLIIEAQAQCTLAILEGGKRENEFFPAGIDEARFKRQVPIPGDQLVFEVLLTSRR
GIGKFNAAVKVDGQVAVEVIMCAKRVV

SEQ ID 7551

ATGATGAGTCAACACTCTGCGCGGACGACGTTCCGCCAAGCTGTGAAGAATCGAATCGCTTGGCGTGGCGGTTGCGTCAATGCTTATTTTGCACAGATTGGCCACCCAAACGGGTTTCA
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ATCAAAACTGGATAAATGTTTCAAAA

SEQ ID 7552

MMQHSAGARFQAVKESNPLAVAGCVNAYFARLATQSGFKATYLSGGVAAACSCGIPDLGTTMEDVLIDARRITDNVDTPLLVDIDVWGGAFFNIARTIRNFERAGVAAVHIEDQVAQK
RCGHRNRKAIYSKDEMDVRIKAAVDARVDENFVIMARTDALAVEGLDAATERAQCEAGADMIPFAMTDLKMYRQFADAVKVPVLANTIFEGATPLTYQSELAENGVSLLVPLSSFRA
ASKAALNVYEAIMRDGTQAAVVDMSQTRAELEYHLNYHAFDQKLDKLFQK

SEQ ID 7553

GGGAATCGTCTCTTTGAGCGGGGCGGGGCAACGCGTACCGGTTTTTGTTAATCACTATACCTCCGCGCGGCAATTTGACCGCAACAAATATCTCGAA

SEQ ID 7554

GNRSL*AGAGQRRTGFC*PTIPSGRHLTRNNILQ

SEQ ID 7555

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SEQ ID 7556

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SEQ ID 7557

TTGATATTGCGCTTCCATTTCTGCGAACCGGCACACAGGCACAAACGCCCTCACTTATGGCTTCGGGACACAGATCCGCTGTAAGGCTTCCACGGCTTCGTGGGTTGTCCCGCTTTT
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SEQ ID 7558

LILPPLRLTAHTGTNALTGYFGDTMPSEGPHGFVGCAPAF*RYIFLKLLEIFTRLLKGNRSFKRCQTERACFCHIKPLSDGGILQCVOQIKHISRPAADAGNAVHLRFIFQPNQTD*F
HDSIGNPAVCFRYFRFGIHTGYAQPDFSGCIRHNPDNAASPEVTAERTDRQSGCDKHKQCAVGADIFARGFHILRFDGKD*NIVGKLRQGCRSFDPQLFSQTFALFRITTVGYMDAVSPL
FDQSARNGSRHISAEEKINIHYPPIQ

SEQ ID 7559

GTGTCCCTGGGTTGAATAAAACCTAAACCGTGGGTTTCTTTTATTAGTCTGCTGAAACTTTCAGACGACCTTTTCCGAACGCTCAAACCAACCGGTTTGGCGCACATAATCACCGCT
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TGGGGATGAGTTTGGATGCTTTTGGCTTCGATGGGAGTTGTACGCTCATGCTGTCTGATTCCT

SEQ ID 7560

VSLGLNPKFVGLFIRSETFRFPFSERSNHAFAHNHFGDGLSVHFGNGVEFADAAPAGQEFDFKDELVAIGDILAFETGVYAGEEEKFVFLAPAFQNRQRAARLRHFRDDEYAGHN
GQVGEALIELGFVYGVDFDGGQGFHRLBGGNAVELEKRVAVGDEFLDVGFGDELIVHVCRIIP

SEQ ID 7561

TTGAACGCTCAATTTAAAAATAAAGATCAAGGGTTAGCGTGAATATAAGGAATCTGTAGTATTTTCTGATTTTCAAGATGGAACCGGTATAAAATGCCCTTAGGAAAGACAAAGCAG
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LKRPFNKKEBSRVSNYKCECISPDFRMEKYKNVRKDKAAELYLNLSLSRFLPHVVSIPETVLNKKIDICPRQEFKDRNRLYDSIQPQTNPAKYQGCFLNNGTKESAELIKVLSKIQ
 NNSGGKFDHNQLVAGLGFGFWRYLFAGGKDAQDAAKGVLKVFPPKKPKSTPSVQYNQKWLPRELSNINNFRNRLAHEPICPSFKGAIKDTGYARNHQSIPELLNMDVDVTASVFSFS
 DQVIAVCEIDKL

SEQ ID 7563
ATGATTGGGATGCCCCACGCGTCGGATGGCTGTGTTTTGCCGTCCGAATGTGATGGAAGCCTGTCCATACTGAAAAAAGTCTATAAAGGAGAAATA

HIGMPDASDGCVLPSECDGSL SILKKVYKGEI

SEQ ID 7565
ATGGACAGGCTTCCATCACAATTCGGACGGCAAAACACAGCCATCCGACGCGTCGGGCATCCCAATCATTAAAAATATATGGGAAAAATTATCTTAT

MDRLPSHSDGKTQPSDASGPIIKNIWEKLSY

SEQ ID 7567

CCATCGGACGCGCTCGGACAGGCCGCTGCGCCGCGCAACCCCTGCTTTTCCAAACAGTCGAAACCTTCTGTGTTGAACTCTCAACCAAGGTTTGCCGTCACGCGTAGCCCAATCCAACCG
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GACTCTCGCCGCGCAATATCCCAAAAATCGATGGCGGCAGGTTTCTCGGCTTACACAGCGCGGACAAGACGAACACTCATACCAACCCCGCCAGCGCGCAGCTGCAACCGTAAATGCAAA
CAACGACGCGCTTGCCGTAATTTTATACCGGAATTTCCAT

SEQ ID 7588
PSDALGQAVAPQFLFQTVEYFLPEPLNQRFVAVTRTPIQPAGFKLEYFPKIKVRFLRGFIVCPDGTIAV* KRYLVVL* RQRTLAANIPKIDGGRFSRLTPAGQGTLLIPRQPACNRKCK
QRSCRIFYYPNPFH

SEQ ID 7569
ATGGGAAAAATATCTTATTGATATTTAAACCAATCAAAGAAAAACAGCAGACCGTTCGGAATTATTGCGGCAAAACCCGAGACAAGAAGAAAAACAGGGGATTATTTCAGAAAAGGGAAAA
ACATC

MGKIILLIFKTNQRTADRSELGKTADKKKTRGLFRKGKNI

SEQ ID 7571

ATGACCCCTCATCCACCGGACCGCGCTCATCGACCCCAAGCGGAAGCTCGACTCCGCGCTCAAAGTCGGCGCGGTACACCGCTCATCGGCCCCAACGTCGGAATCGGTGCGGAANTACAGAAATCG
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TATCGGCAACGGCAACACCATTCCGCGAATTCCACCCTTTAATTAGGCACGGTAACCGGGCATCGGCGAAACCGGTATCGGCGACGACAACTGGATTATGGGTCTACTGCCACCTTCGCGCAC
GACTCGGTGTGTGCGCAACCCACACCATTTTTCGCCAACACACGCTTCGCTTCGCGGACACGTTACCGTTCGGCGACTACGTCGTTTTGGCGGGCTACCGCGCTGGTCTCTCAATTCTGCCCGATCG
GCGACTACGCCATGACCGCCTTCGCGCGAGGCGGTACACAAAGACGTGCGCGCCTACTTTTATGGCATCGGGCTACCGCGCGAACCGTCCGCGACGAGGATATGCGCGCAACCG
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SEQ ID 7572

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DCVVGNTTIPANNASLAGHVTVGEDYVVLGGTTLVPQFCRIGDYAMTAFAGVHKDVPPYFMASGYRAEPAGLNSEGMRNGPTAEQISAVKDVYKTLYHRGIPFEEAKADILARAETQAEI
AVPQDFFAQSTRGIIR

GTGGGCATTGAAATTCCTGGTATTTGGGCTGATTGATTCGATATTAAAAATGCCGCTCTGAAAGGTTTTTCAGACGGCATTTTGTTTGCCAGATATATTT

VGIEILVFGLIDSILKMPSERFSDGILFARYI

SEQ ID 17575
GCCCTTTTCCGCAAAATCGCGCTGCCGATACCGGACGTGTGTCGACCGCACTCAATGGCGGCAAGGCATATCGTTCGACATCCCCATAGACAGCAGCTCGCGCTTAAAGCGCAGCGCATTTGAGCTCGGACAGCAGCTTTTGCATGCTGTGAAACTGAGTTTCAACTCCGTTTTCATCTGCTGTGTCCTTTGGCAACGCACATCAGTCCGCGCAGCAGCAAGGTTGGGCAGCTTTCGCCACTTCCACGGCAAGCGCAGACCGCTTCTTCGGGGGGGACACCGGTGTTTGGCGCGCTGCGCCGCAATGTTCACTCTGCACACACACCTCTGAAGGGCGGCATTAAGGAAGCGCGCTGCTGCTCAGCCGGACGGCGGTCTTCAGACGGCATACGGTATGCAACCCAAATGCGCGCGTTGCGGCACAAATTTGGTTTGTGGACTGCACATCGCCGATGACGTGCGCACAGTGTGGCTCAAACTGCGGCAATTCCTCCGTTTTCGCGGTACCACTCTCTGAATATAGTTTCTGCCGCGAAATCAGCTGTCCGCGCAAGCTTAACTCTCGCGGATGCGCTCTTGAAGGGAGCGCTCTTGTGACGGCAATCAGGCTGACGGGAATCGGGCTCCCTGCGCGCTGCGAGAAACCAATTTTCGGGATACCGTTCGGACACCTCAGCATAACGTTCTTGCAACACCGTCAAT

SEQ ID 1576

APFFPMRAADTIVCRTALNGGRHIVRHPHQHVLNASNRIEVGKQLLHGLKLSFQLRFTAVGFGNAHQSAHDKVGQLRHFHGHKDRDFFGRDVTFCRLARNVHLDTHLQGRH*GATLPAQPD
GGLOPAYGMHPMPRAFGDKFGFVGLHIADVDVPHDVGQIRFLRPAVPLNLTVLARIITLSGSVNFADAV*REGLADGNQADGHRLPARLQNFSDTVGHILTTFVLQHRH

SEQ ID 1577

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SEQ ID 7578

SEQ ID 7578
MDISKQTLDDRVLNKANGTTVRTELMAGLTTPLTMCYIVINWPLILGETGMDNGAVFVAPCIASAGCFVMGFIGNYPIALAPGMLNAYFTTFAVVKMGMPVQVQALGAVFISGLIFILF
SFFKVRREMLVNALPMGLKMSIAAGICLPLALISLKAGAGIVANPAFLVGLGDIHQPSALLALFGFVMMVVVLGYFRVQGAIIITITITIVIASLMLNEFHGVGVGEVPGIAPTFMOMDPKGL
FTSMVSVIPLVFFVLVDLFDSTGTLVGVSRERAGLLVDGKPLRLKRALLDASTAIVAGAALGTSSTTPTVESAAAGVSAGGRGTGTAIVTVGVVLMALACLIMFSLAKSVPPFATAPALLYVGTQML
RSARDIIDDDMTTEAPAFLTIVFMPTTYSIADGIAFGFISTAVVKLCRRGTGDPVPMVWVVAVLNALKFWYLG

SEQ ID 7579

SEQ ID 7579
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SEQ ID 7580

SEQ ID 7580

MQITDLLAFGAKNKASDILHLSSGSPMIRVHGMRRINLPMSAEVEGVNMTVSVMNDHQRKITYQNLEVDVFSFELPNVARFRVNAFTNTRGPPAAVFRITPSTVLSLEELKAPSTFOKIAES
PRGMVLVTGPTSGSKSTTLAAMINYINETQPAHILITIEDPIEFVHQSKKSLINQRELHQHTLSFANALSSALREDPDVILVGENRDPETIGLALTAETGHLVFGTLHTTGAAKTVDRIVD
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SEQ ID 7581

SEQ ID 7581
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SEQ ID 7582

MPSETPKAFOTASVFFKAVCCLIDASFCIVV

SEQ ID 7583

SEQ ID 7583

TTGCTATAGTGGGTTTAAATTTAAATCAGGACAGGCCGACGAAGCCGCAGACAGTACAAGAAGTACGGCAGGCGAGGCAACCGCTGTACCGGTTTAAATTTAAACCACTA

SEQ ID 7584

LYSGLNLNODKATKPOTVQEVROGEATLYRKF~~FKPL~~

SEQ ID 7585

SEQ ID 7585

ATGGAATTGTTTACGACGTGGCGAGAAATCGGCAGTCAAGCCCTGCGGTAAATTAAGTAATCGCGCTTGGCGGGCGGGGTTGCAATGCAATCAATAACATGGTTGCCAACTGTGCGCAGTG
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CCGTTGGCGCAGCAGGAGAATCGGGAGGCCATTGAAGAAGCCATTGCGCGTGCCAATATGCTGTTTATCAGCACCGGTATGGCGCGCGGTACCGGTACCGGTTCGCGCGCGGTGTGTGCT
GAGATTGCCAAGTCTTTGGGCATTCTGACCGTTGCGGTAGTTACCCGTCCGTTTTCCTATGAAGGCAAAACGCGTCCATGTGGCACAGCCAGGGTTGGAAACAGTTGAAGAATAAGTCGAT
CGCTGATTATCATCCCGAACGACAAACTGATGACCGCATTTGGGTGAAGACGTAACATATGCGCGAAGCCTCCCGCGCGCGGCAATGTATGCGCGATGCGGTGCGAGGCATTTCCGAAGT
GGTAACCTGCGCGAGCGAAATCATCAACCTTCGCACTTTGCCGACGTGAAAAACCGTGATGAGCAACCGCGGTATCGCTATGATGAGCTTCGGGTTATGCCAAGTTGCGACCTGCGCGGTATG
GCGACCGACCGAGGCCATTTCAGTCGCGTGGACGATGTAATTTGGATGGTGCACCGCGGTGTGCTGCTCAATATTACAGCTGCTCCGGGTTGCGTCAAGAAATGTCGAGTTGTCTGAAG
TCATGAAAATCGTCAACCAACGCGGATCCCGATTTGGAAATGCAAAATCGGTGCGCGTCAAGACGAGACCATGAGCGCAAGATGCCATCCGGATTACCAATTATCGCTACCGTCTGAAAGA
AAAAGGAGCGGTGCGATCTTCACTGCGGCAAGGAAAGTAGAAGCGGTTGCCCGCTCCAAACAGGAGCAAGGCCAATGTGCAAGGTATGATCCGCAACCATCGCGGTATCCGCACCATGAAT
CTGACGACAGCGGATTTGCGATAAACAGTCTGTCCTTGACAGATTTTGAATTTCTGCAATTTTGGCTGCTCAACACAATTCAGACAA

SEQ ID 7586

SEQ ID 7586
MEFVYDVAESA VSPAVIKVIGLGGGGCNAINNHWANNVRSEVFISANTDAQSLAKNHAAKRQLQGLNLTRGLGAGANFDIGRAAAQEDREAIKEAIRGANMLFITTCMGGGTGTSAPVVA
EIAKSLIGLITVAVVTRFPFSYEGKRVHVAQGLEQLKSYVDSLIIIPNDKLMTALGEVDVTRERAFRAADNVLRDAVAGISEVVTCPSEIINLDFADVKTVMNRGIAMMGSGYAAQGDIDRAM
ATDQAISSPLDDVTLGDARGVLVNIITAPGCLKMSELSEVMKIVNQSAHPDLECKFGAAEDFTMSBDARITITLATGLKEKGAVDPTPARSEVAVAPSKQEQSHNVEGMIRNTRGIRTMN
ITAADFDNOSVLDLDFEIPAILLRQENSER

SEQ ID 7587

SEQ ID 7587

GTGTTGACGACGCAAAATTGCAGGAATTTCAAATTCGTCGAAGCAGACTGGTTATCGAAATCCGCTGCTGTGCAGATTTCATGTTGCGGATACCGCGATTGGTGCGGATCATACCTTTGACA
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TCATGGTCTCTGCTCTTTCAGCGGCACCGAATTTGCATTCCAAATCGGGATGCGCGCTTTGGTTGACGATTTTCATGACTTCAGACAACCGGACATTTTCAGGCAACCCGAGCAGTCGTAAAT
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CGCATACCCGGTGTGCTCATCAGGTTTTCACGTCCGCAAAAGTCGAGGTGTGATGATTTTCGCTCGGGCAAGTTACCACCTTCGGAATGCTCGGACCGCATCGCGCAATCATTTGTCGCG
CGCGGAAGGCTTCGCGCATAGTTACGCTCTCACCCAATGCGGTCATCAGTTTGTGCTTCGGGATGATAATCAGCGAATCAGCATTTCTTTCACTGTGTCACCTTCAGCTTCGCAACG
GACCGCTTTGCGCTTCATAAGAAAACGAGCGGGTAACTACGGCAACGGTCAGAAATGCCAAAGACTTGGCAATCTCAGCAACCAACCGGCGGGAAACGGTACCGGTACCGCGCCCATACCG
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TACCCACATCTGAGATCTCTTCGCGCAATGGTTTTTTGGCAAGACTGCGCATCTGTATTGGCACTGATAAACTCCACACTCGGCACATTTGTTGGCAACCATGTTATTGATTGCAATTGCAACC
CGCGCGCCCAAGCGGATTACTTTAAATTACCGCAGGGCTGACTGCCGATTTCTGCCAGTCTGTAACAAATTCATTCAAAACACTCTGATCGCCCGGTTCAGAGGACGGTT

SEQ ID 7588

SEQ ID 7588
VLITQNCNRFKIVKDLRVLETGCCQIHGADTAIGADHTFDIVALLLFGRCNRFYFPCRSRIDRSFFPQTGSDNGNPDGFIAGHLVFSGTPEFAQIGMALVDDFDFRQLGHPQATRSSRN
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DAFAFIKRTKGNYGNGQNAQRLGNLSNRRGTGTAAHTGRDKQHIGTANGFNGLEIFLCRCRTADIGIRTRAQTACQIRTLQDLSLRNWFQRLRICIGTKLHTAHIVGNEHVIDCTAT
AAAGADYFNRYRADCRFCVNVNKFHSTKTPDRPVORTV

SEQ ID 7589

SEQ ID 7589
ATGGGGATGTGGCGGGCGGAGAAATCATCAATGCTGCCGACTGCCATACTTCTGAAATCTATAGTGGTTTAAATTAAACCGGTACAGCGTTGCCCTCGCCTTCCCGTACTTCTTGACTG
TCTGCGGCTTCGTGCGCTTGTCC

SEQ ID 7590

MMWRRAAEIINAADCHTSETYSGLNLNRYSVASPCRTSCTVCGFVALS

SEQ ID 7591

SEQ ID 7591
ATGAATACCGATAACCTGCACGACATCTTGACGAAACGGTTCAAGTGATTTCTCAAAAAAACAAGCCGATCCGAAACCCCGCGAAATCGGCACACACTTCCACCGCTGCTCGACT
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CAACCGCGCGGCTGCATCTTTACCGAGCGGAAATCGCGCTGACACCATAACTGGCAGACGGCGGTACAAAACGCTATGCGCAATCCCCAGACGTTGGTCTGTATCGGCGAAGTCCCG
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GCCCGCCATCCAGGACTTCTCCTGTAAGGGCGACCTGATGAACATCAGTAAATCATGAAACCGCCAAAACCGGAGATGACAGCATGACCAAAACCTTTTGAAGCTGTACCGTCAC
GGCATCATGATTACGAAGAAGCCCTGCGCCAGTCCGTTTCGCGCAACACCTGCGATTGACATCAACTGCAACAAAGAGGCAACCGCCGAACTCTTTACGACAGGGTCAACGGT
TCAACCTCATTTCC

SEQ ID 7592

MFTDNLHDIIDETVQVYSQKQSRSETPAEIGTHFHPILLRLICETAEAQNASDILISKFPFSLKINSALTPOPKALIGEETAATAASTMNAEQSEIFRRDGEINYSVQSRSGTRYRANA
YYSQGSAGLVLRINHVIPQMRGLPEKLKDLAVAPRGLLIIVGPTGSGKSTMTMLHNRKNTLPGHVITIEDPIEFYKPRRCIFTQREIGVDTINWQTAVQNAMRQSPDVVICGEVR
SRSEMEYAMQLAQTGHLCTFTLHANTAPQSLERILNFPYKEQHNQILIDIALNLGIIQRALALKKDKTGTAVVDLLINTPAIQDFILKGDLMNISKIMETAKTDGMDQNDQLFELTRH
GILSYEBALRQSVSANNLRLHQLHKEGKTPPELLYDRVNLNLIS

SEQ ID 7593

ATGGAACAGCAGAAAAGATACATCAGCGTACTGGATATCGGTACGCTAAAGTCCCTCGCACTGATCGGGAAGTTCAAGATGACGACAAAATCAACATCATCGGTTTGGGCGAGGCTCCTT
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CGCAGGCAACCATCCGACGCTTAATTCGCAAGGTGTGTTAAATCAAGACGGAAGTAAACACAGGCAGACATCGACCGCGCATTTGAAACGGCAAGGCAATCAATATCCCGCCC
GATCAAAAATTCCTGATGCCGTGGTTCAGACTACATTTATCGACACCCAACTTGTGTGAAGGAGCCCATCGGTATGAGCGGTGTGCGTCTGGATACGCGGGTGACATCATTAACGGTG
CAAGTACGGCAGTGCAGAAATGTCCAAAATGTATCGAGCTGTGCGGCTTGAAGGCGATCAGATCATGCTTCAACCGTTGGCAAGCGCGGCGGCTGCTGACTGAAGATGAAAAGACCT
CGCGTATGCGTCATCGACATTTGGTGGCGAAGCAGGATATGCGGTTTATGTAACGGCGCCATCCGCCATACGTCCTCATTCGCGCGGCTGTTAATCTGATTACCAAGATTTGTCC
AAATCGTTGAGAACACCTCTCGATGCCCGGAGTACATTAATCCATTTATGCGCTGGCATCATGCGATACGGAAGGCTTGGGCGAGATGATGAAGTTCGCGCGGTGGGTGACCGGACAT
CGCTCAGGTTTCCAGTAAGTTTGGCAGCAATCATCAGCGCAGTATTTCAGGAGATTTTGGCGTAGTCTGGGCGAAGTGCAAAATTCGGGTTTCCCAAGAGTGTGTAATGCGGG
TATCGTTTCGACCGCGGTGTGTCATGATGACCGGATTTGGAATTTGCCGAAAATCTTCGATTGCGCTGTACGACCGGTGCGCCCAAGAAATGGGCGGTTTGTCCGACCGGTG
CGCACACCGGCTTTCTACCGCTATCGGCTGCTTCATGCGATGCAAGCTGGAAGGAACTTCCCGCAACCGGAAACGGTACAGTGAAGAGAGAGAAGGGGCGGCGGTTTGTGTG
CAAGATTGAAGCGGTGGATTGAAAACACCTC

SEQ ID 7594

MEQKRYISVLIDIGTSKVLALIGEVDKDKINIIGLQAPSRGLRAGMVTNIDATVQAIRQAVNDAELMADTKITHVTGTAGNHIRSLNSQGVVKKIDGEVTDADIDRAJETAKINIPP
DQKILDAVVDYIDITQGVREPIGMSGVRLDTRVHIITGASTAVQNVQKIELCLGSDQIMLQPLASQAVLFEDEKDLGVCLVIDIGGTTDLAVYMNGAIRHTSVIPAGGNLITRDLIS
KSLRTPLDAEYIKIHYGVASCTDEGLGEMIEVPGVDRTSRQVSSKVLAAIISARIQIFGVVLGELQKSGFPKEVLNAGIVLTGGVSMGTGIVEFAEKIFDLFVPTGAPOEMGGLSRV
RTPRFSTAIGLLHAACKLBGNLPQENGTVQEREGGGLLARLKRWIENNL

SEQ ID 7595

GTGTCGGTAATTTTCAGCACAGAATATCAATAAGACAATATGTTCTTTTGAATAATCTTTTGGTTTTTTCACCGAAGACAGGCGGTTCAAGCTGCGGAAATGTTTGAATTTATTAA
AAGCAGAGGCGGAGTCACAATGAAATGTCCGAATGGGATGTGGCGGGCGCAGAAATCATCAATGCTGCCGACTGCCATATTC

SEQ ID 7596

VSGNFSTEYSIRQVYLLKNTFGFTEDRFVQAAEIVCNYLKABAEVMTKCPNGDVAGGRNHQCCRLPFP

SEQ ID 7597

TTGGGTATGCTGTTTCGGCGGCTCCATCGGACGCGAAGGCCCGTCCGTGCAAGTTCGGCGCGGCAATGCGGCGGCTGGGGCGGCTGGTGCAAAAAACACGTTTGGCGTTTAAAGGTATGC
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CGCGCAGATTCTGCTCGCGCTACTCGCGCGGTTTCATACAGGTGCGCATTCAGGCAACAAACCGTATTTTTCGGGTTTCAACGCGCGGCTTTGGAAAATATTTGATGTGGATCGTG
CGCGCGGCGCTGTTTTCGGCGCGGCTGGCGGCATTTTGCCTGATGCTCTATGCGGTGCGCGCGGCTTGCACCGCGCAAGATACGCGCTTCATCGCAACCGTCCGCTGCTGCTGG
CGCACTGATGGGCGTGTCTGCTCGCCCTGCTCGGCAGCTTCTACCAAGGCAAAACCTACGGCACCGGCTACCGAAGCGCGCAAGCGCTGCACGCGCATCAGAACCGCGCTCGGACT
CGCGCGCCCAATGGCTCGCCACCGTATTCAGCTATTGGGCGGCAATTCGGGCGGCAATTTTCACTCCCTGCTGACCATAGGTGCGGTTTGGGCGAGCATATCGCGCCATTCGCGGAC
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TGTTTTGGATGCTGATTGCTGTCATTTTCGCTCGCAGGTTTCGCGCGGCTTTTCGCGCGGCTCCGTTTACACGCGATCGGGAATGCGCTTCCGCGCGCGGCTTCAGGAACCGCGCG
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SEQ ID 7598

LGMFLGASIGREPSVQVGAAMGAWCKKHGLAFKGMQENDLMAAGAAGGLAAAFNAPLAGVIFATELGRGIMLRWERQILLGLVLAAGFIQVAIQNNPYPYSGFNGGVLENILMWIV
AAGLVCAAGGIFARMLYGAFAAPRKIRGFIIRNPLLLAALMGLLALLGTFYQGTGTGTGHEAQAHLHGIYEAAPVGLAAAKWLATVSYWAGIPGIFPPLTIGAVLGEHIAAIAAD
ISQGANIIVLICMAAPLAGATQSPITSAVVVMEMTGGQSLFWMILIACIPASQVSQPSRPPYHAGSMRFRFRVLQETAATGNAPARQAANSKTMPSEN

SEQ ID 7599

TACCTTCCGCGCGGCTTTGACCGCAACAAATATCTGCAAGATTTATTGTGTGCGCATAAATCCCGGACAGCGCCTAAATAAGGTATAATCGCATCCGATTCTGTCGCGGTTTTCGCGGCT
GCAGCGGGATGTCGCGGTTTTCAT

SEQ ID 7600

YPPAGI*PATISCKIYCVIRINAGQPPK*GIIASDSVPPAARRRDVGGFH

SEQ ID 7601

ATGGGGTTTCAGATTGTGGGCTATCATGATTTTCTATTGGAATGTCTTTTACTGATTTTGTCAAAACGCATTTATGCCGCTGAAAAGCTTCAGACGGGATTTCTGTTTGGACTCGA
TTACTCGATATAAG

SEQ ID 7602

MGFQIVGIIISIFVLANSFTDFVKTHLCRLKSRFRDRLDSTITRYK

SEQ ID 7603

ATGCAAGTATTTTACACAATCTCAAAGCCTTTTTCGAAACCGTCAGCAGCTGGGTTTGGGATCTGTTATGTTGATGCTGCTGGTCCGCAACCGGCTATGCTGACCGTTATGCTGAAAG
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GTCCGCGCACATCGGTACGGGTAACATCGCGCGGCTGGCGACTGCAAGTGTAAACCGCGCGCGCGCGCGGCTATTTTGGATGTGGATGACCGCTATTTTCGCGCATGGCCACCAATACGGC
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GATGCACTGATGCTGCGCTCAAGCTGATTTTTCGATGCGTTACGCGCGAGCGGCTAGCAGCGCGGCTATCGGTACGGTCACTCCGCTACGGCGTGGCGCGCGGCGGTGCTTCCAATG
AGGCGGGTATGGGTTCTGCGCTATTGCGCGCGAGCGCGGAAACCGGACACCGCGTTCGTCAGGCTTTGGTTTCCATGACCGGCTATTTTGGACACCAATGTTGCTGCTCGATTAC

CGGTATCTGTTGGTCATGGGCTCTGCTCGCGCGCAGGCGGGCAGTTTTGTGAAACCTGAATTGAGCGCGCGCGCTGACAAACGTCATTTTCAAAAAATGCTGCCCGGCATCGCGGGCTGG
ATTGTGACCATCGCGCTGATTTTCTTTGGCTACTCAACCATTTCTCGGCTGGTGTATTACGGCGAGAAATGCGCGGTTTACGCTCTCGCGGAGAAGTTTGCBCCTTTGTACCGCGCTCGGTT
ATGTTTCTTCCGTCATGCCGGGTACCGTGTGAGCCTTGATTTGGTATGGCTGGCTTCGGATACATTCAACGGCTTGATGGCATTGCCAACCTGACTGCGCTTTTGTGTGATGGCGAAAGT
CATCGTCAATGAAACACCGGACTTCAAAACAAAAATCAACAAACGGCGAATTGCCGCAT

SEQ ID 7604

MQVFLDNLKAPFFETVSSVWVGVSVMLLLVGTGIVLTVMLKGLQFTMLGYALKQAFVPSKKYEGGAGHEGDISHPAALMTALSATIGTGNLAGVATAVVTGGGAPVFMWMTAIPGMATTKYG
EGVLAVKYRVNNSKGEMSGGPHYYIEKGLKNWKMVAVALFGTFASFGIGSSVSQNSVAQAVQTSFGIEPATYTGITLTVLTAVVVLGGIKGLAKAASIVPAMAVFYVLGGLSLIVINS
DALMPAVKLIPSDAFSAQAVAGGAICTVIRYGVARGVPSNEAGMSGAPIAAAAKTDPVROALVMSHTGFLDTTVVCSITGTVLWGLLGAGGEFVKPELSGAALTVTVTQKMLPGIGGW
TVTIGLIFPAYSTILGWCCYGEKCAVYVFGKFAALYRVUGYVSSVMPGTVLSLDLWLASDTFNGMLALPHLITALLMAKIVINETRDFKQKITNGELPH

SEQ ID 7605

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CCGGTATCCGTCGATTCGCTCGGTATCGGTATCGGTGCGCCCGCGTTTCCCGATACCGTTGAGTGGCTGCGTCCGACGAGCGCAAGCCGGTTGACGTTGGGGCGACCATGCTCTGGTGGACGGCGAA
GGCAATGTTTTCGAAGCCCGCTTGGACAGACCCCGAATGCCGTTATTCAGAGGCGCGGAAGGACGTCATCCGCGAATGCTCCGCGGTTATGACGAATTTTTCGACTGTTTGGCAAAACAGG
GTTTGGGCATCAAGAGGATGACCTATACCGGCATCTTCCGGCTGGAATGCTGTTGGACACCGCATATCCGTCAGGCTCGGACGGGAAGAACAGGATGGAAGACGCTTCCGCGCTTATACCGA
AGCGTGGCAGCATCTGTTGCGTAAAGATAAAAAATCGGTTATCTCTATGTTGGATATGAGGTATTAAGGACCGAATTTTCAGTCCGCGCATGCTCCGACGCTTTACCGCGAAAAAGAAATCCGGAAGAA

SEQ ID 7606

MWDNAEAMERLRITRWLLVMMAMILLASGLVWFVNSNHLFVKQVSLKGNLVYSDKKALGSLAKEYTHGNLLRTDINGAQEAYRRYPWIASVMVRRRRFPDTVEVVLTERKPFVARWGDHALVDGE
GNVFEARLDPRGMPVFRGAEGTSAEMLRRYDEFSTVLAKQGLGIKEMTYTARSAMNVVLNNGITVRLGREWEMKRLRLPTEAWOHLRLKKNRNLVSYVDMRYKDGFSVRHAPDGLPEKESER

SEQ ID 7607

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SEQ ID 7608

MLPRFGKKPEAFHLVFPSEPDGDAVVQNDIPRTRCRIGHLFDAQTFLFQNSRKFVITAEHFGRRSFRASEYRHSGSVQAGFKNIAFAVHGQMVAPTGNRIALGQDDLNRIGKTAAHHDREN
PRIPAVGFLCAIDVRPONTIPMDVFFRQTAQCLLIGINQVALQRHLLDGOMIRIVKPNQPGRSKQHRHHDQPAROPFHRFGILPHVVRPSKPOYINRQNP

SEQ ID 7609

TTTCTGATCCGAAAAACCAATGCCGCTCTGAAAACCGCATCCCCGTTTTCAGACGGCATGATTTTATCCGCCCATTCATGTGCCACACTTTATTCAC TTCATAACAATAAACCGGTAA
ACCATGAAAACCCCACTCTCTAAGCCCTCTGCTCAT

SEQ ID 7610

FPDPQNPMPSENRIPVFRRHDFIRPIHVPHFIFHITINR*NHENPTPOASAH

SEQ ID 7611

[illegible]

SEQ ID 7612

MPFVLGIAGGLVLDLNRLLTGRLLKNIATVAFLTSSSLTAQSTLTGLTGLPFIAMLTMTFGFTILGAVGLKYRTAFAGALAVATYTTTLTTPETYLWNTNFMILCGTVLYSTAILPQIILP
HRPVQESVANAYEALGGYLEAKADFPDPDEAENWIGNRHIDLAMSNTGVITAFNQCRSALPYRLRGKHHRPRTAKMLRYFFAAQDIHERISSAHVDYQEMSEKFNKTDIIFRIRRLLEMQQ
ACRNTPAQALRSGBKHYVYSKRLGRAIEGCRQSRLRLSDGNDSPDIRHLSRLLDNLGVSVDQPPQLRHSDSPAEENDMGDFRIAALETSGFNWQAIARPQLNLBESCVFHHAVRISLVVAAC
TIVEALNINLGYWILLTALFVCPQNPYNATKSRVYQRIAGTVGLGVIVGSLVFPYTPSVETKLWTVIAGTTFLFMTTRTYKYSPSTFFITTIQALTSLSLAGLVVAAAMPVRIIDTIIGASLAWA
AVSYLWPMKYVLTIEFTAAALVCSNGTYTQLKAEKRLTGEGTDIEYRITRRRAHEHTAALSSVTLSDMSSSPAKFADSLQPGFTLLKTGYALTGYISALGAYRSEMHECSPDFTAQPHLA
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SEQ ID 7613

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CGGCTGTATCAAAATCGAATGGCTGTGGCGGATCTGCAAAAATGTCACGGCAACCGCTATCAAAATCAATAAAGAGCGCATGGTCAGGATTTCGGAATACAGCCGTGAAATGTTCCGCCGT
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TGGCGTACCGCGCTGTGAAGCCCGAAGATGCGCAGAAATTCGAGCCTGCGCTGGCACGCTTACCGCCAAAATTGTGCGCGGTCTGCACCTGCCTGCGGATGCGACCGCGGACTGCGCGCT
CTTCAACCAAAACGTGACAAATGTGTCTCAAGAGAAGGCGCTACGGTTCTACTTTCACCAAAACCATCAGCCGCAATCGACCAACACGGCGTGCACATGCAAAAGCCGTGAAACCGCCGACCG
CGGTTTGAACAGATGCCGTTCTGCGGCGCTGCGGTCTCAGCAGGACTGTGTTCGCGCATTTGGATCTCAATTCGCCCTTATTCCTCCGCTCAAAGCAATTTCTTGACCTTGAAACGCTGCA
CAAAATTCGAGCGCGCACCGGTGTCCACTGTTTATAGATGAAGACTPACAAAGTCGCCATCGCCAGTGTTCGACACAGAAATTCGCCGCTGCGCGGAAATGGCGGAATGTGCGGCTGCAAAACCA

ACTGCCCGAAAAACGCCGCGAAACCTTGGCTTTGGTCGTCAACGACTTGTTCGCCGAAGCGCGGATTTGAGCCAAGCATTGTCTCGAGCGCGCTCAGGCCGATGACGCCGACAGTACG
CCGTTAATCGGGCGCACCCGCTTTGAAACCTGTTTCTGAATACCGGCGACGCTACTTTGGGCTGGACCATGTCCCGGGTTCGGCAAAATGACGCCGATATCGTGAGCGGCAAGACA
CCGAAATCCGCGCGCAGATTGAGCCTGTGCGCTATCAAAACTG

SEQ ID 7614

MKVLVLGAGVAGVSSVWYLAEGHEVTVIDRTEGVAMETSFANAGQLSYGTTFWAAGPIPTKALKRFLKSHPLFLFRPDGGLYQIEWLWRMLQNCATATRYQINKRMVRISEYSREMFRR
FEAQTDMNFEGRRKGLQIFRQTEVEEAAKQDIAVLERYGVPPYRLKPECAEPALARVTAIVGGLHLPADATGDCRLFTENLYKLCQEKGVRFYFNQITSRIDHNLRIKAVETETG
RPETDAVVCALGCFSTVLAQLDLNLPYVKGYSITLFPVTNSDGAFTVSTVLEBSYKVAITRFDNRIRVGGMAELSGYETKLEPKRRRETALVVDLFPBGDLSQALSWSGLRPHPTPDST
PLIGRTFENLPLWGHGTGLGWTSPGSAKLITADIVSGKDTFIRSDLSLSRYKL

SEQ ID 7615

ATGCAGAAATTTGGCAAGTGGCCGATTGATGGGTGGTTTTTCCAGCGAAGCAAGAAATCTCGCTGGACAGCGGTACCGCCATTTTGAACGCTTTAAAAAGCAAGGCATAGACGCATACG
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CTGCCGTACGCGCGGTGGTTTTTGGCGATTATGAAATTTGAAGCGCGCACATGTGGGA

SEQ ID 7616

MQNFQKAVILMGFSSEIREISLDSGTAILNALKSKGIDAYAFDPKETPLSELKERGFQAFNHLHGTGVEDGAVQGALELLGIPYTGSGVAASAIQMDKYRCKLIWQALGLPVPEFAVLYD
DTPDAVEEKLGLPMFVKPAABGSSVGVVVKKGRLLKSYEELKHLQGEIIAERFPGGEYSQPVNLKGLPIHIIIPATEFYDYEAQYNRDDITVQCPSEDLTAEBSLMLRELAVRGAQ
AIGAGCVRVDPLTDLGKLYLLEINTLPGMTGHSVLPKSAAVTGVGFADLCIEILKAHVHG

SEQ ID 7617

ATGTTAGACAAATCTCCCGCGCGAAATCGAATCAAAACATATCAAACTGGGAAAGCAAGGCTATTTCGCGCGCGATATGGATTGACAAACCGCTCTTTTCCATCCAACTGCCGC
CGCCCAACGTAACCGCGCAGCTGCACATGGGTGATGCTTCAACCAACCAATCATGACGCGCTGACCCGCTACTACCGCATGAAGAGCTGCAACACCGCTGGATTCCCGGTACCGACCA
CGCGGCGCATCGCCACGAAATCGTGGTGCAGCGCTCAGCTTCGCGCGCAAAACGTTGTCCTGACGACTTGGGGCGCGAAAAATCTTGGAAAAAGTGTGGAGTGAAGAAAGTTTCCGGC
GGCAGATTACCCAGCAGATGCGCGCGTGGGCTGCTCCGCGCATGGAAGCGCGAGTATTTACAGTGGACGCGCTACGCGCGCAACCGTGAACCGAGTGTTCGTGCGCTGTATGAAC
AGGGCTTGATTACCGCGGCAAAACGCTTGGTGAACGCGGATCCGCTGCTGCAACGCTGTCTGGCGCGCGCGCGCTGCGGTCAATCCAGAAATGAACGTTACACCCACTTAATTCGGCACA
GCTGGCGCAATCCACCGAAGCGCTTATCGTGGCGACACCGCTGCTGAAACGTTGCTGGCGCGCGCGCGCTGCGGTCAATCCAGAAATGACGCTGCGCAGCATTTCAACGATTACGAAG
GAATTAATCTCGCGCTGACCGGTGCGACCATTTCCGCTTATCGCGCAAGTACGTTGAAAAAGACTTCGTTACCGGTGCGGTGAAAAATCAGCCTGCGCAGCATTTCAACGATTACGAAG
TCGGCAACCGCCACGACGCGCGCTGATTACGCTGTCGACTTAGAAGCAAAAGTCTGCGCAACCGCGAGTGTTCACCTCAAAAGCGCAAGCGCAACCGCTTTTCCCTGCCGTGAAAA
ATACGCGAGGCTTGAACCGCTTTCCGCGCGCGCAAAACAAATGTTGCGGATTTGAGAGCAAGGCTCTTGTGCGAAATCAAAACCGCACGCTGATGACCGCGCAAGGCGACCGCACAGGT
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TGATGACCAACCACTTCACCGCAAGTACGCTTTAAGCGCTGTATCCACGCGCATCTGCGCGGACCAAGGCAAAAGATGTCAAATTCGAGGCAACGCTATCGACCTGTGGA
TTTGATCGATGTTATCGGCTTGGAACAGCTGCTGATGAACGCTAGCAGCGCGCTGCGCAACCGCAAGCGCGCGCAAGTGAAGAGCCACGCAAAACCTCTCCCGCAAGGTATCCCC
AGCATGGCGCGGACGATTCGCTTACCATGCGGAGCTACCGCAGCTTGGGCGCTTCGCT

SEQ ID 7618

MLDKYSPAIESKHYNWESQGYFRPMDLTKPSFSLQPPNNVTGLHMHAFNQTMDGLTRYRMKGCNTAWIPGTHAGIATQIVVERQLAAQNVSRHDLGREKFLKXVWMEVSG
GTITQQRVRGCSADWREYFTMDGVRAETVTEVFRVLYEQGLIYRGKRLVNDPVLGTAVSDLEVESMEBQSGMWHIRYPLADNPTEAVIVATRPETLLGDAVAVNPEDERYTHLIGK
ELILPLTGRITPVIADIEYVEKDFGTGCVKITPAEDFNDYEVGKRHDTLRLINVFDLAKVLANAENVNPKFBAQPGFSLPEKYAGLDRFAARKQMVADLQDQGLFVEIKPHTMTPKGRDTG
SVIEPLTQWTFVMSATPNNGEPDNEFKGLSLADKAKAVDSGAVRFIPENWVNTYQNMNNTQDWCISRLWGHQIPAWYDEAGNVYVARNQAEKQAGKTGLTREEDVLDTWFSFA
LVPFSTLWNPSETDELKFLPLSNVLVTGYELIFFVWARMIMTTHFTGKVPFAVVIHGIIVRDHEGKRKSKSEGNVDPVDLIDIGLIDKLIKRTTGLRKPETAPKVEEATKFLPPEGIP
SMGADALRPTMASYASLGPPG

SEQ ID 7619

ATGTTTTTATTTCATCCGCTATATATTGTGAGAAAAATATGTTGCGCAACCGGTGAGACCTTTAAAAATACCGCTTTACGCACTAAAAACCAACCGGAACGCAACATATGATGAAAA
ATCGAGTAAGCAACATCCATTTTGTGCGTATCGGCGCGCTCGGCATGAGCGGTATCGCGCAAGTCTTGCACAAATTTGGGCTTTAAAGTTTCGCGTTCGGATCAGCGCGCAAAATGCGCGTAC
CGAGCATTTGACGAGCTGGGCAATCAAGTTTATCCCGCCATACCGCAGAACAGTTAACCGTGGCGGATGTCGTGTTGCTCTACCGCGCTCAAGAAAGAAATCCCGAAGTTGTGCGT
CGGTGGAGCGCGCAAAATCCCGTATTCGCGCGCGCTTGTGCTGCGCAGAGCTGATGCGCTTCCGTGACGGCATCGCCATTCGCGGTACGACCGGCAAAACCAACGACACCGCTGACCG
CTCCATCTCTCGCGCGCGGAGACTCGACCCCACTTTGCTTATCGCGCGCAAACTCAACCGCGCGGACCAACCGCGCTTGGGCAAGGCGAATACATCGTTGCCGAAGCGGACGAATC
CGATGCGCTCTTCTCATCTGACCCCGATTATGTCGCTGTTACCAATATCGAGCAAGACCATATGGATACCTACGGGACAGCGTCAAGAAAACTGCATCAGCGGTTTATCGATTTCATC
CACCGTATGCCCTTCTACGCGCAAGCGCTTTTGTGTTGACAGCGAACAGCTCCGCGCGATTTTGCCCAAGTGAAGCAAACTTATGCTACTTACGCTTTGGAGATACCGCGGACATCT
ACGCCACCGACATCGAAACGTCGCGCGCAATGAAATTCACCGTCCATGTTCAATGAAGGACATGAGCAGGGGTGTTGAAGTCTGCTGAATATGCGCGGACACCAACGCTGCT
GAACGCAATGGCAGCATCGCGCTGGGCTGGAAGTCCGCGCATCGGTTGAAGCATCCAAAAAGGCTTGTGCGCTTTGAAGGCGTTCGCGCGCGCTTCCAAAAATACGGCGACATCAAG
TTCGCAACCGCGCGGACCGCTTTGCTGCTGGACGATTACGACACCAACCGCTGCAAGTGGCGGCAACCTTCCGCTGACAGCGCGCGCTTCCGCAAGGCAAGCGGCTTCGCGCGCGC
AGCGCACCGCTATACCGCGACGCGCGATTGTTTGAAGACTTTACCAAGTACTCAATACCGTTGATGCGCTGCTACTGACCGAAGTTTATGCGCGCGGCAAGTGTGATGATGTTTACAGGATGGCGATGTTGTG
CGACTCCCGCGCTTGGCGCGTGTCTATCCGCGTATGGGCAAACTTGAGCGCAATTTACTGCGAAACGCTCGCGACCTCGCGCAAAATGCTGATGATGTTTACAGGATGGCGATGTTGTG
TTGAATATGGGTGCGGGAAGCATCAACCGGCTTCCCTCCGCGCTTGGAAATGTGCAAAACAGATT

SEQ ID 7620

MFFISIRYIFVRKLMCANGQTFKTIPLRTKNQPERNIMMNRVSNHIFVIGGVGMSGLAEVLHNLGPKVSGSDQARNAATEHLSSLGIQVYPGHATAEHVNGADVVAATAVKKENPEVVA
ALERQIPVTPRALMLAELMRPDRGIALAGTHGKTTTSLTASILGAAGLDPTTVIGKLNAAAGTNRALGKEVIVAEDESASFLHLPTIMSVDNTIDEDMDTYGHSVEKLHQAFIDFI
HRMPFYKAPLVDSEHVRALLPKVSXPYATYGLDDPATDIATDIENVGAKMFPVHVQMKHGEQSGFEVVLNMPGRHNVLNALAAGVLAEGVSAVEATQKGLLGFEGVRRFPQKYGDIK
LPNGGTALLVDDYGHFPEMAATLAAAGAYPEKRLVLAFOPHRYTRTRDLFEDFTKLVNTVDALVLTETVTAAGEEPVAAADSRLARAIRVLGKLEPTICENVADLPQMLMNVLDQGDVV
LNMGAGSINRVPSALLELSKQI

SEQ ID 7621

AATAATATCAAAACCAATAATCCGCCAAGAAACATATTTCTTCAATCAGTTCGAATTTCCAAGCCCTGTTCCATTTCTCAACGTGTTTTCCCGAGTAATTCGGCTCTCCATCGTAGGA
TGCAGTTCATACCAACCGCATAGTAACGTTGTACCGTGATGTAATCCTTCAATCAATGCTCCCTATGTTGGTAAATACGTTGCACCAATCAGATGAACGCCAATGTAACGTCG
CATTAAGTTGGCTTGCTAAAATATAAACCGCAGGCTGCAT

SEQ ID 7622

NHKKP*IPPRNIIFFNQLQFFSPVPLQLFFPSNCLHRRMQFIIPNHSNVVP*CKSPNQLPMLVNLHQIRCNANV*RAITLAC*NINRRLH

SEQ ID 7623

TTCGTAAAATATAAACCGCAGGCTGCATATAATACCTTTTGAATTAATTTAAATTTATATTCGCCGGAACACCATCCGGTGATTAATTTAACCTTTCGTATCCCATAGCTTTCCATCAT
TCCCGCAACTCTTTCGTATTCGCCGGAAGCGGAATCCAGGACTCAGGACTGAGAAACCTTTTATCCCGATAAGTTTCCGCACGACAGACCCGGATTCGCCGCTGAGCGGGA

SEQ ID 7624

LLKYPQAAAYTLLNLYLNSREHHPVITLTLRYPHSFSPFQLFVIPAKAGIQDSGPEKPPYPISPRTDRPGFPFPERE

SEQ ID 7625

TTCATGAACACCGAAACCAAGACTCGGCTACGGCGCAACCGCTGCCGAACCGCGGCCATTCCTTCCCGATATGTGGATCATAGGTGCTGTAATCAGACCATCGAGCAGGTTACGC
AAGCCTACGAAACCTACCGCTTGTATTTGGCGCGGAAACCTGTACAGCTTCGTATGGAACGATTAATTTGCCGACTGGTATCTGGAACCTGCCAAAGTACAGCTCCAAACCGGCTGCGCCAG
CCGTGAGCGCGCCACACGCCATACCTTATTCGCGTACTCGAAGCCGCCCTGCGCTGCTGCACCGGATTAATCCCGTTTCATCAGCAAGAACTGTGGCGAAACCGTCCGCCCATGTGCGAT
GCCAAACCGCGGACAGCATCATGCTGCGCCGTTTCCCGAAACCGAGCGCGGAGATTTGTCAGACGGCATTCGGGCAATGACCGTGTTCAGGATTTGATCGGCGCAGTCCGCAAC
TGC CGCGGCAACCGGCTATCCAGCCCAACGTGAAGCCCGCTGTTTGTGAAAGCGCGGACGACTTGGCGGACTACCTCAATACCTGCGGATGATGACCGCGCTGACCGAAGCAGCGCA
AGTCCCGCGCCCTCCCGAAAGCGGAGACGCGCCGTCGCAACCGCGCGCTGATGCTGAAAGTGAATCGCAAGAGCCGCCGAAACCGCCGTTTGAGCAAGAAAGCGGAG
AAGCTGCAAAAGCCTTGGAACAACTCAATGCCAACTCTCCAAACCGGCTACACGAAAAGCCCGCGCATCTGGTGAAGAAAGCAAGCCGATTTGGCGGAATTTGAAGACAAA
TGGCGAAAGTCAAAATCAGTTGGCGAAGTTGAAGAC

SEQ ID 7626

LHNTFNQDCGYGATAAEPRGHSFDMWIIIGRLNQTIETQVQAYETFRDLAAETLYSFVWINDYCDWYLELAKVQLTGCASRQRATRHTLLRVLEAALRLHPPIIPFITEELWQTVAPMCD
AKTADSIMLARFPETDGGELIVQTAFGQMTVLQDLIGAVNLRGETGIQPNVKAFLPVESADLDADLYLKLPMTRLTPEARQVAALPESGDAPVAVCNARIMLKVKIDKAAETARLSKEAB
KLQKALDKLNAKLSKFGTTEKAPHLVEKDKADLAELEDKMAKVQNLAKLKD

SEQ ID 7627

ATGGCGCGTAAACCTTTATGCTGATGCGCGCGGAAACGGCGGACACATTTTCCAGCTCTGGCTGTGGCGGATTCATTCGCGCTGCGCGGTCAATCATGTAATTTGGCTGGGCGCAAGG
ATTCGATGGAAGAGCGCATTCGTCGCCAATACGGCATACGCTTGGAAACGCTGGCGATTAAGGAATACCGCGCAACGGCATCAACAGCAAGCTGATGCTTCCGTTTACTCTGTACAAAAC
CGTCCGCGAAGCGCAGCGGATTAATCCGCAACACCGGTGTGAGTGCGTCATCGCTTGGCGGTTTGTGTACCTTCCCGCGGTCTGGCGCGGAACTCTTGGCGGTGCCGATTTGATG
CACGAGCAAAACCGCTGGCAGGCTTGTCCAACCGCCACCTGTGCGCGTGGCGGAAACGGGTGTGTGACGCTTTCGAAAGCGTTCAGCCACGAAGCGGTGTGTGCGGCAACCCGCTCC
GCGCCGATTAATGACAACTGCGCGTGTGCGCAACGCTTCCAAGGCGCGCGCTGTAAGAAATTTTGGTGTGGCGCGGATTTGGTGTGGCGGATTTGAACAAAACCGTACCGCA
GGCGTGTGGCACTGCTGCTGAAGAGGTGCGCCGCGAGATGTACCACAGTCCGGGCGTAACAACTGGGCAATCTTCAGCGGATTAATGACCGGTGGCGGTGAAGCGGAATCGGTGGAA
TTTATTAACGACATGCTGCTGCGCTTACCGTGTATGCGGATTTGGTGTATTCGCGTGGCGCGCTGACGATTCGCGAGTTGACGCGCGCGGGGCTGGCGCGGTGTGTGTGCTGCTATCCTC
ACCGCGTGTATGACCAATCAACCGCCACCGCGCTTTCATGCTGAGGAGGAGCGGGCTGCTGTGCGCGCAACCCAGTTGACGCGCGGAAACCTGCGCGAAATCTCGCGCAGCTCAAC
CCCGGAAATGCTCAATGGCGGAAACCGCGTACGTTGGCATTTGCCGACAGCGGATGACGTTGCCGAAAGCGGATTCGCTGTGCGCGG

SEQ ID 7628

MGKTFPMLMAGGTGGHIFPALAVADSLVRGHVHVLWLSKDSMEERIVPQYGRILETLAIKGRNGIKRKLMLPFTLYKTVREARQRIIRKRVBECVIGFGFVTFPGGLAAKLLGVPIVI
HEQNAVAGLSNRHLSRWAKRVLYAPKAFSHEGGLVGNPVRADISNLPVPAERFQGRGLKILVVGSLGADVLRKTVQALALLPEBVRPQMYHQSGRNLGNLQADYDALGVKAECVE
FITIMVSAIRDADLVICRAGALTAELETAAGLGLVVPYHVDHQTANARFVQAEGLLLPQTQIAEKLAETLGLSLAREKCLKWAEARNATLALPHSADDAVBAATACAA

SEQ ID 7629

GGACCTGAGAAACCTTTTATCCCGATAAGTTTCCGCAACGACAGACCGGATTCGCCCTGAGCGGGAATGACGCGGAGCGGTTCGTGTTTTTCCGATAAATTCCTAAACTCAAAAT
TCATCATCTCTACAAAACAGAAAACCA

SEQ ID 7630

GPEKPPYPISPRTDRPGFPFPERE*RRSGFCFPR*IPKYNPIIPRTENQ

SEQ ID 7631

TTCGTGTGTCACCGTCTTAGATTCCCGCTGCGCGGGAATGACCGGTTTCATTTGCCGCCCCCTCCCGAAAAACGCAAAAAATGCCGTCCGGAAGACCTTTCCGACGGCATTTGCCGAA
AAACCGGCGCGCGCGGCTCAGAAGAAGACTTCGCGCCAGCT

SEQ ID 7632

LLSHVLDSRLRGNDAPHLPPEKRRKMPSEDLSDGICGKTRAGGSEEDFAPA

SEQ ID 7633

ATGAAACGCTTTATTCGCGGTGCTTTTATCCGCAACACCGCCCGGCTTCTCCGATTTGTCGTTACATGGCATTCGCATCGGCACTGATGAAAACATTCACAGTGATACAAAAGTCAAAAT
ATCTTCAGGACCGCAGCTTCGCTGGCGATGCTATACCTCAAAATCGATGATGACGCGCAATATCTTGGCATACCGTGTGTGTCGTCAGGTAAATGGGTTTTGCCAACAATGCTTAACTCA
AAGCCAAATCAAGTACGTTGAAGTTTACGACAGCAGCAGCCCGAAACGCTGCGGTGTAGAAAAGTCGAGGATGCAAGACTCTTGGAAAGCATGATGTACACCGGATTTGGTCCGCGAG
ATGGCAAAACCGGAAAGATGATGTGTATCACTGGATAAATCAGGCAAAATAGTGTCCGGAAGACGGAATTCCTCGTACGAGCATGTACGAAAGTGGAG

SEQ ID 7634

MKRPIILVLLSATPAPASPIVCTWHCIGTDENIHSDDTKVKYLQDGSFRGDALIKIDDDGNILAYRVVGAGKWRFANNALTSQIKYGEVSRQHSPEFLAWLEKSEDA RLLESMTTGLVAQ
MDKPGKIDVYQLDKSGKLVSDDGTSREACTKVE

SEQ ID 7635

TTGGGATGTATGCTATGTCGACGCGCATGTCTGCGCTGTAATTTTGGCCCTTTCGCGCAGGTGCAACAGACTGGCAGGTGGTTTTTTGAAGATTTCCGAAGTATTTGTAAGTGG
GCGACGGTGTCCACACTCTGCTGCTCGACAGCGCGATTTGTGCGGACGCGGAGAAATTCGACGCGCCGCTTTTGTGGATGTTGCTGATGACGGGCTTCGCGCTGCTGATGATTTATTC
GGCTTCTGTGATTTGGCATCGAAGGAAGCGCGATCAGTTTTTCTATTGACAGGACAGCGGGTTCGTGTTGCCGCGCTTATAGCGAGCGGTTTTTATGTTTCTTTCAGGATG
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GACGGCCAACTGATTTATGTCGCCCAACCAATCCGAGGACGCTGTTGAAACATTAGAAATGTACGCGCGTTTCCGGCGATCATCTCGCGGATTTATGCTGGTGGCGTTGCGTTTGGTGTG
ATAATGTTACAGCCGATTTTCGTTCTGTTGCTGCTATTACCGTCATTACCGTTGGAATGCTGTTTTCGCGCAGGATTCGCGTGAAGAAATTTTTTGTCTGTTAGGACGCTCTTGGG
GGATGCTGCTGATGATTACCGCGCGCTCCCTACCGTGTGCGAGCGGTAGTGGCAATTTTGGACCCGTTGGAAGAACCGCGAGGCTCCGGCTACCGACTTACCCACTCTCTGATGGCAATCG
CGCGGAGAGTGTGCTGATGGTTTGGGTCGAGTTTGGCAAAACGCGGCTTTCGCGGGAAGCGCATACCGATTTTATTTTGGCATCATGCTGAAGAAATTCGCGCTTCTTCGCGATG
TGGCTGCTGATATCTGTTACGCTGGCTGGTGGTGGCGGCTTTCCATCGGCAAGCAGTTCGCGGATTTGGGTTGACTTTCAACGCTATATGCTCTCGGTATCGGATTTGGATCG

SEQ ID: 7636

LGCIVCSGDIVCRLKFLPFAAGANRLAGGFLKISEVLVKVGDVHTLLLRPIVRDGRKDPAPLLMMVLMTAFGLMLTYSASVYLASKEGGDQFPYTLRQAGFVVAGLIASGFWLFLCM
RTWRRLLVPWPIAFGLSGLLLVAVLILAGREINGATRWIPLGLPINQPTPEFLKLAIVLYLASLPTTRREEVLRSMESLGWQSWNRGTANLIMSATNPQARRETLBYGRFATILPLIMLVAFGLVL
QWQPDIFGSGFVVITVITVGMFLPAGLWPKYFPVLVGSVLGGMVLMITAAPVRVQRVVAFLDPKDKPDQAGYQLTHSLMAGRGGEWFGMLGASLSKRGFLPEARTDFIPALIASGFGFGH
CVLIFCYGWLVVRAFSGIQSRDLGLTFNAYIASGIGIWIQISFFNIGVNIGALPTKGLTPLMSYGGSSVFFMLISMLLLRLIDYENRQKMRGYRVE

GTGAGGCATGTACGAAAGTGGAGTGAAAGCGAAGCTGTATTTCACCCCGTCGGGCAAAATACCAAACTCAAATCAAGCGCTCCGAATACCGTTTCGGCGGTATCGTTTTCGGGCAAAATTAATCACGCATCCGGGCATTCGATATCGTCGGCAGTTTCGGCATAATCGCCGTAACGGCAACCTTATACGGCTTACCCCTGTATGGCGGATTAAACAAAATCAGGACAAGCGCGGGCGGCAGGCAGTACGAATGGTACGAAACCGGTCGCCTGGTGCTTGGGCGCCT

SEQ ID 7638
VRHVRKWSKELYFPFPRRAKIPKLLSSRPNTVFGGIVCGKLIITPGIRYRQFAHTCENGNI LRLTLVWRINKNQDKAAGRQYEWYGTGSPGAMAP

TTGCAACCCCTGTGTGACCGGAAGTTAAATTGGGTTTTATAGACAACCTTCAGGGCAGCCTCTGCTGGGGGCGAAGTAGTGTGTGTGGCATGTGACATTTTCGTAGCTGTAGCCCTACCAACCCC
GGGCGGGTTCGTACTAAATCCAATCAACGGCATTCGCCGCCCTTTTCAGACTATCGGTATCAAAACCGGAAACCTTGCCGTAGGGCGCGAGGTAGGTGCCGCCCGGAAAAACGACGATACCGC
CTTTTGTGACCAACAACGCTTATCGGTATTATCGAA

SEQ ID 7640
LQPIILTEGKLGFIIDFRAASAGGEVVVACDIFVAVAYQPRAGRTNPINGIAAPFTIGIKTGNLAVGRQVGRRPENDTAFLSNNVIGIIE

SEQ ID 7641

TTGTTGGAAATCCCGAATAAGCGGTTCAAACGCTGTCGCTGCCCGCGGACCCATATACAGTTGGCAACTGTCCGGTTGTGCCGATGGGTTGCCCTGCCCTGCCCTGAGCTACGCAACGGTT
GTCGTGCTTTGGCGCGGGTGGCGCGCGGGCGGTTTGTGCTATGATACGGAAGTTCGATATACAAGGGCGGGCTTCAGCCGCCAAATCCACCAACTCCGCCGAATCCACCGAATC
CCGCCCGCTCATCCCGCATAAGCGGGAATCCAGACCTGTGCTGCCGGAACCTTATCGGA

SEQ ID 7642
LVEIPNKRFKTKCRGRGSHIQLATVRLCRWVALPLPELRNGCLPWAGAGGGRAVCRYDTEVPIYKGGLOPAKSTNSAESTDSRRRHSRISGNPDLVVKLIG

[illegible]

SEQ ID 7644
EEDFAPA*AFDTAHRAGNIGQAVQIVHQGAHTP*SGEAPVIAGGFFTLFECSSAAACITVCRDGEIVCF*LFVQVTHINRFPVNI*SVRADGFVFP*PHAAYG*GGLAVHFMAGILRN*LVIRHNR
RASRSCQAAVVGSDI*QNGGLCAAPVITRIAD*DGKGGTGYHGRFDGNAL*SP*LIQHYP*PLTPARS*VGS*LVQ*CF*PI*FLFKHLEQG*PASRAVLRY*LNRL*VIVKDT*VNIL*FARI*QYI*IFGQIA
ARETDD*DAFV*QCSNG*GGRGS*NR*LVAF*ENSPYR*PPIRIGIAQIKAVHIAAPVAGIGDIDRAVQI*PIHQRG*GRK*PALAALH*DFD*FNQ*TTTAV*QI*ITYIQ*GPI*IAAANI*FSRI*TGSEEG*GVFA
VLGFADLRRADGVA*P*PHFAIPAVIIAIFDIKQSGSGWII*SVDFAP*IQGIRASAAK*THRT*HKH*EM*LL*VL*VICNA*QDKAAV*HAVAVAHIA*FP*GKGGAQ*LF*GBCRI*VAF*NI*LAHRAGD*VAE
LQIVAAPITAAV*FFEMHHP*VVRGGCQI*PADDRNR*AVD*VQAIAL*VAV*ADAV*SL*VAFV*P*FSVN*FKSTVIGSS*TNR*PQQH*F*P*LVGK*FID*VIR*FLMNA*ESA*VAVG*SKSD*LL*VSIQ*PDK
LYAAIQSDDC*PPHETRL*FTFNII*LIQGYEGIAAG*FAG*FS*FSPQILKVDAAART*VGVGRN*RS*ILHL*LA*ILHRAEP*Q*RG*GGQ*CRRR*GGI*LV*IGVR*F*DL*VAAAC*FDLQRA*IDAFS*FI*PKP
IT*KKSIQ*V*P*SP*RFQDAR*PQGT*Q*INCFAL*RD*IF*DL*GF*IQ*QV*Q*GVQ*IKDGG*GV*LV*PDIT*GR*IF*TVACRINE*VL*V*VL*GV*PT*ILL*HL*VL*VKI*YL*TV*SV*FFD*ALAAQ*IERHAQ*PRI
TROFINGRIVAAPV*FVYIQLVACL*SL

SEQ ID 7645

ATGACATTTCCAAAACAAAAAATCCTCGTGCCTGGACTTGGCGGCACGGGTATTTCATGATTTGCCATCTGCGCAAAAACGGCGCGGAGGTTGCCGCTTATGATGCGGAGCTGAAAGCG
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ACCACGGTAACGAGCCTGCTCGGCTATCTCTGCATCAAGTTCGGGCTGGATACCGCTATTGCGGGCAATPACGGTACGCGCGTTTGGAGGCGAAGTTTCAGCGCGCAAGGCAAAAAGCGG
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CACGAAGCCGATTTTGGTTGGAACCGGGGACGGGCTGTTTAAACAAGGCAATGAAGATTGATTCTACGCAAGACATCCCGCTGCGAGCGTTGCAACCGCGCCGACGCTATTGGCTG
CGTGGCTTTGTGCGAGGCGCGTGTGTTTGCCTGCGCGGACGCACTGCTGGAACAGCTTCAACAGCTTCAACGGCTTTCGCGACGCTGTGGAAAAAATCGCGGAGAAAAACGGCGTGGTATTCA
CGACGACGACAAAGGCAACGAGTATGCTGTTGCGCGCGACCGCGCGGATTCGGGTTTGGCAAAACCGCTCTTCGTGATTTTGGCGGCTATGGGCAAGGGCAGGACTTCACGCCCCCTGCGCGAC
GGCTTGAAGATTAGGCAAAAAGCGGTGTTCTTGATGCGCGCTGATGCGCGCAAACTCGCCCGATTTGGACGGCTCGGCTTGAACCTGACCGACTGCGTCACTTTGGAAGAGCGCGTTC

AGACGGCATACGCCAAGCGAAGCGGCGATATTGTCTGCTCAGCCCCGCTGCGGAGTTTCGATATGTTTAAAGGCTACGCGCACCGTTCCGAAGTGTATTATCGAAGCGTTAAGGC
TTTG

SEQ ID 7646

MTFQNKILVAGLGGTGISMAYLRENGAEVAAYDAELKAERVAQIGKMPDGLVFTGRKLDALDNGFDILALSPGISERQPDIEAFKQNGRVLGDIELLADIVNRRGDKVIATIGSNKG
TTVTSILVGLICIKCGLDVTIAGNITPVLLEALQREGKADVWVLELSSPQLENTESLRPTAATVMNISEDLDRYDLDLYAHTKAELFRGDGVQVILNADDVFCRAMKRAGREVKRPSLE
HEADFWLERGTGCLKQGNEDLISTQDIPLOGLHNAANVMAAVALCEAVGLPREALIEHVKTPOGLPHRVEKIGENGVVFIIDSKGTINVGATAAALAGLQNLPLFVILGGMGRGQDFTPLRD
ALKDKAKGVFLIGVDAPQIRRLDGGCLN/IDCVTLLEAVQTAAYAQAEGDIVLLSPACASFDHFKGYAHRSEVFIKPAKAL

SEQ ID 7647

TTGTTTGTGTCGGTATCCATCGGTTTGGGATTTCGATAAATGTTTCAGATGCAATTGTATCGCAGATTTTTCAGGGAACGGCAACCGCCGGGGCGCGCGGCTGTGTTGGGAGTTGT
TCGGGGGGGGGGTGGATGAGTTGCTACGAATCGCTATCTG

SEQ ID 7648

LFLCGIHRVWDSKCSCTVSQILQNGKRPGRALFGLPGGGGHEQLIAIAL

SEQ ID 7649

GTGTTTCTCTGATTTTAAATTAATTTGTATGGTAAATTTGGGCTCCCTGCTCTTTTGGCGCTGATGAATATGACTGCCCCACTTTTACCTCGGGCAGATTTTGGCGGTTTCATCACA
TAGCGTATTATACGTTTGGCCATCGCCCCCCCCCGCGGTATGGGAAACATCAATATGGCGCATAAAGCGCGTATGGCGGAAACCTGCTTTTCAAAGTTTATTCATATTTT
ATTCTTAAGTTTGGCTTCGCGGACGGCGCGCGCAACCGCGGGTTGCG

SEQ ID 7650

VFLILILKLFVWVNRSLFFGADEYDCPHFTSGRPCTITLAIYVCAIAPPAGMKHQYGGIKRMAENLPQSPITHILFLKFAFAGRRANAGVR

SEQ ID 7651

TTGGAAAGTCATTTTGGTTTGTCTTAAACAAATCATATTGGGAGGAGAGCTGCGCCCTTGGCAAGCGCTTTCAGACGGCATCGCGAGCGGATTAATAACCGGCTTCAGGCGTTG
TCATGTGCGCAGCTGTTTGTCTCCGTTTGAACGCCCTTGCAAGCCATTGTTGAGCGAGCGCAAGGCTTTCGCGCACGCGCGTCCATGTAATACATCAAGCCCAATTTGATTGGG
CTTGGGCATCCCTTGTTC

SEQ ID 7652

LESHFGVILKQIILGRRRPPLPKPLSDGLASRLITRLQALVIVAIVSVL/SLAKPLLSERKVLHAHAASVIHQAIQIVLGLGILP

SEQ ID 7653

ATGGATACCGCACAAAAACACGCTGGGCAATAACCTTATCTACGACGGCAGCGCTTTTACGCTGCGAGAAACAGCGGGCGGCGTACCGACGCTTCAGGCGCATTTGGAACCGCAC
TCGCCGAATCGCAGGAGATCTGTGCCACACAGTTGCCGCGAGGACGACACCGCGCTTCATCGCAGCTGCCCAAGTCTTCATTTTCATCTACTGCGCGCTACGTCGCGCTCAGGCAATG
GATACGCGGCGTAAACGCCACCTGCCCCAAGGCAATAGCGTTTTCGACGCGCGACAGGTCGACCGCGGATTTTCAGCGACGCTTCGACGCAATCCGACGCGGCACTACCGCTACCTGCTCGAA
TCCGCCCCCGTCCGTTCCCGCTGCTCAAAACAGGGCGGGCTGGACACACCTCGAGCTCGACATCGGACCGGATGCGCGCGGCTGCGCGCTTATTGTCGCGGCAACAGACTTCTCCAGCT
TCCGCGCGCGCGGCTGCCAGGCAAAATCCCGCTCAAAACATCTACCGCGCGGACCTTACCAAGCGCGGAGCTCGTGGCGCTCGATTTGCAACGCAACGCGCTTTTTCACCAATGCT
ACGCAACATCATGGGCGCGCTGCTTATGTGCGGAGCGGCGAGGCTCAGCGCTCGAAGGCTTCGCGCGCTGCTGCTCAAGAACGCGCGCGCTCAAGGCCACCGACCTTTATGCCGCGAGCGG
CTTTACCTGACCGCGCTGCACTATCCGCGGCGCATACGCGCTCGCGCCCCCAATCCCGAATGGCTT

SEQ ID 7654

MDTAQKRWAITLSYDGRFVWQKQAGGVPTVQAALETALARIAGESVATTVAGRTDTGVHATAQVVFHPTAAVRPAQAWIRGVNAHLPEGIAVLHARQVAPGFHARFASGRHYRYLLE
SAPVRSPLIKNRAGWTHLELDIGPMRRAALLVGQDPSSFRAAGCQAKSPVKTIYRADLTQSAGLVRLDLHGNAFLHVMVRNMGALVYVSGRLSVEGFAALIQRSLKAPPTPMPDG
LYLTGVDPYAGYIVRPQIPPEML

SEQ ID 7655

ATGCAGAAAAAAGACATTCGCGCGGACACCTTTTCATCCCCACAAGTTCCAAACACATTTTCGGCTTAAATATCCACAGCATTCGCGTCTTAAAGGCACCGGACGCAATTCGGTAAAGA
AAAGCGGATGTGTCGCGCACACAGCAAACTATCCACAAACCTATTCCCCAGGAAACCAATCCACAGGTATGCACAAAGGGAATCTCTCTTACCGACACCGCTTTTAAACCGGCAAT
TCAGATGATTTTAAAAATAAAAAAGTTACCCACAGAAAAATTCCCATATCAATATAATCATCGTTTATPATTTTAAACCTTATATTTTATTTATAACCTTCAGGGAACCGGACCGCA
AAGCGTAAAGGCATCTTTTCAAAAAAT

SEQ ID 7656

MQKRHSRRLFIPTSSKHLISLNIHSIPVLKGTGSHSVKSKMSSAQANYQNLFPPTKNNPQVCTKGNPPYRHPFKTAIQHLIKIKSYPOKIPHINIIVLLFKPYLFTITLQNGTA
KRGIFSKN

SEQ ID 7657

TTGCATTTTACAACTTACTCGGAGGGTATTTGGAGGCAATTGCAAAACCGGGGTTATAGCGGATTAACAAAAACCGGTACGGGTTGCCCGCCCGGACCCAAAGGGAACGGTTCCC

SEQ ID 7658

LHFYNTYSGGYWRLQTCGYSGLTKTGTALPRDPKGTVP

SEQ ID 7659

ATGAAAGCGCATTTGGCGTAATCGGTTTGGCGTTATGGGGCAAAACCTGATTTTGAATATGAACGATTTCGGATTTAAGGTTGTCGCTACAAACCGGCAATCGGTAAAGTGGACGAAT
TTTTAAACGGTGGCGCAAAAGAGACGGGCAATTATCGGCGGTATTCCTGCAAGACTTGGTCGATAAGCTGGCAAAACCGGAGAAAAATCATGATGATGTTTCGCGAGGTTCCGTTGGTGA
CGACTTTGTCGAACAATGCTTCCGCTGTGGAAGAAGGCGACATATTATCGACGGCGGCAATGCCAATTACCCCGACACGACACGCGGACACATTACCTTCCCGGAAAGGATTTTG
TTTGTGCGCGCGGCGTATCCGCGCGGGAAGAAGCGCGCGCGCGCGCGCTCCATCATGCGCGCGGGGATAAGCGCGCTTGGGAAGCGGTCAGCGGATTTTCCAGCGCATTTGCCGCA
AAACCGCGCAGGCGCAACCTGTGTCGACTGGGTGGCAAGGATGGCGCGGACATTTTGTCAAATGGTGCACAACCGCATCGAATACGGGATATGCAAGCTGATTTTGGCAAGCGTACCA
GTTTATGAAGACGGTTTGGGCTGTCTACGACGAAATGCAACCGCTGTTTTCGCGAGTGAATAAAACCGAGCTGGATTCTTATCTGATTGAAATCACAGCGGCAATTTTGGGCTATAAG
GACGAAGCGCGGCAACCGTGGCGGAGAAATCTCGATACGCGAGGCAAAAGCGGCAAAATGGACGGGCAATCAATGCTTGGATTGGGCAATTCGCTGACGCTGATTTCCGAAG
CGTATTCGCGCGCTGTGTTTGTGCTTCAAAGAACGCGGTGACAGCGGCAAGCTGTTCGCGCGGCAACCGGCAACCGCGTCAAGGCGGCAAAAGAAATGGTTCGAGGCGTTGAGGCA
GGCTTGTCTTGGCTCCAAATCAATTCTACGCAAGGCTTTATGTGATTCGCGAAGCGGGCGAAGTTACGGCTGGGGTTTGACTACGGCAACACTGCGCTGCTGTGGCGGCAAGG
TGCATCATCCGCGCGGTTTGGGCAATATCCGCGAGCGTATGAGGCAATCCCGATTGTTGTTCTTGGTTCGGGATCCGTAATTCAAAAATTTTGGAAAACTGCTGCGCGGAT
GGCGCAAGGTGTTTCCAAAGCGGTGGAATGCGGCATCCCTATGCGCTGATGCTTTCGCGGATTCGCTTTCGAGCGGCTATACGACCGCAACGCTGCTGCAACCTCTTGCAGGCACA
CGCGCACTTCTCGCGCGCACATTCAGAGCGCACCGGCAAAACCGCGCGGCAATTTTCCATACCACTGGACGGGCAAGGCGGAGATACCGCTTCGACAACTACGATATT

SEQ ID 7660

MKGDIGVIGLAVMSQNLILMNDGFKVVAYNRTIGKVDEFLNGAAKETGIIIGAYSLQDLVDLKLAPRKIMMVRAGSVVDDFVEQLPLLEBGDIIIDGGNANYPDTRRTHYLAKGIL
FVGAGVSGGEGARRGPSIMPGDKRAHEAVKPIFQALAAKTPOGEPCCDVGKDGAGHVPVHMVHNGIEYDGMQLICEAYQFMKDLGLSYDEMHRVFAENKTELDSYLIETPAALIGYK
DEGGEPLAEKILDAGQKGTGKWTGINALDLGIPLTLISAVFARCVSSFFKEQVQTKLFAATATPVGEGQHEVEALRQALLASKISYAGPHLIRREAGESYWGGLDYGNTALLMRG
CIIRSAFLNIRDATYENPDLVFLGADPYFKNILENCLPAWRKVAVAVECGIPMPCASAITFLDGYTTERLPANLLQQRDYPGAHTYERTDKPRGEFFHTWTKGGDTASTPTDI

SEQ ID 7661

SEQ ID 7661

ATGAAAAAATCCCTGATTGCGCTGACTTTGGCAGCCCTTCTGTTGCGGCAATGGCCGATGTCAACCTGTACGGCGCCATCAAAGCCGGGTACAAACTTACCGTTCGTAGAACATACAG
ACGGCAAGGTAAAGTAAAGTGGAAACCGGCAGCGAAATCGCCGACTTCGGTTCAAATAATCGGCTTCAAAGGCGCAAGAGACTTCGGCAACGGCCGTGAAGGCCGTTTGGCAGTTGGAACAAGG
TGCCTCCGTCGCGCGCACTAACACCGGCTGGGGCAACAACAATCTCTCGTCGGCTTGAAGGCGCGCTTCGGTACCATCCGCGCCGTAGCCCTGAACAGCCCCCTGAAAAACACCGCGGCC
AACGTCAATGCTTGGGAAATCCGGCAAAATTACCGGCAATGTCTGGAAATCAGCGGAATGGCCCAACGGGAACACCGCTACTTGTCCGTACGCTACGATTCTCCCGAATTTGCGCGCTTCA
GCGCAGCGCTACAATACGCACCTTAAGACAATTCAGGCTTCAAGCTCAAAACGGGAATCTTACCACGTTGGCTTGAACACTCAAAAAACAGCGGCTTCTTCGCGCAATACGCGCGCTTGTCCAAAGATA
CGGCGAAGGCATAAAAAAATCGAATACGATGGTCAAACCTTATAGTATCCCCAGTCTGTTTGTGAAAAAATGCAAGTTCAACCGTTTGGTAGGCGGTTACGACAATAATGCCCTGTACGTT
TCCGTAGCGCGCACAAACAAGATGCCAAATGTATGGAGCAATGAGCGGTAATTCGCACAACCTCTCAAACCGAAGTTGCCCTACCGCGGCATACCGTTTCGGCAATGTAACGCCCGCG
TTCTTCGCGCCACGGCTTCAAAGGCACCTGTTGATAGTGCAAAACCACGACAATACTTATGACCAAGTGGTTGTGCGTGGCAATACGACTTCTCAAACGCACCTTCGCTTGGTTTCTGC
CGGCTGGTTGCAAGAGCGAAAGCGCAGACAAAATCGTATCGACTGCAGCGCCGTGCTTCTGCGCCACAAATTC

SEQ ID 7662

EQ ID 7662
MKKSLIALPLAALPVAAMADVTLYGAIKAGVQTYRSVEHTDGKVSQVETGSEIDFGSKIGFKGQEDLGNGLKAVWQLEQGASVAGTNTGWGNQSFVGLKGGFGTIRAGSLNSPLKMTGA
NVNAMESGKPTGNVLEISGMAQREHYLSVRYDSPEFAGPSGVSQYAPKDNSSGNGSEYHVLNWNQSGFFAQAAGLFPQRYGEGTKKIETDGTYSIPSLFVEKLQVHRLVGGYDNNALYV
SVAAQQQDAKLYGAMSGNSHNSQTEVAATAAYRFGNVTPRVSYAHGFKGTVDSANEDNTYDQVVVGAETDFSKRTSALYSAGWLQEGKGADKIVSTASAVVLRHKT

SEQ ID 7663

SEQ ID 7663

AACGGTGGCGGCAAAAGAGCGGGCATTTATCGCGCGTATTCCCTGCAAGACTTTGGTGCAATAGCTGGCAAAACCGAGAAAAATCATGATGATGGTTCCGCGAGGTTCCGTGGTTGACGACTTTGTGTGCAACAGTCTCTCCGCTGTTTGAAGAAGGCGACATCATTTATCGACGGCGCAATGCCAATTACCCCGACACGACACGGCGGACACATTACCTTGGCCGAAAAGGGATTTTGTTTGTTCGGCGGCGAGCGTATCGCGCGGCGAAGAGBGC GCGCGGCGCGGGCCGTCCATCATGCCGGCGGGGATTAAGCGCGCTTTGGGAAGCGGTCAAGCCGATTTTCCAGCGGATTGCGCGCAAAACCGCAGGGCGAACCGTGTTGCGACTGGGTTCGCAAGGATGGCGCGGACATTTTGTCAAAATGGTGCAACAACGGCATCGAATACGCGGATATGCAGCTGATTTCGGAAGCGTATACCGATTTATCGAAAGCGTATACCGATTTTTCGCGGCGTCTCTACGACGAAATGCACCCGCGTTTGCCGAGTGGAATAAAACCGAGCTGGATTCTATCTGATTGAAATCACAGCGCAATTTTGGGCTATAAGGACGTAAGGCGCGAATCCGTCGCGGAGAAAACTTCGATACGCGCGCAAAAGCGCAAGGCGTCCGAGCGGCGGCGCAAGCTGTTGCGCCGAAACCGCCACGCGCTCGAAGGCGGCAACAAAGATGGGTGAGGGCGTTGAGGCGAGCGTTTCCGCCGCTCCAAAATCATTTCTACGCACAAGGCTTTATGTTGATCCGCGAAGCGGGCGAAAGGTATACGCTGGGGTTTGGACTACGGCAACACTGCGCTGCTGTGGCGCGCAAGGCTGCATCATCCGCGAGCGGTTTTTGGGCAATATCCGCGACGGTATGAGGCGAATCCCGATTTGGTGTTCTTGGGTGCGGATCCGATTTTCAAAAATAATTTTGGAAAGCTGCTCCGCGCATCGGCGAAGGTGTTGCAAGGCGGTGCAATGCGGCATCCCTATGCCCTGCATGCTTCGGCGGATTACGCTTCCTGCTGATACGACGCAACCGCTGCTGCCAACCTCTTGACGGCACAGCGGAAGGTGTTGCAAGGCGGTGCAATGCGGCATCCCTATGCCCTGCATGCTTCGGCGGATTACGCTTCCTGCTGATACGACGCAACCGCTGCTGCCAACCTCTTGACGGCACAGCGGACTACTTCGCGCGCACACTTACGAGCGCCAGCAAAAGGCGGCGCAATTTTTCATPACCAACTGGACGGGCAAGGGCGGAGATACCGCTTCGCAACCTACGATATTGATTCCGCTGCGAAAATCGCTCCGAACCGTTTCGAGCGGCATTTGTTTTCGAGGAAATAGAAAGATGTTCCAATGGCTTTATGATGATTTGTTGGCTGCTTCGCGCGGATATGGATACGGCGTTATTTTGGACAACGCTTCGCGAAGTGCCCGGCGCAT

SEQ ID 7664

SEQ ID 7664
NGAAKETGIGAYSLQDLVDKLAKPRKIMMVVRAGSVVDDFVEQLPLLEEGDIIIDGGNANYPDTTRRTHYLACKGILFVGAGVSGGEGBARRGSPINPGDKRAWEAKPIFQALAAKT
PQGEPCDDVWGKDGAGHFVKMVHNGIEYGDMLICEAYQFMKDGGLGSYDEMHRVFAEWNKTELDSYLIEITAILGYKDEGGEPLAEKILDTAGQKGTGWKTGINALDLGIPLTLISEAV
FARCVSSEKQERQVTGKLFARTATPVEBGKQMEVLEARQALLASKIISYAQGFMILIREAGESYWGGLDYGNTALLWREGCIIRSAFLGNTRDAYEANPDLVFLGADPYFKNILENCLPAWR
KVVAKAVECGKIPMPCMASAITFLDGYTTERLPANLLQAQRDYFGAHTYERTDKPRGEFHTNWTGKGDDTASTTYDI*FRCRNAVTRVTRAFVLQIERCSNGFMICYGLRRYGYGVITW
NAPEVPRH

SEQ ID 7665

[illegible]

SEQ ID 7666

SEQ ID 7666
MFLNLAHFSNWLGLNIFQYTTFRVMAALATALFSLMFGPWIRRLTALKCGQAVRTDGPQTHLVKNGTPTMGSSLILTAITVSTLLWGNWANPYTIWLLGLVLLATGALGFYDWRKVYV
KDPNGVSAKFKMVKQSSVAVIAGLALFYLAANSANNILVVPFKQIALPLGVVGFVLVSYLTIIVGTSNAYNLTDGLDGLAAFPVVLVAGLALFAYVSGHYQPSQYLQLPYVAGANEVAIF
CTAMCGACIGFLMFNAYPAQVFMGDVGCALALGAALGTVAIVTRQEFVLVINGGLFVVEAVSVMLQVGWYKTKKRIFLMAPIH HHYBQKWKETQVVRFWITIVLVLIGLSTLKIR

SEQ ID 7667

SEQ ID 7667

TTGATTCCGTTGCCGAAATGCCGTCCGAACCGTTTCGACGGCATTTGTGTTTCAGGAAATAGAAAGATGTTCCAATGGCTTTATGATGATATTGTGGCTGCTTGGCCGATATGGATACGGC
GTTATTTTGGACAAACCGCTCCGAAGTGCCTCCCGCATACCGGGCGCATAGGGACGAGCGTTTCGGCAAGCCGCATCCGAATCCCGTTACCGGGCGGGTTGGATACACGCCGTTTCGGTTCGG
AGAAACGCGCTGACCCGCCCGCTTGATACGCGAGTTGCGGGCGCGTTTCCCGATGCGCGCTGCTGATGACGCAGATGACCCGACGGGACGGGAAACCGCGCAAGTTCTGTTTCCCGAT
GCGCAATGCCGCTATCTCTCGTATGACAAAAACGTTGGGTACGGCAGATTTTTCGCGCAACACCGCCCGATGTTTCGGCATTGATGAAACCGAAATCTGGCCCAATCTGATGAAGGAAT
GCCGGCGAGCGGGTGTGCGCGCTGTTTTTGGCGAATGCGGGCTGTCGGAAAAATCGCTGAACGGTTATCTGAAAGTCCGGCGCTGATCGTCCGCGACCGCGCTTCGCTGACGGGCTGTCT
GGCGCAGACGGAGCGGATGCGCGCGGTTTGGCGAAATTTGGCGCGCGCATTCGTCGAGGTGTGCGGGCAATACCAAAATACGACCTGATGCCGCTCTGAAGACATGAAAAAGCTTGGCGGGCGAG
TTTGAAAAACGCACTGACGGGCGCGCGCGTTTGCCGCTGTGCGGCAGCAGCGCGCTTTATCGGGCGAGAGCAGGCGGAAAAATCTGCTGGCGGGCTGGCAACAATATCGCGCGATGCCCTCG
TGGCGGCTCGTGCCGCGCATCCCGAGCATTTTCAGACGACATTTGAACAGGCGAAACGTTTCGGGTTTAAAGTCTCAGCGGCGCAGCGAGCTTTTCGCGCTGCAACCCGATACCGAGTGTG
GGTAGGCGCAGCATGTGGGCGAGCTGTATGCGTATTACCTGTGCGCGCGATGTGCTTTTGTTCGGCGCGAGCTTGTGCTGCTTGGCGCTTGGCGCTTGCAGAACATGCAACCGCTTTCCTCGCGCGTT
ACGACGATATTTCGGCTTTTCGACCTACAATTTTCCGAAGCTTCCGGCACCGCTTGGCATCGGTGCGTGGCTTCAAGTCGAATCGCGGACGCGTGGCGTGAAGCCGTTGAAAAAACCCT
TATCTCGCGAGCGGGCGGAAATGCAGATGCAGGCGCGCTGGACGGCTTTATCGCAACAACATCGCGAGCGGGCGCAGAAATCGCCGAGCGGTGCGGGAAGCGGATGCAGCAATCGGG
GCGA

SEQ ID 7668

SEQ ID 7668
LIPLPKCRPNKSDGICFAGNRKPMQWLYDVWLWLLAPTIWIRRYLDKRSGSPAPYRAHRDERFGKPHPNPVTGAVMIHAVSVGSETRAAQPLIRELRRRFPDAPLIMTQMTPTGRETAQVLPFD
AQCRYLPYDKKTVWRQFLREHRPMFGILMETEIVFNLMKBCRRAGVPLPLANARLSKSLNGCYLKVRRRLRPAASLTGCLAQTEADAARLAKLGAASVQVCNKTLYLMPSEDMKTLAQG
FEKRIIGRPFVAVCGSTRVTRGEDAEKLLALAWQQYRGDALLAVVPRHPEHFTTTFETAKRFGFKVQRRSDGLFVEPFDQVWVGDSMGLYAYTYLCAADVAVCGSLVSGGCGNLTLEPLSCGV
TTIFGPTSTYNFSEACREHALASGAAVQVESADAWREAVEKTLSGEGGGMQMRADVGLAQHRGAGARIAEAVREAVCGHRGR

SEQ ID 7669

SEQ ID 7669
TTGGGAAAGTCCCTGCACGTTAATCTGCAAAAGCCGTCCGAAACCTTGCCGGACAGCAAGCAAACCTCAAGCGGGCGCAAGCCCGATGTA

SEQ ID 7670

LGKSLHVNLOKPSETLPDSKQTSSGRKPDV

SEQ ID 7671

ATGACGCTTAACCGAATTGCGGTACATCGTCCGAGTCGCCCAAGAACGTCATTTCGGCGGGCGCGCGCGTGTGTTTGTGACGCCAGCCCACTTTGTCTATTGCCAATTAGAAGATTGGAAG
AAGACGCTTCGCGCTCTTTGTGTTGACCGGAGCAGCAACGATATTATTACGACCGGAGGCGGGGAACGTATCGTTGCACAGGCGCGTAAGGTATTGAAAGAGCGGGAGCTTATCAGGCATT
GGCAAAATGAAGAACAAAAACGAGCTGGAGGGTGCCTTCAAACTCGGGCTGATTTTACGGTTCGCGCATACCTGCTGCCGAAACTGATTGCTCGGTGCGCGCTACTGCACCGAAAAATGCGT
TTGATGTTGGAAGAGAATTACACGCTATCTTTGACCGAGTCGCTCAACCGCGGGAGCGTTGACGCGATTATCGTTGCCGAACCGGTTTCAAGAGCGGGGCATTGTTACCGAACCCCTTGATGAT
ACGAACCGGTTTTTCGTGATTGTCGCCGAAGGGCATTTCATTTGAGGAACCTGGATGCGGTTTTTCGCCCCGGATGCTGGGTGAGGAGCAGGTTTTCGCTGACGAGCGGCAACTGTATCGCGGA
TCAGGTACTCTCAAGCTGTTCCGAATTTGGCGCGAAACAGCGCATACAGGGCTGACCAATACATTTGACGCGGACCTGCATCAATACATCGCGGATGAGTGGTCGCCGAGGTTTGGCAATC
AGCGGTTGCGCGGCAACCGCGCTGACCGAGAACGATCATATGCTGTTACGATATTTCGTTTGAAGGTACGCGCGCAACCGCGCGGGTTCGATTGGCGGTATCGCGCGTAATTTTGTGCGTC
CGAAGGCGCTGTGTCGCGCATGAAGGCGGCGATTATGACAGTCGACGCTTCACGGGGTAAGTTTATCCACGAC

SEQ ID 7672

SEQ ID 7672

MTLTELRYIVAQAQZRHFGRAARRCFVSQPTLSTAIAKKEELAVSLFDRSSNDIITTEAGERIVAQAQKVKLKAELIKHLANEQEEQLEBAGFAKLGILFTVAPYLLPKLIVSLRRTAPKMP
LMLLEENYTHHTLTSLKRGDVAITVAEPFQEPGIVTPEPLYDEPPFVIVPKHGSFEELDAVSPRMLGEBQVLLITEGNCMRDQVLSSCSELAQKRIQGLTNTLQSSINTIREHVASGLAI
SVLPAPALTENDHLPISIIPFBGTPPSRVVLYARRNFVRPKALSAMKAATMQSLHGVSFTHD

SEQ ID 7673

SEQ ID 7673

TTGGAGCATCGTATGAGTATTTTATGCCGTCGGCCACATCATCCACTGTATTGCGCCACCGCCTTTGTCGGCGGCGTGTTTTTTGAAGTCTGGTTTTGTCGCTCTGCATACGGGACGGG
TGCTCGCGGAGCGCGCGCGAAGTGGAAAAAGGCAATGCTCTACCGCGCGCTCAGGGTGATGCCGTTTGCGGTCGGAGCTGCTGTTGCCAGCGGCATCGTGATGGCGGCAAAACCGCTACCT
TCTTATATCGGGCGAACCGCTTGGCACTTCCTTCGGCACAAATGCTGACGCTGAAAATCCTGTGGCGTTCAGCGTGTTGGCGCACTTGCCCATCGCGCTGCTCAAAATGGCGCGTTCACG
CTGACGGTCGGCTGGTCGAAATACATACAGCGCGTCGCTTTACCCATATGCTGCTGATTGTCTTTTGGCAAAACCGATGTTTTATATCAGCTGG

SEQ ID 7674

LEHRMSIYAVARI IHLYCATAFVGGVFFVLVLSVLHTGRVSRREARREVEKAMSYRAVRVMPFAGVLLFASGIVHAANRYLPISGEPFATSPGTMLTLLKTLAPSVLAHPAIAVVKHARST
LTVGHSKYTHAVVPTHMLLTIVFLAKAMFYIWS

SEQ ID 7675

SEQ ID 7675
GTGAAATGAAAGCCGACGTTTTTTAAAGCCTTATGCTGATTGCCGCGCTGGTCGGCGCGTTTTATGCCGGAATGGGACGCAGGCGTATCTTTATGAAGATTTATGTTTAGACTTG
CGCGCGGCAAAAAATCCGGGGAGCTACCCGATTTCGCGTATTGGGAAAGTCCCTGCACGT

SEQ ID 7676

VKMKSRFFKALLLIAALVGAFYAGMRTQAYLYEDLCCLDLGGGKNPGSYPICVIGKVPAR

SEQ ID 7677

SEQ ID 7677
ATGTCATTGATCGAACTTTTATTTCGGTAGAAAGCAGAAAAACGGCAACCGTTGCCCGCAGCGCGCTTCAATCATCATTTGCCCAAGAGCGCGCCCAAGAGGTCAGACTCCGGATTACCTGC
CGACTTTACGCTAAAGCTTTGATGGAAAGTCCTGTCCCAATATGTGAATGTTTCATTAGACAATATCCGTATTTCCCAAGAAAAGCAGGATGGTATGGATGTGCTTGAAGTTGAACATTACTTT
GCCCGAACAGAAAAAGGTA

SEQ ID 7678

MSIJEJFGRKOKTATVARDRL011IAOERA0EGOTPDYLPTRLKELMEVLSKYVNVSLDNIRISQEKQDGHVLELNTLPEQKVV

SEQ ID 7679

SEQ ID 7679

ATGGCTACAAAATGGGGGATTTTCTTTGTTCGCAAAAGAAAGAAAACGCTTTATCTTTGAAGGAGGCACTTCTGCCTCCGACAAACTGGTCAACGGCGAAGTATCCGCGTTTACCGAAGAAG
AGGCCTAAAAAATCTGGCAAAACCGCGCATCCGCCGCTGCAGATTACCCGCTGTAAACAAGCTCCAGCGCAAAATCACAAGAAGACATTACCGTTTTCACCCGCGCAGCTTTCCAC
GATGATTAAAGCGGGCTTGCCTGATCGAGGCATTTGAAATCGTGGCGCGCGGACACGGCAACCCGCTTATGACGGAAATGCTGATGGAAATCCGAGGCCAAAGTGGAAACAGGCGAGCTCG
TTGAGCCGCGCATTTCTCAAACCAACCGAANAATTTTCGACGCTTCTACTGCAACCTGGTTGCGGGGGCGAAACGGCGGGTGTATTGGAAAGCCTGCTGGACAAATTTGGCAATTTACAAGG
AAAAAACCCAGGCCATCCGCAAAAAGTAAAAACCGCGCTAACCTATCCGGTATCCGCTATCGCGCTGCCATCGGTTTGGTATTTCGTGATGATGATTTTCGTACTGCCCGCTTTAAAGA
AGTTTACGCCAATATGGGCGCGAGCTTCCCCCATGACCCAAACAGTATGATATGTCGACTTTTTCGTCTCATACGGCTGGATGGTGTCTGATGCACTGGGCTTTGCCATATACGGC
TTCCTTAAATTTGAAGGCGCGCTCGATTAAAAATCCAACGGCGTATGGATGCCATATGCTGCGTATGCCGATTTTCGGAGACATTGTCCGCAAGGGAGCAATGCCCGCTGGGCGAGACGA
CGGCAACGCTGTTTGC CGCGCGCGTGCCTTTGTGTCGATGTTATGGACTTCCATGCGCGCGCGCGCGCAATTTAATCTATGAAAGACCCCAACCGGAAATCGTATCGGCGCTATCCAAAG
TCTGTCTATGACTCGGGGATGCGTGGCAGGAACTGTTCCCAATATGATGTTGCAGATGCTCTCCATCGGCGAGGAATCGGGTTCCTTTGGAGCATATGCTCAACAAGCCGCGCAATTT
TACGAAGACGAGGTGGACAATCGGTCGCGAGGCTGTCCGCTATGATGGAGCGATTTATTTATTTGTGATTTTGGGCTTGGTCATCGGTACGCTTCTGGTGCCTATGTATCTGCCGCTGTCTCA
ACTTGGGCAACGTGGTCCGC

SEQ ID 7680

SEQ ID 7680
 MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAPTEEBARKKLAKRGIRPLQITRVKTSKKRKITQEDITVFTROLSTHMKAGLPLMQAFETVARGHGNPSMTFENLMEIRGQVEQGSS
 LSRAPSNHPKYFDRFYCNLVAAGEFGGVLESLLDKLAIYKEKQTAIRKKVTALTATPVSVIAVAIGLVFVMMIFVLPAPFKEVYANMGAEPLPLTQTVHDMSDFFVSYGHWLVIALGFAITG
 FLAKARSIKIQRRHDDAILLRWPIPGDIVRKGTAIRWGRTTATPLAAGVPLVDVLDSTAGAAGNLIYEATREIRTRVIQGLSNTSGMRATELPFNMMQLMSSIGEESSGLDDMLNKAAEF
 YEDEVINAVGRLSAMMEPTIIVILGLVIGTLLVAMYLPFLNGLNVVA

SEQ ID 7681

SEQ ID 7681

ATGCCGCTTCCACGACGAGAATTCGCGGTTTTTCAGACGGCATTTCCTCCATCCCGATATTGCTCAAAACAAACCGAAGCGTTTGCTATAATTGCACTTTTTTACCGCACACGACGCCCCATGTTTC
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CTTGAACCGTTTGGCCGCAITTCGCAAAACCGAATTCGACGACACCTTCCCGCTTCAAGAAAATTCGAAGAAATCAAAAACACCGTTGCCGAAAATCAGGTACGATTATCTGCGGGCGAA
ACCGGTTGGGGCAAAACACGCGATTTGCCAAGATTGTTTTGAACCTCGGGCGTGGGGCGGCAGGATTGATCGGCATACCCAGCCGCGCGGTTTGGCCGCGCGGTCGTTGGCGGGAGCGGA
TTGCCGAAGAGCTGAAAATCCGAAATCGGCAGCGCGGTCGGCTATAAAGTGGCGTTTACCCGACACACCTCCGCGGATGCTCGCTGATGACCGACGCGCATCTCTGTCGGCGGAAAC
CCGAGCCGACCTTTATCTTCGCGCGCGACGAGATATATCATTTGACGAAGCGCATGAACGACGCGCTGAACATFCAGTACTTCTCTTGGGCTACTTAAAAACAACTCCTGCGCGCGCCCGCGAT
TTGAAAGTCATCATCATCATCAGCCACCTAGACGACGACAGCTTCTCCCGACACTTCAACGGCGCGCCGCTACTGGAAGTGAGCGGGCGCACCTATCCCGTGAAATCTCTTACCGACCGC
TGACCGGCAAGACGAAGACGACGACGAGAAGTCGAGCTGACCGACGCGAATTGTCTGATGTCGCGCGCAGAAATGGCAGCTTACGGCGAAGCGGATATTTAGTATTCTTCCGCGGGCGAACGCGA
AATCCGCGAAGCGCGCAGAAGCCCTCGCGAAATCCACACTGCGCGCGCAATGACGAAATCTCTGCCCTGTTTGCAGCGCTGTGCGACGCGCGAACGACGACAAAATCTTCCACCTTTCAGGCGCA
AATGCGCGCATCTGCTCTGGCGACCAACGTCGCGGAAACCTCGCTACCGTGCCGGGCGATCAAAATACGCTCATCGACACCGGCTTCGCGCGCTCAAAACGCTTATTCGCGCGCGCAAAAGTCG
AACCACTTTCAGCTAGAAAAATCTCCCAAGCGCGCGCCCGCAACGCTTCGCGCGCTCGGACGCGCTCTCAGCAGCGTGTGTATCCGACTGTTTTTTCAGAAGAGATTTTAAACAGCCGTCG
CGAATTTACCGATCCGAAATCTTCCGACGACCACTTCGCGCGCGCTCATCTGCGCATGCACTGCTGAGTATGGCGAGCGATGACGATCTCCGCTTTTGAAGATGCCGATTTCGCGATAT
ATCAATGACGCTTTCTCAGGTTGTGCTGGAATTTGGGGCAGTGGAGGTTGTC

SEQ ID 7682

SEQ ID 7682

MPSEQRQNAVVRHPPPTILLKQNRVCVNCFFYRTRTPMFPDFSQTLKSDRHFLQSAFKNPNKYGLSKIEEKYRKSHEIFLKRLLAALPKPEPDDTLVPEHKELEEIKKTVAEQVVTIICGE
TGSGRTPTLQKICLZELGGAAGLIGHTOPRRLLAARSVAERIAEELKSEIGSAVGKYVRFTDHTSRDCAVKLMTDGIILAEQTDTRYLAAYDTIIDEAHERSLNIDFLGYLKQLPRRPD

LKVIITSATIDAERFSRHFNGAPVLEVSRTYPVEILYRPLTGKDEDDAEVELTDAIVDADELARYGBGDLVFLPGEREIREAAALRKSTLRRNDEILPLPARLSHAEQHKIPHPSGA
KCRIVLATNVAETSLTVPGIKYVIDTGLARVKYSARAKVEQLHVEKISQAAARQSRGCRVSAGVCLRFSBEDFNSRPEFTDPEIVRSNLAAVILRMASLNLGDDVAAPFPLEMPDSRY
INDGFQVLELGAVEVV

SEQ ID 7683

TTGATGGGAAATGCCGCTCGAAAGGCTTCAGGCGGCATTTTGTATTGGGCATTGGGTAAATGTCTTTAGAAAAGATATTGCAAAATTTAAAAATCCCGGTGTTCTATTCTGCTT
TCTTACGCTATTCTTTAAAGGTGGGAATCTGGAAACCAAAAAACAACAGGAATTTATCCGAAACAACAAACCTATCCGCGCTCATCCCAAGCGGGAATCTAGTTTGTGTTCAA
A

SEQ ID 7684

LMGKCRLLGFRHRFCLWALGKMSLEKNIANLKNPRVLISAPLRHSPKGNLTKKQEFIRNNKTYPPSPRKRESSLLFK

SEQ ID 7685

GGAGATTGAACCATGACAGAATATCCCGCATCGGGTCGCGGTGTTTTACGGCGTTTTTTTTGCGCGCAGTGTGCTCATGATTGCCCTGGATATGTTTTTCGTGAAGAAAAACGGCAGCC
ATAAAGTCGGCATCAAGAAAACTTTGGCATGGAGCGGCTGTGGGTTCGCGTATCTCGCTGTTTCGAGAGCTGGCTGTATTTCGAACCTCCCGCGCAATCCCGCTACGGCGCGGCGAGCGC
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CGCGTGTCTGTACGGCGTATTGGCGCATTTGGTATTGGCGACCGTCATGATTTTCGTGGCGCGGCACTGGTTCCGCGAGTTGAGTGGATTCTGTATCTGTTTGGCGCGTTCTGCTCT
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TGAGTTTTATCGGTGAGAAATGCTGGTAAATGATTTGGTGTGAT

SEQ ID 7686

GD*TMTEYPIGSPFYGVFFAAVLVMIALDMFLSKKNGSHKVGIKETLANSGLWVAVSCLFAGWLYFELAGNPGYGAAAAKEKVLFFPTGYILEKSLAVDNIPVFLMIFGYFKVAPQPH
RVLLYGLVGLVLRVMI FVGAALVRQFEWILYLFAGFLLYTG IHEMKPBGDEKEDLANSRLNNAVKVVPVGTETPHGEKFTTVENGKKIATPLFLVLVMIELSDVVFVAVDSIPAVFAVTT
DPFIVLTSNIFAILGLRAMYFLLADVAERFIFLKYGLAFVLSFIVKMLVMHNVH

SEQ ID 7687

GTGTTTTACACAGCAAAACAGGCGATAAAAAATCAGCGCTACCGATGTGTCCGCCGCCGAATATTAAAGCAAGCAATATGAAACCACTGGACCTAAATTTATCTGCGCAAGCCCTC
AAGCTCCGATGCCGTC

SEQ ID 7688

VFYHSKYGDKKISRYCVRPNINESKYETTGPKFHLPSQASDAV

SEQ ID 7689

GTGGCAAAATATTGTAGTAACCTCAGGCAAGGGCGGTGTGCGTAAAAACGACTACAGTGAAGTATTGCAACAGGTTTGGCATTTACGCGGATATAAACTCGCGTAAATGATTGATG
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AAAACCTGTTTATTGTCGCGCTTCCGAGATCCGAGATTAAGACGCTTTGACACCGGAGGCGGTAGAAAAAGTGAATGCAGGAGCTGTCCGGCAAGAAAAATGGGCTTTAGATATATTATTGTC
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GTTATTGCCCGCTTTTGGGCGAGAACCGTGAAATGCGTTTCTTGAAGCTGAGAAAAAAGCTTCTCAAACGCTCTGTTCCGAGGA

SEQ ID 7690

VAKIIVTSKGGVGKTTTSASIALGLALRGYKTAVIDFDVGLRNLDLIMGCERRVVDLINVIGQBATLQALIKDKNCENLFLIPASQTRDKDALTRGVKVMQELSGKKMGFEYIIC
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VIARLLGENREMRFLBAEKKSFKRLFGG

SEQ ID 7691

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TAAA

SEQ ID 7692

MTEYPIGSPFYGVFFAAVLVMIALDMFLSKKNGSHKVGIKETLANSGLWVAVSCLFAGWLYFELAGNPGYGAAAAKEKVLFFPTGYILEKSLAVDNIPVFLMIFGYFKVAPQPHRVLL
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SEQ ID 7693

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SEQ ID 7694

MPSENKPVSRIVTDSRDIRBGDVFALAGGRFADHDFVGVLVSAGAAVVSREDCAALGGLKVDVDTLAAQLTAKAWRDVNPFPVGTGSGGKTVKEMLAALVLRFPDGDVAVSATAG
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KPLSCFDFLVCGDERTAVVLPVPRHNVHNAALALALAGLSLNDVABGLQGFSSNIKGRILNVKAGIKGATLIDDTYNANPDSMTAAVDVLARMPAPRIIPVMDMGEDEDEAAAMHAEV
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SEQ ID 7695

TTGCGCGGTAAACTTACATCAITAAAAAATTCATGATGGTTTATATAATGAATGCCCTTCGATATAAAGTCGACAAAGATGGACGTATGTCTATATCTTTGCATACATCAGACTTGTTCG
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CTGGGTGAGTTGAGTGCAGAAAAACGAGGATGGTCAGAAAGCAAGGAAACAGTATTGATTACATCCCTGTCCGTACCGGTGAGCAGGTTTATGCCGAAGATGGCGATTGATTGTTA
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SEQ ID 7696

LRGKLSLFLNSMVMYDINADIKSTKMDVLSISLHSDLFLEDLVLKLGKFKQESGVVFFVLDVQEFDPYPSLDLALVSLFSRHGMQILGLKHSNERHAAMVAMKYLFLCLSHSENVKE
LGQVEVQKTEDQKARKTVLITSVPTGQVYAEDGLIVTGAVSQGAELLDGNMHIYAPMRGRALAGAKGDT SARIP IHSMQAELVSVAGTYRNFEDLDLHLKQPVQILLQDNRLVI
SAIGSE

SEQ ID 7697

GTCCGTGAGACGAGCGACTTTTAATCCGTTGGTTCGAGCGTTCGAATCGCTCAGACCCACAGATAAAGCAAAAAAGCTGAGTTTCAAACTCGGCTTTTGTCTTCCGACAATCCTT
GTTCCGAAAGCGCGCATTTCCGTCAA

SEQ ID 7698

VGRAADF*SVGRAPESL/THQIKQS*VFKTRFLSSDNPCSESAAPRQ

SEQ ID 7699

TTGAATTTGGTGCACAAACCGGCTGCTGAGTAATTTTATGTCATATAACGCCATCTGCCGAAAAGCAGGTGGCTTATTTTGCATATCTGATAGATAATATGGTATTGGCTATCATGTTTA
AAATATTAATTGAA

SEQ ID 7700

LNWL/NRLLSNFSHITSAEKQVALFLQYLIDNHVLAIMFKILIE

SEQ ID 7701

AAACTCGGCTTTTGTCTTCCGACAATCCTTGTTCGAAAAGCGCGCATTTCTGCAAAATCTTTGGTGGCGCTTCCGTATTTTCCGAAAAATCCCTTATAATTCGCCCTCTGCAACCT
TCATCGGGTATGCTTTATGCGTTTCCGAGTATGAAATATTTATAGTGGATTAACAA

SEQ ID 7702

KLGPFCILPTLLVRKARHVPKFGAAVFFPKIPYNSASATFIG*CFMRCPEY*NIIVD*Q

SEQ ID 7703

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CGCAGACTTTGGGGCTGCCGGGAGCGGAACATAACATTTGTCAGCTTTGCGAAGCAGCGCGGTTTTCGAGCGCGTGGCTGTCTAATCAAGGAATGTTGGGCGATTTCGCAACGAAAT
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SEQ ID 7704

HKQSARIKMDQTLKNTLGICALIAPCFGAALASGVHLEYEYGYTRYSAVGALASVVFLLLLRGFPVRSVVLLIYVGTALYLPVGMNLYGAPSYQIVGSILSNPAEAREFVGNLPGSLY
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RSDYMNVYGFPLPDTFFLSRTKGLLINGYQSTAHATNLSLPQTGLPGEPNNINISLAKQAGFRATWLSNQMLGHFANEISTYALRSYDYPWFQRGDYKGSAGLSRDLPLPAFKRVLTGN
AGTKPRLIVMHLGMSHDFCTRLDKDARRFYQTEKISCVYSTIAQTDKFLBDFVTKLLNENKESWSLVYFSDHGLMHVKGGERITLTHGEWRQSYGVPLVLKISDDTTRREMKVRRSAFN
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SEQ ID 7705

ATGCGTCATGTAATGGCAATTCGCAAAATAACCGTACACGAGTCATGCTGCTCAATGCTGCGTAATATGGCGAATTCATTATTGACTACGAAACTATTGTAACAACTCTGCCAAGG
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CGATTGGGTCCTCGTTTACTGCTGTAACGCTGTTATGTTGAGTGTGAAATACGAGTATCCGTAAGGTTGATAATGCACCTCTGGCACTGCTGTAATTTGATTGACAAACCGGCTGCT
GAG

SEQ ID 7706

MHRHNGRKLNRNTSSRAAMLRNMANSLTHETIVTTLPAKELRRVVEPLITLKGKPSLASRRLAPDRTRDRDVVVKLFGDLGPRFTARNGGYVRVLKYGPRKGDNAPLALVELVDKPA
E

SEQ ID 7707

GTGGATAAATCGAAATCTCCGCAACCGGCCGCTCAACGGGAAATAACGGTCTCGGGCGGAAAAACCGCGCATTCGCGCTGATGTGCGCGGTTTGTGACATCGGGTACGTTGCGCC
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GTCAAGGCGACGGATTTCGCTGCGCTCCGCAAGCCTCGTTATCGCCGGTTTGGCGGCGCGCGCGAAACCGTGGTCGAACAGATTACCACTTGGATCGCGGTTATGAAANTATTGAAAAAA
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SEQ ID 7708

VDKLKSANGPLNGEITVSGAKNAALPLMCAGLLTSGTFLRLKNVPMFLADVTTQKLLQGMGARVLTDNISFEFENGGTVNNTCAPYELVTRASTLVLGPTLARFGEAQVSLPGGCAIGS
RPVDQHLKGLGEAMGAETVIEHYGVKAKGKLGTRVAMDVVTVGGTENLLMAATLAEGTTVLENCAIEPEVVDLAELCNKMGAKISGIGTSTMIVBGVDELHGCEHSVVPDRIEAGTFLCAV
AITGGRVVLNRNAAPKTMEVVLDKLVRAGAVIEAGDDWIAIDMRQPKAVDIRTVVHPGFPPTDMAQFMALNAVAEGSCRVETIFENRFMHVPELNRMGANITTEGNTAFVQGVRLSGAV
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SEQ ID 7709

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SEQ ID 7710

MNQNSTEFLKPRQIDVMTFSATRAKVSQMPPFERGPGHTLGNALRRLLSSMNGFAPTEVAIAGVLHEYSTVGGVQEDVDVDDLNLTKIGTVFKLHGSRQVQVLVKSGSGVVSAGDIELPHDV
 EILNPGHVICHILADNGQIEMEIKVEQGRGVQSVSGRQVRDENRQIGAIQLDASPSISRVSFEVEPARVEQRTDLDKLWLDITFDGSDIDPEEAVRSAARILIDQMSIFADLQGTVPVEVE
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SEQ ID 7711

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ACATC

SEQ ID 7712

IHTYSTH*ERTINVDKLKISANGPLNGEITVSGAKNAALPLMCAGLITSGTIRLRKNVPLADVTKTQKLLQGMGARVLTDNISEFEINGGTVNNTCAPYELVTRMRASILVLPGLTARFGEA
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 DRIEAGTFLCAVAITGGRVVLRNAAPKTMENVLDKLVEAGAVIEAGDDWIAIDMRQPKAVDIRTVVHGPFTDMQAQPMALNAVABGSCRVVETIFENRPFMEVPELNRMGANITTEGNTA
 FVOGVERLSGAVVKATDLRASASLVIAGLAARGETVVEQIYH

SEQ ID 7713

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GGGACGGCTTGTGTTATGATAAA

SEQ ID 7714

MFPSKLSPLAETGIPILSCANAGRLHSDSRQIKQGDIFVACPGEYADGRSYIPAAVANGAAFPVWDDGRFAMNPWKVPNQGIKDLKRAGILAAQVYGVNSDGLKXVNGVITGNGKTSI
TQWLAQAADDLGEKTAITGVTVNGFWGALETAHTTAPAVDVQITLYLRFQRQAGATAAMEVSSHGLDQSRVNGVPFRPSAIFTNLTFRDHLVDYHGTMTEAYGAIKSRLPFYWHGLKHAVINTDQ
YGAELAGRLKKDCPDLAUVSYGFSSEHDIRITDFTASSDGHNAVQTPWGGKCRTRLLGRFRNAQNLAACIALICANGYPLDKVLDVLAKIRPASGRMDCIMNSGKPLVVVDYAHTPDALE
KALSTLQEIKPQGAALNCVFCGGRNDCGRKPLWGAAGVQADKVVVTSNPRLENPHDIINDILPAPAPCEVADRAAAIRYAVEQAAANDIILIAGKGHENYQDVQGVKHRFSDLETV
GQALVTRK

SEQ ID 7715

ATGGCCAGCTGTATATTGGCCCTAAATGTAAGTGGCCACGTGCGAAGGTACGCGATTGTGTTTTGAAGAGTGC GCGCCGCTCTTTGGATTCTAAATGTAAATGATTCCGCTCCCGGTGAGC
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CCGTAAAGGTTTACTGCGCGAGTTCTGTGTCAGTTGCTGGAATCTCGTTTGATATAAGTCGTTTATCGATGCGGTTTCCGGTTTCTACCCGAGCTGAAGCAAGACAGCTGTTTCTCATAG
GCTATAGTTGTAATGGACAAGTTGTCAATATCTCTCTTCCAACTGAAAGCTGGTGATGTTGCTCTCAGTTCTGTAAAAAGCCAAAAACAGGTACGTATTCAAGAAGCATTGGGTTTGG
CAACTCAAACTCGGCTTGCCGGGTTGGGTTCTGTAGATGTCAGATAAACTTGAGGGTGTTGTTCAAAAAATGCCGGATCGCTCTGAATTGACCGGTGATATTATGAACAGCTCGTGTGTA
CTTCTACTCTCAA

SEQ ID 7716

MARYTGPCKLARRREGFDLFLKSARRSLDKCKDISAPGQHGAKKPRLSDVGLQLREKQKTRRIVGLERQFRRYFAEADRRKGSGTGELLQLLESRLDNVVYRMFGSGSTRAEARQLVSHK
 AITVNGGOVWNPSPFOVKGADVVSUREAKKQVRIQEALGLATOIGLPGHVSVDADKLBGVFKNMPDRSELTDINEOLVVEPYSK

SEQ ID 7717

ATGCCGCTCGAAGCCTTCAGACGGCATCAATTGTTTCTGTATCGCAAACACCGATTAAAAAGGACGTATTATGGCAATTTTAAAACTGACCGAACAAAACGTGCAGGGCAAAACCGTCTC
ATCCGCGCCGATATGAACGTGCCGTTCAAAGACGGCAAAATCAGCGACGACACCGGTATCCGCGCTCGATTGCGTCCGT

SEQ ID 7718

MPSEAFRRHQLFLYRKHRLKRTDYGIFKTRTKRAGONRPHPRRYERAVQRQRNRRHPYRLDCVR

SEQ ID 7719

ATGGCTAAAGCAACACAGCTTCACGTGTACGTAAAAAGTACGTAAAAACCGTGAGTGAGGGTATTGTGCAAGCTTCATGCATCTTTCAACAATACCATCATTACAATCACTGACCGTCAAG
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GGTTGCGTCCGCTTAAAAACGTCTATT

SEQ ID 7720

MAKANTASRVRRKVRKTIVSEIVHVASFNNTIITITDRQGNALSWATSGAGFKGSRKSTPPAAQVAAEAAGKVAQYEVGNLEVRKPGPGRESSVRNALNLFKITITSITDVTPLPHN
GCRPFKKRI

SEQ ID 7721

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TCGACCAACTCATCGTCCGCGCGCATTCGCCAACACCTTCTGTGTCGAGAAGCAAGCCATCGGCAAAATCTTGGCGGAACACGATTGTTGGGAAGAAATCCAAAAAATATGCGGAA
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CGGTTCTTGTGATTCTTGAAGGCAAGAGCTGCTGCGGTAGCTGCTTTGGAACAAACGCGCGCG

SEQ ID 7722

VINGASVIVMTHLGRPTGEFHPEDDVAPVAHLGSLGKDVKVLNDWRENKPALNAGDVMVLQNVRLNKGKNDLELGKAYASLDFVNDAPGTAHRAQASTEVAQAAPVACAGVLH
AGELDALGKALKQPARPMVAIVAGSKVSTKLITLESADKVDQLIVGGIANPFLAEGKAIGKSLAEDHIVERSKKIMAKHAAGGSVPLTDVWVAKAPADAABAVKDIADVAEDHI
LDIGPKSAALADLLKAAADTVVWNGFVGVEFDQFAGGTALABATAQSKAFSLAGGDTLAAIAKFGVTEQIGYISTGGGAFLEFLGKELPAVALEKRG

SEQ ID 7723

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GACGGAGTCCCTGTTTTCGCGCTTAAAGATATGAAGAAATCGGCTTCGCGCCCAATTTGGAACGCTGTCCGAGCTTGTGATGTCGCGGTCGATGTTTGGAGAACAACTCGAACG
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GCAACTCTTTGACACACGTCATCGATTACCGATATTGACGCGCAAGGTCAGGAAGGTTTGAACCTTTGCGCTTGAAGACAGCCTGTATGGCGAAGCGCGGAAAGTTTTCGCGGA
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CGCAGCGCTCAAAACACCGCT

SEQ ID 7724

MLPKEBQVKPMTISNGRISFVLMAMAVLFACLIRGLYLQVTYTNFLKEQDNIRVTRQALPATRGTVSDRNGAVLALSAPTESLFAVPKDKMEMPAAQLERLSELVDVVDVLRNKLQ
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KAVEYHQAAGTVVWLDARTGEILALANTPAYDPNRPGRADSEORNRNAVITMLPEGSAIKFPFVIAKALDAGKTDLNERLNTQPKIGPSFVRDTHVYPSLDVRGIMKSNVGTSKLSA
RFGAEEYDYFHELIGIVRMHSGFPGETAGLLNRWRPIEQATMSFGYGLQLSLQLARAYTALTHDGVLLPLSFEKQAVAPQGRKIPKESTAREVRNLMSVTPFGGTGATGAVDGF
VGAKTGTARFVNGRYADNKHVATFIFGPAKNPRVIVAVTIDEPTAHGYGVGAVGPPFKKMGSLNLIGISPTKPLTAAAVTTPS

SEQ ID 7725

ATGGCTCGTATTGACAGGGTAAATATCCCTAATAACGCACACATCGTAATTGGTCTTACGGCTATTTCAGGTATTGGTCTACTCGTCTAAATGATTGTTGAGGCTGCAAAATTTGCCG
CTGATATAAGCAAAAGATTGGACGAGACTCAATTAGATGCTTTGCGTGATCAAGTTGCCAAGTATGAAGTAGAAGGTGATTTCGCTGCTGAAGTAACTATGATGATCAACAGATTGAT
GGACATGGGCTGCTATCTGCTGCTTCCGTCACTCGCGGCTTACCATGCGCGGCTCAACGCACCTGCTACAAATGCGCTACTCGCAAGGTTCCGCTTAAAGCATTTGCTGTAAGAAA

SEQ ID 7726

MARIAGVNPNNHIVIGLQAITGIGATRKLICEAANIAPDTAKDLDETQLDALRDQVAKYVEGDLRREVMSIKRLMDGCTYRFRHRRGLPCRQRTETNARTKRGPRKAIAGKK

SEQ ID 7727

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TAACGATGATTTTATGACAAATAAATTCGTATAGGCTTACTCAACAGTATGTAAGTTAATGACTCGTTCAGAAATGAATCATTTTCTCGGAA

SEQ ID 7728

VANQOTSSGSSKFGDLKRLLFLPGALIVFRIGAHIPVPGVDAVALAKLYESAGNGILILNMFSGGSLERPSIFAIGIMPYISASIIIVQLASKILPSLKALKKEGACRKVITKYTRYGT
VLLAILQLSLGVASFVPOQGIIVTSSFEHVSTVSVLTGTMLFIMWLEQIETRGIINGISLIIITAGIASGIPSGIAKLVITLWQGSMSMLTALLIVFGALLIILYLVVYFESQQRKIPIHTA
KROPNRAGSQSTHMPFKIIMAGVIPPPIPASSIILFPSTLLGWFGSADTNSVLEKIALGLLQHGQLLYMALFAATVIFPCYFYTALVSPKEMAENLKSAGFVPGIRPGQTSRYLEKVVIL
RLTLFGAFYITITICLPEFLITLNVPPYLGSTSLILLVVIMDSTQINSYRLTQQYDKLMTREMKSPSRK

SEQ ID 7729

TTGGGCAGCATCCGGGGCTTATATCGCTTTAATCAACATTTTACTTCTCGTTATTATTATCTCGATGCAGGAATCCGATCCGGGCACACAGGCTGCTTCTATCTT

SEQ ID 7730

IGSIRGLYSILLINIFTSRYYPDAGIRFRHTGCFYL

SEQ ID 7731

TTGTGCTTTGGCAGCCCATCTCTGCCGGTGTAGCGGTACCGAAATGGAAAGTGCCTGCAGTTCGTGCTTTCCAGTTGGGCTTTGAGTCCGCTTTAATCAGGCGGTGGCGCGCAGGCGT
GCCTTGCCTTCAAAITCTGATGAAACGATGACGGCGAAAAAATGGTCCGCTCTACTTCGATGTGTGCAATTTGCCACGCCAGCAATCAGGGCTTGAATTTGTCGGGTGTCA
GCAT

SEQ ID 7732

LCFGSPFCRCSSGRNGKCVQFVAPQLGFESVFNQAVAREACIAFKF*NDDEKMNVSVAFYFDVAFCHASNQGLDLFGCDH

SEQ ID 7733

ATGTTTTTGAATACAATCAACCTGCTGTGTGCTACCGATGCTGGTCTGCTGTGGACGCGGTATTGGTAGTGGTCTTGGCAAAACGGGTGGTGTGTCATAAAGGTCAAAGAGCC
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ACTGGAATCAATGCTGTTAATGAGATTGATATTTAGTCTTAAAGCAAGAGGCTGATTCATCTACAGTCTCTAATGTTAAAGTTATTGCTTCTGGTGAAATTTCTAAGGCAGTTGCT
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SEQ ID 7734

MFLNTIQPAVGATHAGRRVGRGIGSLGKTGGRGHKGQKSRSGGFHKVGFEGGQMPQLRRLPKRGFKSLTVSANAQLRLSELESIAVNEIDILVLKQAGLIASTVSNVKVLAISGEISKAVA
LKGIKVTKGARAALIEDVGGKIM

SEQ ID 7735

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GACTACTATGATGTTGATTATAAATAATATGCGGATATGCT

SEQ ID 7736

MTVFRCCNWNQWRLSENRIQIRLCPTTLLSLLGINVTMIKEFMSNYTNHPVLFIGTGMSLYLNDNSYTWDLGSKIAIDLPGDDREYLNISKRYCEDGRFOYEELAEELQSKFKVLE
NDPDRFKPKINDKPFENMRAGNTLSRFKIYISTLLSQLNKDINSNTLSELKARKNVGSIITPNYDKLAQDIFEFNPLIGNDILLSNPFYGVYKIHGCVDDPSKLIITKKDYKFKPKYB
LIRAQLLSLFIHNPIIFLGVNVDENIKELKTIPTVYBQNSPANKIRNPLIVEYEPESNNEDIVEDHIDIITGFTIRINKIKTDNFSQIKALAEILPLISAMDVRFQSIKAEITYG
GNIKVSTPEMDNLNNSDKVVAIGSTKPTISYNFTTSEMSNYFKIIEBENSQLLKLDKHSIASTQYPPITYGFSRICSDIHKAEVLKROQKEKLHPIIBEINRCKNNHSSIQSILDDEN
ISDTYKNDIAWGIWNNQLSEDEVENYLNKFNKNTNHYKRLLCMFYDKYADTV

SEQ ID 7737

TTGAGTCCGGAGGAATGTGATGAGTATCCAATCCGGCGAAATTTTGAAGACCGTCAAAATGGTTGCCGACCAAGATTTTGATGTCCGCACCAATACCATCGGCATTGATTGCACGAGTCA
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SEQ ID 7738

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FSALVQKMSPSDEVILRSVPBAMKTTDIVCSSINIGSTRAGINMDAVKLAGETIKRTAEITPEPGCAKIVVFCNAVEDNPFMAGAFHSGGEADAVINVGVSGPVVKAALENSADVSLT
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SEQ ID 7739

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SEQ ID 7740

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SEQ ID 7741

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SEQ ID 7742

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SEQ ID 7743

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CATAACGACCAATTTTATGATTTTCAACGGGCGTTTGGCCATCTTGAAGAAGTAGGGCGTTATCCCTGCGAGAAGGTGCAACATTCGCAATCGTCCCTCGTAATATGTCTTTAA
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SEQ ID 7744

LGMENGFPKIMAGHODETFMHSACGLSDINLKLALIPKNGNRLAFAHIPBLQLECFIKGDNKFDTFGRLLWMDKPAPTTTTKPFPSISNGRFAHPERDRALSLRREGATLQSPFRNYVFK
AGSRDKIARLIGNAVPPMYTEKIGRAIVDNIEC

SEQ ID 7745

ATGAACAAATCGAATTTCTTTCTGCTGCTTGGCGTGTGCGTTCCGCTTTTTCCTGTTGTGATGCAGCAAAACAGTACAGGCTCAACTTCACAGCTTTGGACAAGCGCAAAAAACAGGAA
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TATGTTGAACATCAAGA

SEQ ID 7746

MNKSNTPLLLAVCSAFSVVMQNNYRLNFTALDKAKKQETALEQDYAQMRLQOARLANHEAIRAAEKQNLHPVSGNTFVHEHQ

SEQ ID 7747

ATGGCTGAACAAAAAAGATTAGGGTTACATTTGGTTAAAGCCTGATTGGTACAAATTTGAATCTCATCGTCATGTGCACGCGGTTTAGGTTTCCGTCGTCGCGAGCATACGGTAGAGGTTT
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SEQ ID 7748

MABQKKIRVTLVKSIGTIESHRACARGLGLRRREHTVEVLDTSENRMINKISYLLKVES

SEQ ID 7749

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SEQ ID 7750

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SEQ ID 7751

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AGGATAATAATAACGAGAAGTAAAAATGTTGAT

SEQ ID 7752

VWRSGLPVRYRNNREKRLNGNEQIEFLSAACGVFRFRFCDAAPVQAQLHSPFGQEKTNRLGAGLCANEATGAFGESRSQGGGRKTPPSAGFYQYLYGTSKIEAACVPESDSCI
RIIITRSKNVD

SEQ ID 7753

ATGCTGCGCAGTTAACCGTGAACCAAGTAGTTAAAGGTGGTGCATATATGGCTTTCTCTCGCTAACGTGTGTTGGTATGAGATGGTGTATGTTGGTAAAGGTAAAGTCAAAAG
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TATGACGCTGCTAAAGAGGTTAGTGGCTTAAAGCCGTTGAGCTATGCGTTTGGTTTATGCTATGGGCATTATAATATTCCGCCAAAGTGCAGGATCTACTAACCCATATAAT
ATCGTACGTGCAACATTAGATGTTGTCTAAGTTGCATACCTCTGATATCGCAGCAAAACGTGGCTTGACAGTGAAGACATTTTGGGAGTTAACCATGGC

SEQ ID 7754

MVAVNRVTKVVKGRIDAFSALTIVVGDGDRIGMKGKSKEVPVAVQKAMDQARRSMIKVPLKNGTIHHEVIGRHGATKVFMPAKEGSGVKAGGPMRLVFDAMGIIHMSAKVHSGTNPYN
IVRATLDGLSKLHTPADLAARKGLTVEDILGVNHG

SEQ ID 7755

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CGGATCGTCCATTTCTGCTCTTTCAGGCGGACTTTTCGATGGCGATGCGGGCAGCTCTTCGCTTTTTCGCGCGGATAGCCGATAATCCGAAGCGGAGGATGACGTTTTCGAGGAC
GTTGCGGTCGTAGAGGATTTTGTGCTTTTGAACACGATGCCGATGTTTGGCGCATAAAGCCGATTTGGTTTTCGGAACAATGTGCCGAGATCTTCCCGTTAAACAGGATTTTGGCCCTG
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SEQ ID 7756

CESSFRQAQDAVSVVRHQGFVMCGDDGCSRFEVGEQFENIERVGAIVEVGGFVGNQAGLVNDGAGDAQALLFTAGEGYGVVQSSQADFFDAGTLFGFARRIADNPKRQDDVLQD
VAVVEDFVLEHDAVDLVAHKADLVVQGCAEILPVKQDFAPARLDARNQLEDGGFARTGVSRRDKYHFAVDLEADVQGFKTAGIGFNLFTEDHRRSCKEGRHIVSGGCVRRMDPSEQ

SEQ ID 7757

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SEQ ID 7758

MDKHPTLRRLRRARRIADLKMVRLCVFRSNHIIYAQVISABGDKVLAQASTLEAEVRGSLKSGSNVEAAIIVGKRIAEKAKAAGVEKVPFDRSGFOYHGRVKALAEARENLSP

SEQ ID 7759

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SEQ ID 7760

VSGAESYKHITVLLINEAVDALAVREDGVYVDGTFGRGGHSLILSLRIGDAGRILIVFDKDPQAIJVAEELARSDKRVGVVHGGFASFQALDGLIGIKVDGALFDLGLSSPDIDGSRGFSF
RFDAPLDMRMDTRGMSAAEWIAVASEQDLHEVIKNYGEERFSRQIVRAIIVQRAESPIDTRKLAQIVQNVTRERQDPATRTFQAIRIFINRELEEVGAVLPQVMCRLEKGGRLAVI
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SEQ ID 7761

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SEQ ID 7762

MSRVAKNVTVTPAGVEVKFTEALVIKNGKNGSLPLHSDVAIEFNDGKLTFFVANNSSKQANAMSGTARALVSNMVKVSEGFKKLQLMGVGYRAQAQKILNLSLGFSPHPIVYEMPEGV
SVQTPSQTEIVLFGSDKQVVGQVASEIRAPRAPEYKGGVRYVGEVVMKBAKKK

SEQ ID 7763

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CTGCGATAACCGCGGAAATTTTGAATGGGACAGCGCGCGCAGGTTGCTGGTTCTCGCCGAGCTGAGGAAAAGGGTGGATTTCGACCGGTGAAGTTGTTTGGTCCGCGCTGCCAACCGTTG
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SEQ ID 7764

LGHVMPGGAHLSIDSKGRLAVPAKFRDILSRLYTPAVVATLESKHKLIMYPVAEWKVAQAQLNLKLVADNPVLRPFQNLILLHNAETLEWDSAGREVLVPAGLRKRKRVDFDREVVLVGRANRL
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SEQ ID 7765

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CGGTTTGGTATTTATTAAGCGTCTAGTGAGATTCCAAGTGTATGAATGGCTTGGGTATTTGCTATGTTAGTACTTCTAAAGGTGTAATGACTGATGTAAGCAGCTTCTCAAGGTGTT
GGTGGTGAATGTTATGCAATGTAGCC

SEQ ID 7766

MSMHDPIIDMLTRIRNAQRANKAAVAMPSSKLKCAIAKVLKEGYIEDFAVSSDVKSILEIKLYYAGRPIVBIQIKRVSRPGLRIYKASSEIPVMNGLGIAIVSTSGKVMTRKARSQGV
GGELLCTVA

SEQ ID 7767

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TATTAATAATCCGTGAATCCGATCGCTGCGGAAATTCGGGCTGTTGTTAAAGCCAGCTGG

SEQ ID 7768

MAKKALINRDLKQALAKKYAAKRAAIKAVINDSNATEERFEARLRFQSPRNAFPVRQRRRCALTGRFRTFRKFLGRIRKIREIAMRGEIPGVVKASW

SEQ ID 7769

TGCTTATTGGTTCGCTCACTCTGTACTGCAACCGCGCTGCGGTTGTCGTCATTTTATCTTATTGTTTAAACAGAAATAAAAAATTCAGATATGTTAATGAGTTTTCATGCCCTGATT
TGACCGAGTGTTTAAAAATTTCTTATAGTGTGATTTGGTGGGAATTTGGGGCAAGAGTCTCTCTTTTACCCCTTG

SEQ ID 7770

LFIGSVLYCTRRRAVVIFYLIVFKQKNFRVYNEFSCPDLECLKFLIVSIGGELNGKVSLLPL

SEQ ID 7771

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SEQ ID 7772

MARLEFYKFTVPELVKQPGYKSVMEVPRIEKITLNMGVGEAVADKVMHEAVSDLERIAGRPVVTVARKSIAGFKIRDNPVGCCKVTLRRDQMFELDLRLITIALPRVDRFRGVSGKS
FDGRGNMNVREQLIFPEIEYDKIDALRGLNITITTAKTDEEAKALLSLKPFKFFRG

SEQ ID 7773

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CGGGGATTTTATTACCGCACCGACCCCTCACCCCTCTGTTTGACAGACACTGGCAGCCAACTTCAAGAACTCTGCCCCAAACGCGGGGCAATATCTATGAATTCGCGCGGGGAACCGGA
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SEQ ID 7774

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SELHPQYAFIRTLASRLRGGMIFIDYGFDAQYHYHPQNGTLIGHYRHVHINPFDIFGLADLTAHVNFDTLDAQAGTDAGLDLTGYLPQSHFLNLGITELLAOTGRTDSAAIYIREAA
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SEQ ID 7775

ATGCGTGGCATTAAAGGCGGTATTATTACTAAAGAAATGCCTTTGGATATTCTTAATATCGCAATCTGAATCCGAAACTAATAAGCGGACCGTGTGGTATTAGCTGATTGAAAATG
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SEQ ID 7776

MRGIKGGIITKEHPLDISNIALINPETNKADRVGIKLIENEGKVKVRPFKSNISIIQA

SEQ ID 7777

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SEQ ID 7778

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PRGTASLTATLIIISPTFA

SEQ ID 7779

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ACCTCTGTCATGCCATGCAAGCGCTCTACCAACTGAGCTATACCCCCGAAATCTGGTAGCGAATCAGGACTCGAACCCCGACACAGGATTA

SEQ ID 7780

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SEQ ID 7781

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TTA

SEQ ID 7782

MIQMOTIILDVADNSGARRVMCIKVLGSKRYASVGDIIKIVAKDAVPRGRVKGDVYNAVVRRTAKGVRRPDGALIKFDNNAVLLNNKLEPLGTRIFGPVTRRLRTERFMKIVSLAPEV
L

SEQ ID 7783

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SEQ ID 7784

MSDLSVLSFFAVPLAALVGLLVGSFLNVVIYRVPMERGWTVFAKEHLNPLTDDSRFTNLAKPDSCCPKCRVPIRAWQNIPIVSYLLLRGKASCQTKISIRYPLIELLTVGLFGLVA
WQYGSWITLGLLITAPLISLTFIDATQYLPDSMTLPLIWLGLIFNLDDGFPVLPQSAVLGAVAGYSSLNLLCAVYKLLTCKTGMNGDFKLIALGAWLGSALPLVFLVSSLLGLVA
IVMRVAKGRHFAFGPALTVSGWLIPTANDSVNRVNWNLTHPVR

SEQ ID 7785

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SEQ ID 7786

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SEQ ID 7787

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SEQ ID 7788

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SEQ ID 7789

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TGAGAAAGCACGTTCTATT

SEQ ID 7790

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SEQ ID 7791

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SEQ ID 7792

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SEQ ID 7793

ATGAAAGCAAATGAATTGAAAGACAAATCCGTTGAGCAGTTGAATGCAGATTGTTGACTGTGTAAGAGCTCAGTTTGGCTTACGTATGCAAAACGCTACCGGTCAATTAGGCAAAACCA
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SEQ ID 7794

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SEQ ID 7795

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SEQ ID 7796

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SEQ ID 7797

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SEQ ID 7798

MLQPTLKYRQKQGRNTGIATRGNKVSFGEFLKAVGRRLTARQIEAARRAMTRHKKRGRIRIWRVFPDKPIITEKPIQVRMGGGKGNVEYYIAEIKPGKVLVEMDGVPEELAREAFELA
AAKLPIPTTFVVRVQVQ

SEQ ID 7799

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SEQ ID 7800

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QOLEKRVQFRAMKRAMQNAIRSGAKGKIMTSGRLNGADIAREWYREGRVFLHTLRANVDYATSEAHITYGVGLKLVVYVTEGNIKSSKEPHESKQKAGRRNAAAN

SEQ ID 7801

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SEQ ID 7802

MFMNKFSQSGKLSGFFPGLILATVIIAGILLYLNQGGQNAFKIPAPSKQPAETELIKLNQPKEDIQEPADQNALSEPDAKEAQSDAEKAADKQFVADKADEVEEKAGEPEREEDPG
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SEQ ID 7803

ATGAGAGTAAATGCACAACATAAAAAATGCCGATATCTGCTCAAAAGGCTCGTTTGGTAGCTGATTGATTTCGTGGTAAAGACGTTGCCCAAGCTTTGAATATTTGGCTTTACGCCCTA
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SEQ ID 7804

MRVNAQHKVARIASQKARLVADLIRGKDVAQALNLAIFSPKKGAELIKVLESAIANAEHNGADIDELKVVTFIVDKGPSLKRFPQARAKRGNRIEQTCHINVTVGN

SEQ ID 7805

ATGGCTCGTTTCAATGAAAAAGGCCCATATGTAGACCTGCATTGCTGAAAAAGTAGATGCTGTCGCGCAAGCAACGACAAACGCCCGATTAAACCTGGTCTCGTCTTACCATTC
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AGGCCACCTGGCGGATAAAAAGGCTAAAAAGAAA

SEQ ID 7806

MARSLKKGPIVDLHLKKVDVAVRASNDKRPKIKTWSRSTILPFIGLTIAVHNGRTHVPVPIIDNMVGHKLGEPSLRTTFKGLHADKKAKKK

SEQ ID 7807

ATGGCAATCGTTAAATGAAGCCGACCTCTGCAGGCCGTCGCGCATGGTTCGGTGGTAACAGAAGGTTTGCACAAAGGTGCACCTTATGCACCTTCTGCTGAAAAGAAAAATCTACTG
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SEQ ID 7808

MAIVKMKPTSAARRGMVVRVTEGLHKGAFYAPLLEKKNSTAGRNNNGHITTRHKGGGKHHRVVDPRKNDGISAKVERIEYDPMRTAFIALLCYADGERRYIIAPRGIQAGVVLVSGAE
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SEQ ID 7809

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SEQ ID 7810

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SEQ ID 7811

ATGACGTTTAAAGTCTTGGCAATGCAACCAACCTGAAATCAAAGCTGCTGTCGAGCTGCTGTTTCGGTGTTCAGTTGCTTCTGTAACCTACCGTTACCACTAAAGGCAAACTAAGCGTT
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SEQ ID 7812

MTFKVLNATKPEIKAAVELLFGVQVASVTTVTTKGTRKFRGRLGRRSDVKAYVSLVDGQELDLAEEAAADKE

SEQ ID 7813

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ATCGTACAGATGCCGACGCGGTCTTTACCGATGACCGTGATGACTGAATTTGTCACAGGCTTACTCTCTGCAGATATCCGT

SEQ ID 7814

LDTHIIPPTQMRICIAWKISSFCIRMSSASFLLSANKSKISCRDLGHFEVSTKIIIVKSSISWLLRLIRPSAKILETSYTMPPRSLPMTVMTLFTGLLLADIR

SEQ ID 7815

TTGGGGCTCGGCAACGGTATCTTTCAGCAGCTATCTGTTTACAGATTGTTTTTCAAAAAACGAGGTGTCTGAAAGTGGTTTGTCAATTTGTCGAGTGTGTGTTGGCATGAATGCTGAGCT
CGGTGCTGATTTT

SEQ ID 7816

LGLNGILQQLSVYRLFVKRGCLKVCHLSDCVGECLSCVLF

SEQ ID 7817

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SEQ ID 7818

NKLYEIVNPPQHNPISVVCKALKWLKPKSLKRCASEKSFRTAYCFVVSNCVIGRCAEYIEIRFQAAGVSKCNFSNRKGGAVCFDDYPPVFRHRFSLYNSRLNLICSGRMQIMFGKQLFEE
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SEQ ID 7819

TTGAAGATAATTTATCCGAATCCCTTTTCGGGTATCCGATTTCCTGTTACTTTTATAGAAAAACATTTACAGGCGCAAGTTGCTTGCATTTCAAGCCCTGTAAATCTGAAGTTTATG
ACGAGGAA

SEQ ID 7820

LKIITYPNLSGIRIFRCTPIRKTFQAQVACNFKACNSEVLDEE

SEQ ID 7821

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SEQ ID 7822

MELKVIDAKQVSGSLSVSDALFAREYNEALVHQLVNAVLANARSGNRAQKTRAEVKHSKKPWRQKGTGRARSGMTSSPLWRKGRAPFNKPDENFTQKVNRMKMYRAGMATIISQLARDE
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SEQ ID 7823

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SEQ ID 7824

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SEQ ID 7825

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SEQ ID 7826

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SEQ ID 7827

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SEQ ID 7828

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SEQ ID 7829

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SEQ ID 7830

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SEQ ID 7831

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SEQ ID 7832

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SEQ ID 7833

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SEQ ID 7834

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SEQ ID 7835

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SEQ ID 7836

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SEQ ID 7837

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SEQ ID 7838

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SEQ ID 7839

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SEQ ID 7840

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SEQ ID 7841

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CGAC

SEQ ID 7842

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LFLILGKKYDIGINDAEENRLLESLDLMEALVSDPDLGAGYKIGIFVVQYQKRCFPVIVYDLIDLARRNNQKMLRLVKGAAYWDSIEKMAQVDGLNGPYTTYTRKVTHTDI SYHLCAACKLSLA
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LYGKVRFLNSQVDLSINENVLQQLQEQPNKMAAQQDFHAASITVGKARDGVGAQPTKPNADGGVDVGTVSFADAALAQEAUGAAVAAP PENSATPAEAARAACLRRFADLLEQHTPALMHMLAVR
EAGKTILNNAIAEVR EAVDFCRYYANEAEHTLPQDAKAVGATVAISPWNFLP LAITFGEVVSALAAGNVTVIAPABEQTSLLAGYAVSLMHEAGIPTSAQLILGAGDTGAALTNDASIGGVIF
TGSTVEARLINKALAKRGDNPLVLAITEGQGNAMIVDSTALAEQVCADVLNSAPDSAGQRCSALRIILCQVEDVADRLMLHIGKAMDELVVGKPIQLTFDVGPVVDABEQNLLNHHINMKGV
AKSYHEVKAADVDSSEKSTFVRPILFELNNLWELQRBVFGPVLHVYRYADELDSVIDQINSKGVALTHGVHSRICTEVRHRSRIEAGNVYVNRNIVGAVGVQVFFGGHLSGTPGKAGG
SFYLOKLTRIPWVAPTL SQIGQAEADALKRLEALTHKLPFNAEKKAAAAAALLHARFETLRLRAEFTVLGTPTGBRNSISWHPKRWVTHGGSTVQAFALTGLASQVAVVEPDSPLASTY
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SEQ ID 7843

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SEQ ID 7844

MAGGQVLADPSGEMTANVVLGTGGIGSGKSAAAQYFADLVGPRIDADAHAHSLTASDGIALPEIRRLFGDTVFDTQGLLRDRLRKEIFASPSRKALLESVMLPLIFSEIKKQQTFTDAVY
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SEQ ID 7845

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CGGTGCAGCCCGACAGCTATATTGCTCTCTGTTTGTACAGCCCGGATAAGCCGCTGCAACAGGCTGCCAACAGGCTTTTGGCCCTTGCAGATTGCCCTCCATCAGCAGCTTTCAAC
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TATGTTTATCCGCAA

SEQ ID 7846

MAETFAUTFMIAALYLFARYKASRLLIIVFPAPSMIANNVHYAVYQSWMTGINYWLMLKEVTEVGSAGASMLDKLWLPALWGAEVMLFCSLAKFRKTHFSADILFAPLMIMIFVRSFDT
KQEHGISPKPTYSRIKANYFSFGYFVGRVLPYQLFDLSKIPVFKQAPSPKIGQSGIQNTIVLIMGESASAHLKLFYGRSTSPFLTRLSQADFPIVKQSYASAGPMTAVSLPSFFNVIPHA
NGLEQISGGDTNMFRLAKEQGYETYPYSAQAEQMAILNLIGKKWIDHLIQPTQLGYNGDNMPDEKLLPLFDKINLQQGRHFIVLHQRGSHAPYQALLQPDQKVFGEADIVDKYDNTLHK
TDQMTQTVFBLQKQPDGNWLFAYTSDHGQYVRQDIYNQGTVPQDSYIVFLVLYSPDKAVQQAANQAFAPCELAHFHQLSTPLIHTLGYDMPVSGCREGSVTGNLITGDAGSLNIRNGKAE
YVYFQ

SEQ ID 7847

TTGGTGTGGAACACGCGGGGCGAGCGTTTGTGTTTCTCTTACGCGCGAGCAGTTATTTGGCGAAGAGTGAGTTGGAGGAAATGCCCTCTGAAGACGATTGTGTTTTCAGACGGCATT
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SEQ ID 7848

LVGNRQRFRFCPLDARAVIGRRVSWREMPSEDDLSGDIPTIHCFFDANLRFYHIVKLIIVFYIAIMKKLSRIVFSIVLLGFSALPAQTYSVVFNQNGKITATMSSAAYIRQYSVA
AGTAAHQDFYYPMSKKYSEPIVASTQIKSFVPTLQNGMLILWHFNGQKMKAGGFSKGRPDGEWVWYYPNGKKSAMVMPYKNGLSEGTGYRYYRNGGKSEIQPKQNKANGVWKQWYADGSI
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SEQ ID 7849

ATGGCAACCAAAAAATCCGTATCCGCTGAAAGCTTATGATTACGCCCTGATTGACCGTTCTGCAACAAGAAATCGTTGAAACTGCAAAACGTACCGGTGCTGTTGAAAAAGGCCGAGTC
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SEQ ID 7850

MANQKIRIRLKAYDYALIDRSAQEI VETAKRTGAVVKGPIPLPTKIERFNILRSPHVNKTSREQLIETHRLRMDIVDWTDTTDLMLKLDLPAGVDVEIKVQ

SEQ ID 7851

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GTGCAGACCGTCAATCAGGCGTAAATCAAGCTTTTCAGCGGATACGATTTTTTGGTTTGCATTATCAATATCTCTCAAT

SEQ ID 7852

LDNFYINTGRQIQLHQRIGSFIPGIDHVDQMGADFQLFTGSPVHVRRITQNVETLDFGRQRNRAFNTSTGTFCSFNDFLCRTVNGVVISFQADTDFLVCHLSISFN

SEQ ID 7853

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TGACGCGGTGCGCGTACGATACGACACGTCAGACACAGCATCGATTGCAACAAAAAACAACAGATGTATTACCGCCCCCCCCACTACTCTGACGCGAGCACCTACAACATTATAATGCT
AATCCACAGACGCAAAACCTTTATCACCAGCGACAGCATCCGCGCGTGGGCTCGGGTTCATCGCCGCGTTCGCTTTCGACATCAGCCCAACCTGACCTGGACACCGGCTACCGCT
ACCACACTGGGACCGCTGGAACACCCGCTTCAAAACCAAGAGCTCATTTGGGATGCGCTACCGCTTC

SEQ ID 7854

VSVGYDFGSWKIADYARYRWNNKYSVNIRKVENKNGSGKKLQDLKTENQENGTFPHAVSSILGSAYVDFDTGSRPKPYAGVRVSYGHRHSIDSKTKTVDVITAPPTSDGAPPTYN
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SEQ ID 7855

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TCGTCACCAACGTGGATGATACCTGCTTACACGCGCGGTGACTACGTTACGCGCGCGGAAATGAGGAACACGCTTTCGA

SEQ ID 7856

LPFINILQLSDNRNHAHTHGTAAFPANRKAQTFPHSDRRNQFYSNGYVLTTRHYHFHTPFQSNRAGTVSGTEVELGTVVGEKRGMAAALFPAQYVHPCFELGVRSDSTRFQYLTAIFYVFTF
GTAQQYAYVVARLTFVQQAEPHFNAGTGGFLGFFQTDFFNLVTNVDDTSLYTAGDYGTAAQKWRTELK

SEQ ID 7857

ATGTTCCGATTATACGTGTCAGTTATGCCGTTGAAAAATGCCGTTTGCCTTAAAAATGCCGCTGAAGGTTACAGCGGCATCGGTATCGGGAAATCAGAAGCGGTAGCGC
ATGCCAA

SEQ ID 7858

MFLYQCLRLKMPFARSCALKMPSESDGIGIGSEAVAHQ

SEQ ID 7859

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SEQ ID 7860

MFRKLLDEQAGDNVGLLRGTKRDEVERGQVLAKPGTITPHTKFAEVVLSKEEGRHPTFPFANYRQPYFRFTTDDVTGAVTLEKGVEMVMPGENVITVELIAPIAMEEGLRFAIREGG
RTVAGVSSVIA

SEQ ID 7861

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CCGATTCCGTCAAATCCATCAATCCCGCGAATCAAGCTTATCCCAAAAAACCT

SEQ ID 7862

VQADLAYAYEHITRDYPEATGAKKGTITISTVSDYFKNIRTSVHPRALGDFGGMVFSAPAVAAGLHQSLEYRSHRCRRFRQIHQFRITPIQPKP

SEQ ID 7863

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SEQ ID 7864

VVFWVSFRPTISISSPTWMIPTSTRPVTTVPRPENGHEVFDQWQWVHGTGSRDVAQVCGSQFEDFFVSGIAPQGFQCGTLYDRAVAVAGEVAVQVADPHFNQFQQLGTVHVAFVH
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SEQ ID 7865

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SEQ ID 7866

LPPASTNPFNITDPAIADSVKSINSAESRLFPKNDLAAG

SEQ ID 7867

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SEQ ID 7868

MAKEKFKSPHNVGTIGHVDHKTTLFAALITLAKKPGGAAYDQIDNAPEEKARGITINTSHVEYFTETRYAHVDCPHADYVKNMGTAAQMDGAILVCSAADGPMPTREHL
LARQVGVPYIIVFMKNCMDVDDAELELVEMEIRDLLSSYDFPGDDCPVQGSALKALEGDAAYEERIKFELATALDSYIPTPERAVDKPFLLEIEDVFSIFRPRYRSHRPRARYHFRH

SEQ ID 7869

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SEQ ID 7870

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SEQ ID 7871

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SEQ ID 7872

MARTPISLYRNI GISAHIDAGKTTTTERILPYTGLTHKLGVEHDGAATDYMEQEQERGITITSAAVTSYWSGMAKQFPEHRFNIIDTPGHVDFTEVERSMRVLGDGVNVYCAVGVQP
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PQVAYRETIRKAVRAEYKHAKQSGGKGQYGHVVIEMEPMEPGGEGYEYFIDEIKGVIPREFIPSDVKGRDTPMGIVAGYPPVDVIRLRFVSGYHVDSSQLAFELAAASQAPKEGHRQAS
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SEQ ID 7873

TTGATGCGCGCGGCTGAAGCCCGCGCTGCAACCTCTCTATGCAACCCCTTTCGAGCGCGGACACTACGCAACATCTTGAGAACCCATCTGTCAGAAATACCCGAAACCGTCCCGATACACC
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SEQ ID 7874

LMRRAEARPATLSMHPASPTLRNLI LRTHPKNTRTPVPIHRNPKTRHSRAAMGHRQRGGFPFARTVSALPHRYAQHGDDASAGRCNPFDAHGPARQPTWASKSRACRTTIVD

SEQ ID 7875

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TGGTGCAAACTACCAAGTTCCTGTTGAAGTTCGCTTACACCGCTGCGCTTGGCAATCGCTTGGGTTCGCGACGCGCGCCGCAACCGTGGTGAGAAATCCATGGATTCGCGTTGGCA
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SEQ ID 7876

MPRRREVPKRDVLPDPKPGSVELTKPMNVLMIDGKKSVAERIVYGALEQIEKKTGKAAIEVFNEALANSKPIVEVKSRRVGGANYQVPVEVRPSRRLALAMRWVRDAARKRGEKSMDLRLA
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SEQ ID 7877

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SEQ ID 7878

MVSDPMAAPRADDAAEQPYFRFVDVYVRQARMVGLGI

SEQ ID 7879

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SEQ ID 7880

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SEQ ID 7881

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SEQ ID 7882

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SEQ ID 7883

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TGCAAAACG

SEQ ID 7884

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CKT

SEQ ID 7885

TTGCCGATACCGGTCAGGCTCGGTCCGCTACGATGTGAAGGTACGTTTTTTTTCGGATGTGGCTGCGGTTTCGGCGCAAAATCAGGATAAACCCGCTGTTTCGGGAAAAATCGGGTAA
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SEQ ID 7886

LPPIGAGSVGYDVKVRFPADVAASQAQITINPRCFGKNRVISG

SEQ ID 7887

TTGCCGACCATGTGCGCAAGAGCGGAATTATATTTTATTGCAAGCAGACAGTCAAGCATAACGACAAGAAAAAGATGATTTTCTGTGTTGCCGATAAATATTTACCGACATCCCTCA
CAATCAGTCGGACGCTGGAGAAAATACGTGTCAATACGTTTTTTCATAC

SEQ ID 7888

LPPTCRQERNYIFIASRQSSITTRKKMIFLPADKYLPTSLTISRAGENTVNTFFPY

SEQ ID 7889

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SEQ ID 7890

LLIVVRFDICTEGNAMTFKPTVVLTASALALSGCVADPVTGQSPNKSAMYGLEAAVCGIVGALTHSGKGARNALACGAIGAGVGGYMDYQERLRQLNLAGTQIETQROGNIRLVM
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SEQ ID 7891

ATGGTTTGTGAGTATGAAAAACGTATTGACAGTATTTCTCCAGCGCTCCGACTGATGTGAGGATGTGCGTAAATATTATTCGGCAACAAAGAAATCATCTTTTTCTGCTGCTA
TGCTTGACTGTCTGCTGCAATAAAAAATA

SEQ ID 7892

MVCQYGRNVLTFPSAVRLIVRDVGKYLANKKIIFFLVVMLDCLLATKI

SEQ ID 7893

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SEQ ID 7894

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SEQ ID 7895

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SEQ ID 7896

MDNVSEFFAGKQIAAGGVQVGPQLQTLPPYRDTPTVSSKQIFNQNAV

SEQ ID 7897

ATGAGCGCGCTTTATGGCATAAAAACTGCTGGAAAGGATTACACCCCAATAAATTCCTGTACAACAAGAACACAGCAATATGCCCGCTTTTATTCGCACAGCGGCAAGGGAT
GTTTGTGAGTATGAAAAACGTAT

SEQ ID 7898

MSAALWHKRLSNKGFPTQINFRYNNNSNMPAFYSHSGKWFVSHKTY

SEQ ID 7899

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SEQ ID 7900

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RHFIMAGNHFARLIGSGSVHYWNARDFSEQAFHAEVGYRYRNSRLEWGFPPVKQNLGNRYTANTGIVLDYSRRLNEKNRSTQSFQYGRKQYHDEYLAKRYNSKTLISVSGTFSYAHNS
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SEQ ID 7901

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SEQ ID 7902

MKFTTNVNSLAVRLPQVQNLVLDNPPDILVLQELKLDQDKPAAALQMHGHCWVSGQKTYNGVAIVSRSPQDVHFLPSLPDDPQRRVIAATVGGVRVINVYCVNGEALDSPKFKYKE
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SEQ ID 7903

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CGCGCGAGCGCGGATGTTTCGAGGCGCGGATCTATACCG

SEQ ID 7904

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SEQ ID 7905

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SEQ ID 7906

VVARTLQARLQIDADILQNRHFGCNQYVMDTQAQFALEHRAAIVEPGERIAPGMDLAQAVQSQIQVVKLPFPDGRVDFPIPFRRVTVRIGRRDIEIAQQHQFVAVAGHFIADKLQ
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SEQ ID 7907

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SEQ ID 7908

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SEQ ID 7909

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SEQ ID 7910

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SEQ ID 7911

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SEQ ID 7912

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SEQ ID 7913

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SEQ ID 7914

MHNLFARRYGTLLGLISTRILKMTKTLVFPALIGQRKTASSRLAVFY

SEQ ID 7915

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SEQ ID 7916

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SEQ ID 7917

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SEQ ID 7918

MVHIMFQAQELTTIRDLRFAVSRFNEAGLFFGHGTDNAHDRAVYLILHTLNLPLDMLAPYLDKILLEAKKEVLAVERRAVEHIPAAYLTHQAWQGEFDYVDERIVIPRSFYELL
GDGLRPHWIEYDELVHNLALDCTGSGCLAIQMAHYPDQIDAVIDVSLDALEVAGINIEYDLLEERILQLHTLDFBGLGTYDLIVSNPFFVDAESVGLPBEVLEHEPRLALGSGADGLDAP
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SEQ ID 7919

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SEQ ID 7920

HIPFGRNRVQGRGGSPMPSESLRLFAKIVGKGYNPVQ

SEQ ID 7921

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SEQ ID 7922

MEEFDAIKIGIASPETIRSWSYGEVKKPETINYRTYKPERDGLCAKIPGVKDYELCKYKRLKFKGVTCCKGVEVTLTKVRRERMGHIELAAPVAHIWFLKSLPSRLGMVLMHTLR
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SEQ ID 7923

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TATTTT

SEQ ID 7924

LCSSVFLKPPFAKRIDGRQIMILIFINFIINQLFISHCTGLYVPPFTTIFANKRRRLSDIGKILPPLPCLTLLPNGIIRIF

SEQ ID 7925

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TTCGGC

SEQ ID 7926

NDIFRESRPFCAATGCTPTTSGSAFHRRRRYQDRIGRAFLTMHRLDKENQIHTDMLALFAVVKDAVAIWADMDLDRCSG

SEQ ID 7927

ATGCCATAATCGCGCTCGCTGAAATGCTGTTTTTCTAAAGCATCAGACCTTCAGGAAAAATGCCGTCTGAAGAATATTTTCAGACGGCAATCCCTCCGTGAGGCAA

SEQ ID 7928

MPKSRLEPMLFFLKHHDLHEKCRKKNISDGIPLRLQ

SEQ ID 7929

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SEQ ID 7930

VCMNYSFTEKKRIRKSFARENVLVFFLLATQIDSYAKFLQLENAPDKRTDDGLQAAPNSIFPIVSHNGYARLEFVYVYITLGEPLFDIPECLRGITTAAPLRARIRLVILDKKASKPTVK
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VQTDVLVAGRLKGETAKVDILDKEGNVLVAKGRITAKNIRDITNAGITRLDVEQESLLGKALAADLIDSETGEVLSANDEITZELLAKPFDINGVKETITLYINELDQAYISNTLRDDET
AGRQARVAIRVMRPGEPPEEAVEQLFNRLPFSBDSYDLKRVGRMKFNTRTYEQKLESAQQNSWYGRLLNETFAGAADKGGTVLSVEDIVASIALVELRNHGEVDDIDHGNRRVRS
VGELTENQFRSGLARVERAVKERLNQAESENLMPHDLINAKPVSAIKEFFGSSQLSQFMDQTNPLSEVTHKRRVSAALGPGLTRERAGFEVRDVPHYGVCPPIETPEGPNIGLINSLS
VYARTNDVGLPETPYRRVIDGKVTREIDYLSAIEBGRVYIAQANADLSDGNLIGDLVTCREKGETIMATPDRVQYMDVATGQVVSVAASLIPLFHEHDANRALMGANMQRQAVPCLRPEK
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SEKVAADRYTISIHELNVVARDTKLGAEDITRDIINLSERMONRLDESIGVYIGAEVAGDVLGVKVTPKGETQLTPEEKILRAIFGEKASDVKDTSLRMPMGSGTVIDVQVPTREGI
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SEQ ID 7931

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TTCAGCGAGCGCGATT

SEQ ID 7932

MSGKBIPLNRNPIVIAAGRECLKYSSDGIFREGRDALEKTAPOAGAI

SEQ ID 7933

TGTGTTACATTATTTCGATAGTTTTTATCAATCATTCGAAATAAATGTAATATCAGATTGATGCGTACCGTTGTTTTCAGACGGCTTATTATGAAAAATACCTTTTCGAGGTGTGTA

SEQ ID 7934

LPFFICIVFIKSLQINVINRLMRTVFFRPIIENYFSECV

SEQ ID 7935

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ATCAAA

SEQ ID 7936

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SEQ ID 7937

SEQ ID 7937

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SEQ ID 7938

SEQ ID 7938
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SEQ ID 7939

SEQ ID 17939

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SEQ ID 7940

SEQ ID 7940

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DAERTALNYLTHLSGLIATATARAFAEVAEYGTDIVCSRKTIPLLEVLQKYAVRAGGGANHRMGLDDAVLIKDNHLAYCGSIAQAVRQAKQAVGPLFCVEIEVDTLQLODEALAGAEIRILL
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SEQ ID 7941

SEQ ID 17947
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GCGCAAGCTGCT

SEQ ID 7942.

SEQ ID 7942:
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VAELASTPSREEELSKLLFVMQAPVSGFARGLAALAEKKAGEAA

SEQ ID 7943

SEQ ID 7943
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CGGACATCGGACTGCGCTGGGCGAGCCGT

SEQ ID 7944

SEQ ID 7944

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WANSADTEEVQRKRLKHILCWGVEPNWSEYVLQRVEMYESGLIAEAAEPQANFDFAITGQTHRHDRHRLVATALSRLRAKIKYRPVIFELMPGPTLLQLQNSVEAISGRLLHQNPF
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SEQ ID 7945

SEQ ID 7945

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SEQ ID 7946

SEQ ID 7946
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VEVCLRLGHTARYQTAFIQHFIALQNVFFRPVFRDPTPTQNMMLLEPLADFLVRVRVCPNAQAADGVALPAVGAQVFPWETAVALVLFPRVHGQDAIGCLAHQPOIADVQHGHAVFVAAGVI
DKGVLGLHTRHRLSLGDPOLYARLQGLQAGGKRAVGQERALGDGQHPAAVGNNGNYQNGQLDDALQSRFGVGVGHARLSAGGKGFIVNQSGLSERSGSVLRYRKPFRPCILYSS

SEQ ID 7947

SEQ ID 7947

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SEQ ID 7948

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SEQ ID 7949

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SEQ ID 7950

MGNLIQWEGTGLVAGKQWITAKDDKVSVDVNCANGMGVIGLHEPFSHGALTPIEPHNGRCVAVPVVGTGKLAGSRAMETGDRQVRLFPYRAANWGNLQKRSFVKRLCSMRVITLSAK
AMSKAAGNN

SEQ ID 7951

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GTCGAGCTGGTTCCCGTAT

SEQ ID 7952

MFPCSWFSDGMKVCRLPFKFLHYAQLEYNQRLKTLRLYRKTDFLRSDKPLWFTIKFPFPAESRAWTPTPKPLRCKASSSWFPY

SEQ ID 7953

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SEQ ID 7954

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SEQ ID 7955

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SEQ ID 7956

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SEQ ID 7957

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SEQ ID 7958

MSKMYVQAYSQFPEKNVQRILEERLAREEMGDYFGQILVPVEKVDIRNGRKTISERKSYPGYVLVEMETDDSWHLVKSTPRVSGFIGGRANRPTPIQREAEIILQVQGTGIEKPKPK
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SEQ ID 7959

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GTTATTTTGTATGATTGCTGAGAAGGAAGGT

SEQ ID 7960

MTEHTPEKKNVKNVLVVQDKESASNSGKEGFFAYFNSNSWSEFKKVVWPKREDVMTVPVIVFVAVLSIFTIYAADTAISMLFPDVLRLREG

SEQ ID 7961

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SEQ ID 7962

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LISEAVRGGGILTNQSGERFMPHYDRRAELAPRDIVARALAAETAKTQDFVSLDISRQPAFVRRHPSIHRHCLSQGLDITRQAIPIVPRVQHYTCGGIQTDFSGRTSLPQLYALGET
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SEQ ID 7963

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TTTTTTAGC

SEQ ID 7964

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TAQQYAYVVARLTFVQQFAEHPNAGTGGFLGFFQTDNFWVNDTSLYTAGDYTAGNGEHVDFRQENFVHGTLSRDVAVQCSQFEDFFPVSGIAPQFQCGTLYDRVAVAGEV
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FFS

SEQ ID 7965

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SEQ ID 7966

MAKEKPERSKPHVNWGTIGHVDHKTTLTAALTTILAKKFGGAAYKDIDNAPEEKARGITINTSHVETETETRYAHVDCPGHADYVKNMTGAQMMDGAILVCSAADGMPQTRHIL
LARQVGVPIYIIVPMNKCDMDVDAELLELEMEIRDLSSYDFPGDDCPIVQSGALKALEGDAAYEEKIFELATALDSYIPTPERAVDKPFLPIEDVFSISGRGVTVGRVERGI IHVGE
IETVLKETKTCTCTGVEMFRKLLDEQAGDNVGVLLRGTKREDVERGQVLAKPGTITPHTKPKAEVYVLSKEEGRHPTFPANYPQFYFRITDVTGAVTLEKGVEMVMPGENVTITVEL
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SEQ ID 7967

GTGTTTGGGTTTCGATGTCGAAGGAAGGGCTTTTTCGAAAGGCTCAACCAACTTACGCAACCATAAAACTGAATGCCAATCTCTTAACCATGCTATTCAAATTTATTGAACGATT
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SEQ ID 7968

VFGFRMSKEGLFCKGLNPTATIKTECQSLNHAIQIYLNDPFLTSQF

SEQ ID 7969

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GTTAAA

SEQ ID 7970

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SEQ ID 7971

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CGGCGCGGATTA

SEQ ID 7972

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SEQ ID 7973

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SEQ ID 7974

LGRKQLKTCVWSDVEGRAFLQRQPPLNRNHN

SEQ ID 7975

ATGGCATCATTTGGGCACTTCGGGTTTCGATACGTCGCACTGTGATGCACTGCTCGGTAATAAAAAGCGACATTTCTTTTCTTTTCCACTAAATTTATCAAAACCGGCGGCGCGGATTA
GCACAAGGTTTTT

SEQ ID 7976

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SEQ ID 7977

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CATCACCCGATCGGTTTCAACCTGTTTGCCTTTTGACGGACCGGGCATCCCGGTTGCAGCACTTATGCCGCTACCGTAAATTCGCTATCGCGGGCAGCCTATTTCGGGCTGCTC
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SEQ ID 7978

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SEQ ID 7979

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SEQ ID 7980

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SEQ ID 7981

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SEQ ID 7982

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SEQ ID 7983

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SEQ ID 7984

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SEQ ID 7985

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SEQ ID 7986

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SEQ ID 7987

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SEQ ID 7988

LGIGIDRFNEQLKGVSRDLSLKRILAHGGKTVGETEFAELTCRKNWYLEMTQAVKPEDVYPGLIPLEALRANGKIALASAKNGPFLERMG/THFFDTVADPAVAHSPSPDIPL
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SEQ ID 7989

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SEQ ID 7990

MKKAPEALMAATPAAAYVRTHALGGGKEDVGGGFGMRDGGRVGDGVEEVQPHAFEPQERAVFTGGREGDFFAVCPQCFOQRQNAVHVHFGFCLNHLQVVVVFAAGQFGEIGFADGFAAVR
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SEQ ID 7991

TTGAGTTTTCGACTCCGCGCAGGACTGCGCCCAACCCCGCAGCGTGCCTGAAAAGCTGTTTAACTGGCTGGGACAAGATTGACGGGAAAACCGTTTGGATCTCTTCGGAGGCGAGCG
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AAGTGGCTGAA

SEQ ID 7992

LSFASADGLRPTDSVREKLFNWLQDLTGKTVLDFLGGSGALGMEASRNARVVADNNRQTVQTLKNSRELGLGQVQTVCSDLAYLANLKEKFDVVFLLDPPFAWQSWESLFWVLGT
RLNDGAYVYIEAGRPDKPDWLTGYREGKSGGTFLRVFQVAE

SEQ ID 7993

TTGGGCTACACCGCGAAGCCTTGGCGAAATACCGCGCTCCGGGTTTCGAACGTGAGCGCCGCCGAGTTGGA AAAATGGGCGGACATCAGCGGAAATATGTAACGTCGCCATGACGAAGAAC
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SEQ ID 8007

GTGCCGTCGATATAGGCCGCTCCGCCGCCGCTGTTGCAAGCCGACGCCGCCGCTGATCAGCATATACAGCGACCGCAACGGCTTGGTCACTTTACCGCCGCCCGCAGGATTTCGGCG
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TGCTTACGGCATCGAATCCCTTTCT

SEQ ID 8008

VPSDIGRPAVLQAGRRRISITYSDRNLVIFTAAPPDFARHDAGVYDALATEAQTLPSLHWPEFGNIRLNKGDTRATIAYGIESLS

SEQ ID 8009

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SEQ ID 8010

VRRSTSTVGLTAWRPKAGTRCTAVRTGWPLFVSTRWQTDGYPNDLDSYRLDEBGLTVTYRATALGDTVFDPTLHTYWRDAGLHDAVLHHPQGGHIADAELPLVTVSDGLEVFD
PSRPKPPDAVAALRRRTGRF

SEQ ID 8011

ATGAGCGATACCCCGCTACCCCGGATTTCCGCCCTGATCGACGGGGGGCGGTAACCGGCTATGTGCTGTCCAACCGCGGTGGTACGTGCGTCTTCGTGCTGGACTTGGCGGGATTGTGC
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CATCCGCGGTGCGCGCTTCGACATCAACGGTAGGACTTACCGCGTGGAGGCCAACGAAGCAGGAACCGCTGCACGCGGTTGCAACGCGGCTGGCGACGCGGCTTACCGCTTTCAACCGGTGGCG
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TATT

SEQ ID 8012

MSDTPATRDFGLIDGRAVITGYVLSNRRGTGVFVLDLGGIVQEFVSLADGVRENPVVSFDAAASYADNPPQINKQIGRVAGRIRGAAPDINGRTYRVEANEGRNALHGGSHGLAVTRFNAVA
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SEQ ID 8013

TTGTTTATACGGATTGTCGTAGTTACGATGTATCAGATTGTAAGCGGATTGGCGGTTTCCGTATCAATCGCGGCACACATTTTCCGGAACGGCAAAACCATATCAACGCAATTGGGAAC
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CATTTTAAACAATTTGGTAAAGCAGGATTATCCCGGCTGGCGGGGATTTTAAAAATAAATACATCTCT

SEQ ID 8014

LFIRIVRSYDVSDCKRIWPPYQSRHTFCRTAKPYQRNWLLESCKRHLKFDGIPKEHFGLYLKECGRRFDSNGVKVRISILKQLVKQDLSRLAGILKNKYIL

SEQ ID 8015

GTGAACACGCTGCGTCAAAATCGAACAGCATCGAATTTCCCTTATGTCGCGCTTGATAAAGTTTGTATGAATGCAAAATATGAAGGAAGTTTCTTAACAAAATAGGGAGGGATCATA
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CAAA

SEQ ID 8016

VKHAASKSNSIELSLMVALDKVLMNAKYECSFPNKLGRDHI IAVHKYSTGVPRGNKVLKIRI IAREKFDGKHYDHFILKDK

SEQ ID 8017

ATGCCCTTTCTTAGGGACGCAATATATAAGGTTTATACCGTCTGTCCCTAATGCGCAATCAGCGACATTTGTCCTAATTAACGAAAGAAAGTTAAGCCTGATGGCATTTGTATACACGG
ATACCTTTCTGATGTTATGATGTCGTTGATGTAGTGAATTTAGCCATTTACGTAAGTTTAAACGGCATTTCCCAAGAGCATTTGGGGCTATATTTAAAGAAATGCCAATGGCATTTGAAA

SEQ ID 8018

MPFLRDAIKYVTVVVPNAQSATLLPIIRKKVKPDGIVYTDTRSYDVLVSEFSLRKFNGIPKEHLGLYLKCKQWHLK

SEQ ID 8019

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CCCCATCAGCACTCTGTGGCGCGGATTAATGACGCAATCAAGAAATCGAATACTGAACACCTCGCAATCAATGCCGCAAGCGACTTGGGCGAAATGACACCGCTGTAAGAACGACGATCGG
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SEQ ID 8020

IVGICRYLFQ*SNALHNQNTGPAQIHHTLLIGNVQNTHTFRTVHNHTLHFFADGHNLIHARTPLITLPPATVATDGAVKPPIFCILIGETDFLQSRGRRAHFLFAARTQPA*KTLRHN
QADRTGNIKRRDTHIQTRQRRIIRVQCGKHNPCLRLNRNIGSFQITNLTDHNDVRLVTOERLQSSGKSQTLIIIDVNLIDARQVNLGRVFRRCNIYRLRNIQTGIERHRLTRTR
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KLENDVGCPTAQIRQSFMDKPRNRAVFLVVDIQVAFLLPLPLKLLKQRCRTRTHPIEQTRQLVLTDNDQLNRNPGRNGFNLRLHGRIGNRKYPVAPENRHTVELHLLLRQH
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SEQ ID 8021

TTGGCAGATCATCGGGAACCTTCCCTTACACGCAATTTGGACGAAATCTGCGAAATATGAGGAGCATACGACATATCGTTTACGATTACTTTATCCGTCAAAACAGTCCGCAATTTGGAATG
TA

SEQ ID 8022

LAHRENFLYTHLDRICKIMEAYDISFTTTPSKQSAFGNV

SEQ ID 8023

GTGATTGTTCGTTTATCTGGCAAAAGTACCGAATAAATACATAAGCGGGTTATTTTCGGCTGTTGGCTTTGGGCGCGCTCGGTTTCTTCTCTATCTTCTCATCTACAATCAATACG
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CGGCTCTGTCTGTATGCCGCAAAATCGTCTCTGCTGTTGAGTTTCGTCTCTTTCCGATGCTGGGCGGCGCATCAGGCAACCATGTTCTTGGTTGCGGCGGAGTCTTGTCTGCTGGGAGCC
TTCTCAGTCTGTCTGATTAAGAGATCCACGCGGGGT

SEQ ID 8024

VICSFILAKVPNKYHKAGYFGCLALGALGFFSIFFIYNYALILSYILIGIAWAGIITYPLTIVANALSGKHMDTYLGFPNGSVCMFQIVASLLSFVLPMLGGHQAHTFLVAGAVILLGA
FSVCLIKKHGGV

SEQ ID 8025

TTGGCAGCAGTTAATCAAAACACGGCAGCCTGTTATTTCTATGGCGAAATAGTGTTTGGCACATCATCGGAAACCTTCTTTACACGCATTTGGACGAAATCTGCGAAATATAGGAGC
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CGGCAAGCGCGGTATTCGGCTTTTGAAGCGCAACGGCAAGGTTGTACGGTTACTGTGCGGACACTCGAACCGCTATTTTATGCGCTATATCCGCGGACGGGTGAAACCGGCGAGCAT
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SEQ ID 8026

LAAVNQNTAACYFLWRNSVWHIIGKTSPTRIWTKSAKLWRHTTYRLRLIRQNSPHLEMYDGEAGAGESYFRKGRRGRSAAGKAAVFGLLKRNKVCVTVTVGHENRYPIAYYPTGETRQH
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SEQ ID 8027

TTGCGGTGACGGCGTTCGATTGTGTTCTTCCAGCGCATTTCTTTTTCGGGCGAGACTTTTTCACGCCCCGGCGTTTGGTAGTTTGTATGGCCAGTACCGGCCAATGGCAGTTCGGGCAT
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SEQ ID 8028

LRCRRFDLFFPAFFLRADFFHAPGSPFDGQYRPMVAFFNGRVPVGVAVGIGAAATVKQFVAVAGFALDEVAFFALRALDAGIFGFFQRLDVFAPGVVGATDEFTAGAAVFFVHQPAA
FGAFATVEFDLFGFRFGDAPGSPFGFVDVAGVTFALGITGTNETAFAELDLQFVFAAFRAGFVKFLRSEFGAFDALFFPHLFDERPEFVHEGNPAFAVGVDFVKLVFEPGGEVVIDVL
GEVFGQEFIDDVACVGGHEAFLLKGNVPAVFERRNAGVGRGAADAVFFBGNQCGFVVARRRGGEVLFAVEFVDRQFVFAHFGQFVAVFALFVAAFPVNAEACBGLHLSGYSEHAF
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SEQ ID 8029

TTGGACGGGATTCGACGATTAAGAGGTTTTCGCCATTTGTCGTTCTCTGATGTTGTTTTCGACGCGGTGTTTCAGACGGCATCGGCGGGCGCGCGCGCTC

SEQ ID 8030

LDGDSIKRFFAICRSLDGGFDAGVSDGIGRAGAV

SEQ ID 8031

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SEQ ID 8032

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SEQ ID 8033

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SEQ ID 8034

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LYGTLIAVIMLMPNSGSPFGYASLAALSFGALMIALLDVSSNAMQPFKMMVGDWNEEQSYAYGIGSFLANTDAVVAAILPFVAYIGLANTAEGKVVQTVVVAIVYVGAALLIT
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SEQ ID 8035

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SEQ ID 8036

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 AERIKAAEAEBQVLELGDRECPKCGKGLRVLYKYSRTGSKFICGANYPKCKHVEPLEKPKDITGVQCPQCKGNLVERKSRYGKLFYSCSTYDCNCYATWNPVPAEECPNCHWFLAIKTTKTRGV
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SEQ ID 8037

SEQ ID 8037

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SEQ ID 8038

MTEVIAYLIEHFQDFDTCPPFPEDIGMLLEAGFDTEIGNFTLMMHEVLINSSEPSAEPAGSGALRVYSKEETDNLQPEVMEGLMOYLI EEKAVSCBQREITIHALMHIPGDEITVDTAKVLT
 LLLLWANKSELVVLVGDELSALILLDNKPTMN

SEQ ID 8039

SEQ ID 8039
ATGAACCGGGTGCAGAAACCCATTTTATCCAGTATGCGCGCAGCGGCTGTGCCGCTGCCGCCCTTCAGACGGCATTTTTGCGGCAGGCGGCGGGGGCGTATGCCGCTGAACGGCGCGGGCG
CGCGTGCGGGGCTATCCTTATTTATAGAATA

SEQ ID 8040

MNRVETHFI OYAADGCAACRPFR RHFCGRRRGVCRLNGAAARVGRILTYRI

SEQ ID 8041

2TGC AAAACCGTCAAAACCTCGCCAACAGGAATCGAACCTGTATTTTACGCTTAGGAGGCATACGTTCTATCCGTTGAACTATGGCGAGCCGAAA

SEQ ID 8042

MOTVKPROOESNLYFTLRRHFFYPLNYGEPK

SEQ ID 8043

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ACATTAAACGGCATTTGGAACTTTTGAATCAGCAAAACCGGCTTCGAAATAACAACGGAATCGACGCGCAAACTTTCCGCGCGTCTTTGAAGGAATGCGAATTCGCACTTAACCTCG
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SEQ ID 8044

SEQ ID 8044

MKITHCKLKKEVQKEPLRSFVPEVTARSADILGHPDAAALFYRKIRITVTNHRLLAAAEVFFEGPAGPGASCFGGRRKGRRGGAAGKAVVFGIPKRNGRAYTTVAADDAEPELTLPAVKK
KTPMDPGTVVADSPGSRGKSDAGGFFTRCIRNRSKEFADRRNHNGIGNFMNOAKRALREKYNGIDRKPPFPPLKECEPFLNGFTGPSROLKILRDWCGI

SEQ ID 8045

SEQ ID NO: 8045

TGTTGTGACCGAATCGAGAAACTATGTCCCAACAATACGCTTATTCTATGCTGCGCGTGAGCAAGTTGTGCCCGCGCAGAAAACCATCATTAAAGATATTTCCCTTTCTTTCTCCCGG
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GCGT

SEQ ID 8048

LFRDRIEKTMSQVVYNSLRVSKVVPVQKTI1IKDISLSPFFGAKIGLLGNGTNGKSTVLRIMAGVDKEFEGEAVPMGGIKIGYLPQEPELDPEKTVREEVESGLGEVAAQKRLEEVYAEYA
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 LDRGHGIPWNGYSSWLEBQEKRELENAESEAARVAMKQLEBWVQNAKGRQAKPKARLARFEEMSNEYEQKRNETQIFIPVAERLIGNEVIEFVNSKSPFGDKVLIDGLSPKVPAGAI
 GTIGPNGAKSTLFRMIAGKEQPDSEGVKIGTQVVKMSLIDQSRGLQNDKTRVFDNIAEGREDTLQVGQFELPARQYLGEPFGRFSDQSKLIARLSGGERGLHLAKTLHGGGNVLLDEFSN
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SEQ ID 8047

ATGGATTTTTATGACAGGAGCAACGTTTCGCGTGGCTGCAATTGGCGTTTACGCCCTATATACGGCGCGAAAGTTTCTCGTCTGATGCGCAGTTTCGGCAGCGCGCAAAATGCCTTGT
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SEQ ID 8048

MDFMTEDEDFAWLQLAFTPYIGAESFILLMRSPFGSAQNLSAPAEQVAPAVNRHKHALAEWRNAEKRALARQAAEALEWETDGCRLMLLQDEDFPELTQGLTAPPVLFIRGNVRLHKP
SAATVGSRHATPQAMRIAKDFGRALGGKGIPTVSMASGIDTAAHQGALEAGGTAVWVGTDIDRIYPANKNLAYETAEKGLIVSEPTIGTRPYAGNPPRRNRLIALSQTVLVVALE
SGSLITAGLAAMGREVMVPGSIDNPHSKGCHKLTKDGAKLTECLDDILNECPGLLQNTGASSYSINKOTFDTGRRAVOTAYAPPPAAKMPSEGAAGSTAVGGILDKMGFDPVHPDVLG
QLAMPAADLYAALLELDGSAVAMPGGRYQRIT

SEQ ID 8049

TTGGCTGATTTTAAACCTGACTTTGGGTGGCTGTGTAAACGGCCGCTGTGTTTTTGGCTTTCGGCTTCGGCAGCGGGCTGGTTCGGTTTGCGCCGGGCACATTCGGCACTTTGGCGGCAC
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SEQ ID 8050

LADFKPDFAWLLKRPCLFLAFGFGSGLVFPFAGTGTGLAALPLAFVLILGIDGLLLAFVCIVLPMAGIRICACAERETGVSDHGGIWDEIVAMLVPLAFVPPFWTWWLLAFLVFLRLFDA
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SEQ ID 8051

ATGCCGTAGCAGCGATATTTTTAATTGTAGACGACGAAGTCGGGCATCCGGACCTGCTGTGCGAAATCTCGCAGACGAAGGCTATTGCGTCTGCGTGGCGGAAAAATGCCGAAGAGCGCGCA
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SEQ ID 8052

MRSSDILIVDDEVGRDILLSEILQDEGYSVALAENAEARKLRHQARPAMVLIDIMPPDCDGITLLKEWAKNGQLNMPVVVMSGHASIDTAVEATWKIGIDFLEKPIISLQKLLSAVENALK
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SYAAGSDGISCEEKLAGLFSVSVRIPPLSMQHEDIPFLIQIACNVAESQKITPTAFSDDALAVLSRYDWPNGFEBQLQNVVTTLLLEADGQEQIGGAASSALGRGVPADGTGHMACGDFD
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SEQ ID 8053

TTGCAACACAGGTACGATGAAGGATGTCGTATTGGGCATAGGCAGCATGCGCGCATPTGTCGCCGCCGCGCAAGCGTTCGATTGTGTTTCAGTGGCGATATGCTTTTGAAAGGACAGGCATT
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SEQ ID 8054

Q1767001.1: LQGTGDKDVLVIGIGDAAIVRPREGFDLCSADMLIKDRHFFADVKEPLGANKVLAVNISDMAAMGAIPRWVLLSALPELDEFWLLERFCGSFFGLAKKFGVTLLIGDVTYKGDMAFNVTII
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SEQ ID 8055

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SEQ ID 8056

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YALFFRQPIPENVAQDAVLEKARAKYAEISYKGLQTFPLVTLTLLIASLLSIFLALVWALYFARRFVEPILSLAEGAKAVAQDFSTQTRPVLNDEPGRILTKLFNMTQELSLAKEADER
NRRREEARHYLECVLDGLTGVVVVDEKGRKLTFFNKAABEQILGMLAPLWSSRHGHWGVAQSSLLAEVFAATGAAAGTDKPVQVEYAAPDDAKILLGKATVLPEDNGNGVVMVIDDIT
VLIRAKKEAANGWEVAKRLAHEIRNPLTPIQLSAERLAWKLGKLDQDAQILTRSTDTIKQVAALKEMVEAFRNYARAPSLKLENQDLNALIGDVLALYBAGPCRFEBELAGEPLMMAAD
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SEQ ID 8057

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SEQ ID 8058

MAFTITRLFKSIKQNLVLPILSVLPDAAEGIAATRAEARIIDGRLSISRRFQTELPDQLQALRRGVLPNFTLSWQLSAPTASYRFLKQLIGDDNDIDYKLSFHLPTNRYRVTVGAF
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SEQ ID 8059

GTGTTTCAGCGTATTTCACCTTTAGCTTTAGCCATACCGTACCGGTATGCACCGACACCTGTTTCAACACAAACGGCATATCAAAGCACGCACTGCACGCCGCCCGGAATGCAAG
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SEQ ID 8060

VFQRISLLALAIPIYPYPTTLFQHTNGISKHRTARRPECKAATSATD

SEQ ID 8061

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SEQ ID 8062

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SEQ ID 8063

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SEQ ID 8064

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SEQ ID 8065

ATGATGATAAAACCATATCCGCGCATACAGTCCGCGCACATCGGGCAGGATTCATCCATTTCCTCAATGAGGGGAAAGGCGTGAATTTGTATGAATTAATCCCTTTCGCGGCTTGATACAG
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SEQ ID 8066

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SEQ ID 8067

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SEQ ID 8068

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SEQ ID 8069

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SEQ ID 8070

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SEQ ID 8071

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SEQ ID 8072

MIPEKSINGWKYRAVMEIRTTQKELAINSLYTTDRIE

SEQ ID 8073

TTGGGCGGTTTGGCGGAAGAAGGTGCTCATGGGAAATCCCTAAATGCCTTGGTGGGAATTTAGGGGATTTAGGGGAATTTTGCAAAAGGTCTTCGGGTTTGATTATAAGATTGGGAAG
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SEQ ID 8074

LGGLPEGAHGSFKCLGNNLDFRGIQJRSSGLYKIEWEGWRMPALPFFRTSIPMLVQNMESIFNHNKDAIFLEGWSLGDAAHIMELLWQNIPTSRRELTKLFLYKNFVGCTR

SEQ ID 8075

ATGGGCTTAAAGTGTCTGCCCCGAAAGACGTTAATCACACAAGGAAACCAAAAAATGAATCCAACTTCAAGGCCACATCGTCGGCGTTAAAAAATCAACGGCAAAATCGAAGGCAAGA
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GCCCAATTTCCGATCGAAGCAAACTGAACGTGGAATCGTCACTACGGCGCAAACTCAAAACTGAAAGTCATCGGTTTCAACTCGTTAAGAAAGGC

SEQ ID 8076

MGLKCLPERRLITQGNQKNIQLQGHIVGVKFNQIEGKSPDYCRILIVATPLDSSQGNALGSSTTYDFGGSANFBQFRNAQFPIEANLNVIEVITGKTQKLKIVIGFQLVKKG

SEQ ID 8077

TTGCAGCCTGAAACCTTGAAAAAGAACTCGGCTTAAAAAGAAATGATGATGATTGATTCCTATAGTGTAGTCTTGTCAATATGGAGTGTATTCAACAGACAAAAAGAAATCGG
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TTTCATAAAGTTTATGGAAGAAAGAGATTACCGTCCATTTCCGTTATTCACAATACCGCTGATTACGAATTTCCCAAGCGGTAAAAGATTTCGTTAATTGCAACAGAAATACCAAA
AAAAGCTGGAACCAAGTCAAGTATTCGGGCAACCGCTTACGGTACCGGATGTTTGGGAATGGAAGAACGCTTTCCCAAAATATGGCAGGACATCAAGACGAGACGGATTTTATGCATAG
TTGTGCGGGATTATCCGATATCAATT

SEQ ID 8078

LQPETLEKELGLKNNDDLILIGCSPCYWSVIQTDKRSKSKSLLEFQRFVEYFNPYVVVENVPGILSRMKESGLDNFIKLEEKGFVHFHGHNTADYGIQSRKRFTLIANRITK
KSNWQSSIRANGLRYAMPNEWKTAFFKLWQDIKTRRILICIVVRDYPISI

SEQ ID 8079

TTGTTTACATCATCGATACCGGCGGAGCTTTCACGAATATTGCAACAGTACCCGGTACAAAATCCGCTAACCTCATGCATCGGCAAGATATTACC

SEQ ID 8080

LFHLIDTGRFRFTNIATVPGTKSANLMHRQDIT

SEQ ID 8081

ATGACCAAAACAGCTGAAATTAAGCGCATTTATCGTTGCTATGCTCGCTTCCGCGCACTGCTGTTCCGGGCGAGGCGTCCGTTACAGGTTACACCGTAAGCGGCCAATCGAAGCAAAATCGTAC
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SEQ ID 8082

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SRTNVQSVRVEGHTDFMSEKYNQALSERRAYVANNLVSNGVPASRISAVGLGESQAQMTQVCQAEVAKLGAKASKAKKREALIACIEPDRRVVKIRSVITRQVVPARNHQH

SEQ ID 8083

ATGAAAAACAGCGCGCTATCCGCCGAGGAAAGAGAAAAATATGGCTTTACTGAATATCTTGCATATCCCGACGAGCGTCTGCACACCGTGGCAAGCCTGTCGAACAAAGTTGACGAGC
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SEQ ID 8084

MKNRRRIIRRRKEMALINILQYDERLHTVAKFVEQVDERIRKLVADMFTMYESRGIGLAATQVDVHERVVMDLTEDRSEPRVFINPVIVEKDETTTTEEGCLSVPGIYDAVTRAERV
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SEQ ID 8085

ATGTTAAATGCGGAACATTTGTTATCACACGACATCCCGAGGGGCTGCCCGCGCTTTTCCAAACCAATCAAGCAAGACAAACCGAAATTTATCAGATAAGGGGAACGGTTATGCAAC
GTCGATTATTAACCTGCTCTATATTCAG

SEQ ID 8086

MLACGTFVITRHIPRCRRFPQPNQARQTEIYQIRGTVMQRRIITLLYIQ

SEQ ID 8087

GTGTGGGCTGTGTGCGGCTGCGTGAACATTGTTTATAATTTATCATATTTCTTCCCGGTACGGTATGGGGCTTTGCCGTTGTGTTGTGTTGTTTGTGCAACGCGCAATCGTCGATATGG
AAAAATCCCCCTAAAG

SEQ ID 8088

VWVCVGLNIVYNLSYFLAGTVWGFVAVFVVFVQRCSDMEKIPK

SEQ ID 8089

ATGGCTTTACTGAATATAGACGAGGTTTATAACGACGTTGCATAACCGTTCGCCCTTATCTGATAAATTTCCGTTTGTCTTGTGATGGGTTGGAAAAAGCGGCGGACGCCCTCGGG
ATGTGCGCGTGTGATAAAATGTTCCGCAATT

SEQ ID 8090

HALNTEBQYNTTFLHNSPYLINPGLSCLIGLEKAAAAAPRDVPCDNKCSAF

SEQ ID 8091

ATGAAATTACAACAATTTGAAATACGCTTAGAAGTTTACCGGCACAACCTGAACGTTTCCGAAGCGGCGGAAGCCTTATTCACATCAACAACCGGCATCTCCAAACAATCAAATTCGCTGG
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SEQ ID 8092

MKLQQLKYALEVYRHNLVSEAAEALFTSPQGISQIKLLEETIGIQIFIRSGKRVSVSPQKGVLDIAERILRDVQNIKNIGSEFTQDQSGSLTVATHTTQARYALPLIVADFVKRYPK
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 GLMAKWAYNPDTGDQLQVDAHLFEPSPWTIALRSDTYLAGYADFIOQAFAPHLTREKVDRILYTPISEDFTS

SEQ ID 8093

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SEQ ID 8094

NRILTSNYPYHHGNYEKQAAYPPKERENYGFTEYRAGL

SEQ ID 8095

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CTCA

SEQ ID 8096

MKACGTFVTRHPIGRCRRFPQPNQARQTEIYQIRGTVMQRRRIITLLCAAGMAFSTQTLANLEVRPDAPQRYTVYKQGDTLWGISGKYLSPFWQCRWLWGANRDQIHNPDLIYPGQVLVLRL
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 TDSALBQRSKQAEERLKDNEYTRTHPLTIPVTRTSIQPLVVTETAISEYQGGDYLMKMPEDTORFMVPEHPSRPVQAKIVSVFEGVGVGQGFKTITIDKGGDGLDKGAVLSLYKKRRTM
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SEQ ID 8097

ATGCAAAACCCCTGATTTTAGTCGGACAAAATGCCTTTTATCCGATGGAATCGGTTTCCGCCCGAACGGAAATCAGACGGCTGTCTCCCTTCAGACAGATATAGCGAATTAAACAAAAACCG
GTACGGCGCTTGCCTCCGCCCGCGGCTCAAAGGGAACGATATCCC

SEQ ID 8098

NONPDLVGQNAFYPMESVSARTEITAAVSLADRYSELTKGTALPRPGSKGTIP

SEQ ID 8099

ATGTGTCACCAAGCATAATCCGGATGGGGCAAAAACACAGAAAAGGTACGGTATGGCTTCGCATAATACTACACATCAGATGAAAACCGCTGTGTCTCTCCGTGCTTTGCGGGAACTCT
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SEQ ID 8100

MCQQAHNRDGAKHTKRYGMASHNTHTWKMTLCSLCLPVGLLPNEFSQLDAVIRQSRRLKKGYLEFRAGGAPTSLFAIRSGFPKTTVASQDGRDQVTGFFMSGELIGMDGICSYVH
SCDAVALENSEVCLPPTHIEELGONTPSLRTHFFRMISREIVRDQGVMLLLGNMRAEZERTAAFLNLNLSQRLYSRGFAANDFILMSREEIGSYLGLKLTQVSRITLSKFHQEGLISVZKH
IKILNLOVLKMGVSCSHAI

SEQ ID 8101

ATGATGATGTCACGCGCTTCGTGCCAAAGTCGTTGCGCACGCGATACCTTTATGTTTGTATTTCTTTGGCCGGTTTTTTGACCGCGCAAAATCTGGTTCAATCAGAAAGCCCTATATCGAAGAGCTGC
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SFO ID 8102

MSHASVQSRFPILYVLIFFAFGFLTAQIWFNQKAYTEELPFLLSALSAVALVWLAWAFVSVRKAKAEKFFYREKMIQNESIHFPVLHASLQHLHKPMLALLVKNHGKGMARVVRPKAEV
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SEQ ID 8103

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GGCGATTGAAATCAACGTGGAAGACGACGCGAGAACCCTTTTCGGGGCGCATATCGTCGATCCCGTTCGAGTGAAGAAAGTCAAAACGGGCGTTTCAAGGGCTTTTCCATCGCGCGCAGC
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SEQ ID 8105

ATGAGCACCTTC

SEQ ID 8106

SEQ ID 8107

SEQ ID 8108

SEQ ID 8109

SEQ ID 8110

SEQ ID 8111

SEQ ID 8112

SEQ ID 8113

SEQ ID 8114

SEQ ID 8115

SEQ ID 8116

SEQ ID 8117

ATGGTCGATACACCGTGCCTTTTTCGATGGCTTCGACACTGAGTTTTTCGGCTTCATATCGGTTCCACACTCTTCGTGTTCAACACCACGCGACAATATCGCCATACGCGCATAAACGCCG
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CGCGGTATTATCGCAGATTTCGCTCCAAAGTTTACCGCAGGAATCCTGTATTTTTCAGACGGCATAATCAAACACGCCGCATAAAGCATAAGGTATAATCGGCCAGACATTTCTTTT
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SEQ ID 8118

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AVSAVGFQQLFQNNVGHREAGRRDEGKFAAPAFQRLTQRMHGAVPVQVARHGDFKLVTPLRFINRYQVQQGLAGLVRAVAGVDDGDARKLRHARRAVFGMALINRVGVAGNDTGGIGK
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SEQ ID 8119

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SEQ ID 8120

MLICNPYEVVHIGTSSGKIFRPGDWAERICGLISSTFKONRLSYSEKVVPRMLVDNIRCAVDDKKLETDNPOMFRLPMDFAADNDLRVIDCKALLERERQGGQNDPANERVLLAAQALEKH
AAETQEQBTASGASVYLREIGADDTATAFAALSVLRSSITDIGRFTQINKIQRPQGYRLLGIFEECKHNAVAVCGPREACTLAGGRHIHIDDIVTLPSRRKIGYASRLLEEVRKIGASTG
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SEQ ID 8121

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SEQ ID 8122

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 VFIMMSALLAAALWLFASRRKGLPVSTHATIGGIVGSGALCMFTFNNADGVALRWGKLGEIGMSWLSPLVGLGAASYFLFSRVKKNVLDYNAWAGTLLKGIRQEKKAYKERRHLRFFEGLS
 EAEKVYATKMAHDAQIYDEPEFDPQELQSEYYRGLYAFDRNRKNVNDVSYKALHSWIPIIASFGTMMISAMLIKGLKLNHLGMSNVNSFLTIPMIGAAVVMGTFVFAKSLKRKDLGKSTFQ
 MFSNMQVFTACGPAFSGHAGNDIAANLGPFAALNDVLRTHNSVAAQSAVPPIAMLITFGIALIVGLMFLGQKEVIRKTVQTSLSAEMHPSAGFTAELSAASVVMHGLSMLGLPVSTSHLILGAVLIG
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SEQ ID 8123

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SEQ ID 8124

MINGVLIFFLITVPILGFCATINYFIINKFKLPKYMAYLLPSLSILFIFIHAIKLEHILFFYVSCVYSAYTTYDKSL

SEQ ID 8125

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GATGGCTCTCGCATATTCGCCGAACGGCAGTTTCGACCGGAGGCAGCAATACAGTGTGGCGCAACCTCATGATTTCACCACATTAAAGGAAGATTGCCATGSGCTCAATCCAAA

SEQ ID 8126

VERKYYPATSSSRSVIOTVSGSSPAFGOVWGYSDAVOKEGCVCHIPKROFDRROQYSVGNTHDFHHIKGRLPWLKSK

SEQ ID 8127

TTGCGGGCGCATATAATATTTTCCACCCGTCCTAAACATTTTATTACACTTTATTTACACTGCGGGCGGCAAAATCGGTATACGAGCGTCAATACACGTTAAATATGGCGTTTTCACACAG
TTTGGGGAG

SEQ ID 8128

LEAHYNIFFPVLKHLFTLYLHCGGKSVYEROYTLKWRFPVWE

SEQ ID 8129

TGGCTTGGCCCTATGTTTGTGTGACCCCGCTCTCTACCAAAACATCCATGTACGGAGTTGGAAAGCAGCGCGAGATTCGGGCATAGTAAACAAGATTGGATTTTCTTGCGGCGCGGCTT
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 ACTGGGTTTGTGAAGCACAAAGGTTATGCTTTGCCATTTGAAACAGTTGGTCAACATAAAATTCCTGTAATTTGTGTATTATAAAATACCGGTAAACCAACCACTTTTTCGGTATTGAACGGTATT
 AACGGAGAAACTGTTTTCCTGGCTGATCTACGCTGGGGCGGCTCTCAACGACGAATACCAATCTTTGAGCGCATGGAAACATGCGATGGCGGACATGGAAAGAAAATTTTAGCCATCTG
 TGGCCAAAATATCTGATTTTGTGTGAAATCAGATGTTTTTAAATAAAAATCCCGTTCGTCAACACACGTTTTCACGGTAGAACAAATCCAAATGCGGCAAAAACGA

SEQ ID 8130

LLGLCLLPASYQNIHVRSWKARRDSGIVKQDLDFSCGAASTATLLANFYGRHYSEAILDKMDKTMQRTSFDDQRIPELGFBAQGYALPFBQVLQKIPVIVLYKTRKNNHFSVLNGI
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SEQ ID 8131

SEQ ID 8151

ATGGCGTTTTCACCAAGTTTGGGAGTGATGATGGAAACACAGCTTTACATCGGCATTATGTCGGGAACCAAGTATGGACGGGGCGGATGCCGTGCTGGTACGGATGGACGCGGCAAAATGGC
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SEQ ID 8132

MAPCTSLGVMMETQLYIGIMSGTMDGADAVLVRMDGGKWLGAEGHAFTPYPDRLRRLDLQDTGTDLERSEMLSQELSLRYAQTAELLCQNLAPCDITLGGCHGTVRHAPHEGYS
IQLADLFLAELTRITVTVGDFSRDLAAGGQAPLVPAPHEALFRDRETRVVLNIGGIANISVLPAPGAFDFTGPNMLMDANTQAHQWLPYDKNGAKAAQGNLPLQLLGRLLAHPTF
SQPHKSTGRFLFALNWLETYLDGGENRYDVLRLSLRPTAQTVCDVSHAAADARQMYICGGGIRNPLVMDLAECEFTRVSLHSTAEINLDPQWVEAAFAWLAACWINRI PGSPHKATG
ASKPCLLAGYGY

SEQ ID 8133

GTGCTTGGCGCTCTAGGGAACCGTTCCTTTGGGCGCGGGCGGGCAACGCGCTACTGGTTTTGTGTAATCCACTATAAAGCAAAGAAACCGCATTAGCCTACACCCCCCAAGCTG
CGGCTGCAACACATCGGCTGCTCTCGACGCAACCGCTGAAAAATCGCGCTATCGCGCGCGCTTACCGCACCGCTTGCCTTTCGCCACCTGCCGATGCGCT

SEQ ID 8134

VLGRRLRPPFLRGGATPYWFLIHYKSKETAISTTPQAAAHHIGCFSTHPLKNAFYPPAL/TAPPATLPDAV

SEQ ID 8135

AACCTTTCGCGCAACAAAGACAAGATGTCGGCGCAATCAGCGGCGGACAGGGATACCGCCATAAATGCCACCGCATGACCGTACCGATCAGCAAGCGCTTACCAATACCGGCTGC
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GACGTAATCGAATGTTGTGCTGACCAACCCCAACAGAAATCAGGTAACAGAAACAGGGGAACAAATCGAAATTCAT

SEQ ID 8136

NLSGNKRQDVGRNQRDRDTHAKCHPDDRTDQARYQYRLPSHRHAASRQPSHENIDKNGYHFKIKFGNRRNLRLS*NQRTQNPYGQKNDTVEQVPLLDQRDLQYCLLHQDQYVGR
DGNRIIVADHPQONQRNQRGNKTEIH

SEQ ID 8137

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GGTTCAGGCTTCAGACGGCATCGGCGAGGTGGCAAAGGCGGGGTCGGTCAAGCGCGGCGA

SEQ ID 8138

MKVLNGWSDRKMVRVLSALPIGVVFFDLIYGFVLNVLQGLDLQRAVPDSEGLAVTPDIAFNLSLQIVANGMAAVVCFGLAVVFLNRSVRRRQVLEIGVFMGLGLVAVLAFSAPSLWENA
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SEQ ID 8139

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SEQ ID 8140

MKTLILLIPLVLTACGTLTGIPAHGGKRFVEQELVAASSRAAVKEMDSLALGRKAALYVSMGDQSGNISGGRYSIDALIRGGYHNNPDSATRYSYPAYDITATTKSDALSGVITST
SLINAPAAALTKNNGKRGERSAGLSVNGTGDYRNETLLANPRDVSFLNLIQTIVPYLRGLVVPPEYADTFVVFVDVFGTVRSRTELHLYNAETLAKQTKLEYFAVDRDRKLLIAPKTA
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SEQ ID 8141

TGCTCTGCTTGGCTACTATTGTACTGTCTCGCGCTTCGCTGCTTGTCTGATTTAAATTTAATCCACTATACCGGACCGCAAGCGCGGCAACAAAAACAGGGCGCTGTCTAG
ATAAC

SEQ ID 8142

LPRLAVLVLSAASSPCPDNLHYTRPRKPNKQGPVLDN

SEQ ID 8143

GTGTCGGGTATAGTGGATTAAATTTAAATCAGGACAAGCGCAGCAAGCGCGAGACTACAAATAGTACGCGAAGCGGAGGCAACCGCTACTGGTTTAAATTTAATCCACTA

SEQ ID 8144

VVGYSGLNLNQDKATKPQTVQIVRQGEATPYWFKFNPL

SEQ ID 8145

GTGAAACCGCTGCGCAGACTGACAAACCTCTTGCCTGCGCGTACGCGCGGTGCGACTCATACAGCCCGCCCTCGCGCGGACTTGGCGCAAGACCGCTTCAATACCGATAACACCC
AACCGGACGACTACGAAACCGCGCGGCAATATACCACTCTTTCGCGGACCGCGCGCGGACGCTTTCGAGCGCACCGGCAAAATCAACGTCAATCAAGACTATACCCACAGATGGGCAACCT
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SEQ ID 8146

VKPIRLRLTWLLAACAVAAVALIQPALAADLAQDPFITDNTQRYHEPGGKYHFGDPGRGSVSDRTGKINVIQDYTHQMGNLLIQQAIIQGNLYTVRFSGHGHHEHAPPDNHAADSASEEK
GNVDDGFTVYRLNWEGHEHPADAYDGPFGKNYKPTGARDYEYTHVNGTARSILNPTDTRSIQRIFDNYNNGSNFSDRADEANRKMFEHNAKLDWNGNSHEFVNGVAAGALNPFISA
GEALIGDILYGTRYAIDKAAMRNIAPIPAEGKFAAIGGLSAGFEKNTREAVDRWIQENPNAETVEALVNVLPFAKVKNLTKAAKPGKAAVSGDFSKSYTCSFPHGTLVKTADGYKAI
ARIQAGDRLSKDEASGETGYKPVYARVGNPYQETVYIEVSDGIGNSQTLISNRIHPYSDGWIKAEADLKAGSRLLSESGRTQTVRNIVVKPKPLKAYNLVADWHTYFVKGNDQETBGV
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SEQ ID 8147

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GAGCGAATTAGCCATTGAGCTTCGCTGAAACTTCGTTTTCGTATCAATCACAGCACACATTTTGGCGAAGCAGCAAAACCATAT

SEQ ID 8148

MFDGEVEADESYFGGQRKGRGAAGKVAVFGLLKRNGKVTVTVPNTQTATLPIIREQVKPDSIVYTDCTRSYDVLVDVSEFSHFSAETSFVSQSQHTFCRTTKFY

SEQ ID 8149

ATGGGAAATGGACACCAAAATAATCAATCTTCTTAGAAAAAAGAATTTTTATCTGGAGCATTCGGGCGAGTATCTGATGATTGCGCCCTATCGGATTACTCCAAAAATAACATACG
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TGAAAAGGCAATTAGCCATCATTTAGAAGACTTTTCG

SEQ ID 8150

MGNHGQNNQSSLEKRIFFYLEHSGQYLMICALSDYSQNKHTVVMANFLYPNEKMDWRNLDDLPLELVLLELQSSFMWYPTIEKAISSHLEDPS

SEQ ID 8151

TTGCAGGTAAATATCAAAACATTAATTTAAATCATATTTTACAGAAATTTCCGCCGCTTCAACAAATGACATCAAAACCGGTTCCAAATTTCTGTAATTTTGAACAAAAATACCGCAA
AACACCGGATTGAGACCGAAAGGACTTTCATA

SEQ ID 8152

LQVKYQITINLNIHPTFYSAAFTKWTNRFQISVILQONTAKHPIETERTPI

SEQ ID 8153

TTGAGTTATCTCTCTGATAGAGAAAAATCCATACGCGAAGCCGTTGACCGGTGGATACAGGAAAAATCCCAATGCCCGCGAAGCCGTCCTTCAACGTTGCGCGCCGCAAGTCG
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GCTAATTCACATGCTGAAATTTGGTGTATCCAGCAGGCTTATAATGCAGGTGAAACGAAAGGGCATCTATGACAATGACAGTTTCAGGAAAGATGTTTGGCGTTATTGTAAGAGAGATA
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A

SEQ ID 8154

LSYLSIRENSIREAVDRWIQENPNAETVEAVFNVAAKVAKLAKAAGKAAVSGDFSISYKNFSTVKPKVIAKGTINGKTRFVUNQSAKIGSPDSPTLIAQRVNAKIQADGKPRPNATV
ANSHAEIGVIOQYAGNETKGAASMTWTVSCKDVCYKCGDLAAAQASGLKSLTVNATDNVTGNKNTYTWTPGMSIKBRK

SEQ ID 8155

ATGAAACATCAACAAATGTTTGGTGGATTTTTATTACAGATAATGGAGAAGCAATCCAAATCCCTATTTTAGAAAATCCTAACATTAAAGAAATAAATACTTTTCTGTATCAA
ATTTTGAAGAAAAAGCGGAGTCTTGTTTTCAGAAATATTCTGAGCTGAATTTGGCAATCTGAATTAATCTATTTTGAAGAAAGATATTATTACCAATAATTCAAACAAATTTT
AGAAGATGGAGATATTGAAGTAAAAATCTTAAACAGAAAAATTATAGTGAAAAATCAATGAAATTTTGGGAGACGCTACCTATTGAGCATATCTTAAAAATATTCTATATTCAA
GATATAATTTCTGAATTTATTATGAAAAATAAACCAATCACAATAATGATT

SEQ ID 8156

MKTSTIVFGGFTITDNGRIQIPILNPNKEINNFFSVSNFEKKAGVLVFRPIPEPEFGNTELTITYPEKGYLPIIQTILEDGDIIEVKNLKTEYNSGNTWELGDVUPIEHISKNISIIQ
DIISEFINKNPITIMI

SEQ ID 8157

ATGAACACAGACAGCCGCGATCTGACCGCATCAGCCACAACACCAAAATCGTCGCCACCTTTGGGCGGGGAGCAACACGTCGAACTGTGGAAGACATGATCCGCGTCCGCGCCCTGA
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GAAGTCTGCGCGTCAAA

SEQ ID 8158

MNQTSRDLRI SHNTKIVATLPGSNVVELLEDIMRVGLNVVRPNFSGHTPEFHQENARIVREAAKRAGQETAIADLQPKIRVKGIAAGGTEINKGETLVLDAALEGEGBREAVGLDY
ROLDDVAAGDVLWLDGLTLTVESVBSRIITRVNSHLKSNKINKRGGLSAGALTEKDFRDLKTAIAIGCDYLAISFVKSAEDLHIAKAVEEMKSGTAVRPLVSKIERVEAI
ENLDEILLAGDGLMVARGLAVEVGAHVPAALQKRMIRARELRPSITATQMMESMITNPVPTRAEVSVDVANAVLDGTDVAMCSAETAVAGATPFETVSQMAIICAAAEKBQDSLNGVABQ
TEYPEAVSTNLALAGGAVSVARAVHAKAIVALESGSTAFELSRHNLTLPIPALTPSVAQRMMANYRGVRPLILATSTDHDTALNEVETMLVEHNLHSGDQYIITSGSQMRBSGNTWL
EVLEVK

SEQ ID 8159

TTGAAAAGTTCAACAAATCAAAAGGTCGCGTGAATCGTGTAAATTTTCAGACGACCTATTCTCTCATTTGAAACAGGATATTGAAAAC

SEQ ID 8160

LKSSTPIKRSPEIVFNQPTTYFLHLKQDIEN

SEQ ID 8161

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GCGTCGACCATCTTCTACAAATCCCGCGGCGC

SEQ ID 8162

VQTRQHRKSSAYTKAKQGLSDCLFYLSVRLPTETETPTFLKPKSCCSALPLPPLSLSTHPATTSASRSRSTRKARQMPPTRRPSSTIPPA

SEQ ID 8163

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AAATGAAGGAAATAGGTGCTCTGAAATTAACACGATTTTCAGGCGACCTTTTGATTGT

SEQ ID 8164

VVADPTGNGFVAVCRFDQGAVERAGVGLKNLVNLFQMKIEIGRLIKHDFRPFDC

SEQ ID 8165

ATGTCGCGGCAATCAGCGGCGGACAGGATACCGCCCAATAATGCCACCCCGATGACCGTACCGATCAGCAAGCGGTACCAATACCGGCTGCCGTCCCATCAAGGCGACGCGGATC
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CAAAAGATGATACCGAGGTCAACCCGCTTCTCGACCAACGGGACAACTGTACCAATGCCGCTGCTGCATCAGCAGCAATATGTTGCCGAGAGCGGTAAATCGAATTTGTTGCTG
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SEQ ID 8166

MSAAISGPTGIPPINATPTVPISEKPVITGCRPIKGTTPHPASQATRIPIKTADIILKPKNSATGGTCAPPETNGLKTPMVKRMIPRPNPCFSTNGTNTNACCISNNVAETVIELLLL
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SEQ ID 8167

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TTGCCCGCGCGGCTCAAAGGGAACGATTCCCTAAGG

SEQ ID 8168

LHRFIPRYSAGLSPAISLNPKEQKSAGGSRCPFLYRFYFLTAGSTGLAGPFGAGAPTEAWSFSFASTAGMPFTLIKSSDNLNAPFCARYSAMAFAGPMPGSASSSCCAALMFTAAREK
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SEQ ID 8169

GTGCTGCCGAGCATTCATTATGAAGCAGATTCCGCCACCGACTTTACCGGGCTTCCCGTCCAAGGTTCTAAAAACGCGCAAAATCACAAAAACCGGTGCGCACCCACATTTACGGCGCAT
ACAAAGTCAACGACAATCTGACCGTGGGCTTGGCGGTGTACGTCCCTTCGGCTTCGCCACCGAATACGAAAAAGATTCCGTGTTGGCGCACACATCAACAACTCGGTCTGACCAGCAT
CGCGCTCGAATCTGTGCGCGGTGGAACTCAACGAACGCCATTCTTCGCGCGAGGATCATGCCCAACATAATTCGCCGCAATATGCGCGAC

SEQ ID 8170

VLPSIHYEADSATDFTGLPVQSGKNKIKTTVAPHIYGAYKVNNDLTVGLGVYVFPFSATFEYKDSVLRNINKLGLPSLAVEFVAWKLNNRHSFGAGIIAQHNSAELRYAD

SEQ ID 8171

TTGGGATATAGAAAAATAAAGAAAGAACGAGAAATGATGCTGCTATTTTTAAAAAGGAAAGAGTTATATATACCGCGATGTAGATTACATAATGGAAGGGCTTGAAAGAACATCTT
CACCCAAAAATCTGAACAGAAAGAAACAGAACCGGTACATTTGATAAAAACCTAAATCGTATTGAGAT

SEQ ID 8172

LGRIKIKERTNDAAIPKKGKSYLSRDVDSHNGGAWKEASSPKNLNRKTRNGTDFKNLNRIGD

SEQ ID 8173

TTGAGCAGCGGCGAGTAGGATTAGAAGGTGTGCTTGCAGCATTTGCGCTTTTTTGGGATTCTTCAGTCCGCATATTTGCCAGTTTCGGCGGAATATGTTGGCGGATGATGCTTGGCGG
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SEQ ID 8174

LSSGSRIRRCLOHLRFWDSSVGIIPAQFGIIMLGDDACBGMFVEFPRGRFDGAGQTEFVDVVAHQHIFVFGGRAEGDVHAQHQIIVDFVCAVNVGCDRGDFAVFRTLDGKP
GRVGGGICFIMNAGQHDVGVGDLAAVEFGQAGGIVEDGRRVGGICRALRVDRICAEVVGACVDRCGGKSABQQDGFPSVKGVISSVSKRRFVDEK

SEQ ID 8175

ATGTGCGAGTTCAGGATTTTGAAGAAACATCCCTTGTTTGAAGAGTATGACGAAAAATTCATTTATGGCAATGGTATGATGACGGAGTGTGGGATGATGAAGAATATTGGAATTTGG
AGAAATGCTTTAATCGAGGTTAGAAAAAATATCCTTATCCGATGGATATACCAAGGACATCGTGATTGGAATCGGTACCATTTATGATTTTTAATGTTTCAAAATTTGAAACTTTTTGA
AATTAAGCTTCTCTGTTGCTTAAAGTGTCAAAATTAATGAGCGTTATGAAGGTTTACAGATATGCTCCGTTATATTTTACTGATCTAGATGACAGGAGTGGAAATTTTTTAC
TTTCAATACACATAGTAAAGGTAGATTGAGA

SEQ ID 8176

MCEFKDFRNI PCFEYDENSFIGKYYDDGVWDEEYWKLENALIEVRKKYPYPMIDIPRDIIVIGTILIDFLMVQNWKLFEIKASFWLPSVKINERYERFVNLRYIPTDLDAEDWKPFP
FPIQHSKGLR

SEQ ID 8177

ATGCTGCAAGCAACACCTTCTAATCTCTACTGCGCTGCTCAAAATCAAGGCCGACGGACGCGCATGTCAAGGCGAGGATTTGGGCGTGGCTTACCAACTGGCGTGGATGTGGGACATCA
ACGACCGCGCGCGCGTGGCGGTGAATACCGTTCCAAAGTTTACACACGCTCAAAAGCGGATGGCGGCGAGACGCGCGCGGGAACACAGTGAATGACAAATATGCTCAC
ACCGCTCGGTTACAGCGGGAATGAAAAAGCGAGTGTCAAAATCGTAAACGCTGAGCTTTTGGTCCGTACACGGCATGTACAAAGTGTCCGACAAAGCGGACCTGTTGGCGGACGTAACTTGG
ACGGCGCACAGCGCGCTTCAATAAGCGGGAATCTTTTTTGAAGAAAGAAAAATAATGCTAATGGCAAAAAATCCGACCGCACCATCATCCCCAACCTGGCGCAACACCTACAAAGTGTG
GCTTGGGCGGTCTTATCAAAATCAGCGAAACCGTGCACCTGCGCGTGGCATGCTTTTGACAAACCGCTGTCCGCAACGCGGACTACCGCATGAACAGCGCTGCCGACGCGCAACCGCAT
CTGGTCTCGCGCGCATGAATACCATATCGGCAAAACACGCTGCTGATGCGCGCTACACCCACATCCACATCAACGACACAGCTACCGCAGCGGCAAGGCAAGCGGCAACGATGTG
GACAGCAAGGTGCGTCTTTCGCGACGTTTCAAAACACCGCGACATCATCGCGCTGCAATACACTACAAATTCAAA

SEQ ID 8178

MLQATPSNPTAAQIKADGHDVKGSDWGVGYQLAWMDINDRVRVGVNYSKVSHTLKGDAAWADGAAKQOWNMLTFLGYTANKEASVKIITPESLSVHGMKYVSDRADLFGDVTW
TRHSRPNKAELEPFKEKNLANGKSDRTTITPNWRNTYKVGGLGSYQISEPLQLRVLGAFDKPPVRNADYRMSLEPDGNRIWFSAGMKYHIGKNHVVDAAYTHIENDTSYRTAKASGNDV
DSKGASCARPKNHADIIGLQYTYKFK

SEQ ID 8179

ATGTGTGAGTTCAGGATATTATAAGAAACGTTCCTATTTTGAAGGGTATGACGAAATTCATTATTGGCAAATGCTATGATGACGGGGTGTGGGATGATGAAGAATATGGAAGTTGG
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AATTAAGCTTCCCTTGGTTACCTGATAGCTGGGAATTAACGAACGTTATGAAAGGCTTAAAACAATGCTCCGTTATATTTTACCAGAGAAAGACATAGTCAACGTGCAATTTGATTAT
TACAACAAAAA

SEQ ID 8180

MCEFKDILIRNVPYFEGYDENSFIGWYDDGVWDDEEYWKLENDLIEVRRKYPYPMIDIPRDIIVIGITIEFLMVPWNKLEIKASFWLPDSVGINERYERLKTMLRYIPTERDIVNVQFDY
YNKK

SEQ ID 8181

TTGAATATGGCGATGGCTTTGTAGCCGTCTCCGTTCTGACCAAGGTGCTGCCGTGGAAGAGCAGGTGTAGGATTTTGAAGAAGTTAGTTCCCAATATCCGTGTTAAAAAAGGGGAA
GGTCGCTGAAAAA

SEQ ID 8182

LNMGDGFVAVCRSDQGAVERAGVGLKNLVPNLFKIRGRSPEN

SEQ ID 8183

ATGGCCGCTGCTGACCGACTTGGAAAACTGTCTGAAAAATACCTCGAACAGTTCGGGCGGTATCGGAAAGTATCGAAGCCTGTACCGCCAACTGCAGGAGCAACCGTCTCTTCA
ACAGGCTGATGAAGCCAAACGACAGCTCAACAGGAGATTGACGTGTTGCAGAACAGTCCGACGCCATCCACAAAGACCTATATCGAAATGAACACGCTGCTTTACCGCCATCGCGA
AGTAGTTTCCATCCCAACCGCAAGCAGATTATCGGAAAAAGGGCAAGAGCGGATTCGCGTGTTCGCCGCGGTTTGAACGGCATACCAAGCTGCTGCCGCCGTCTGTGCCCGAG
CGTCCCTACCATTTTGATATGAAGGAGGTTCGTATATATTTCTCCGAATACCGAGA

SEQ ID 8184

MAGCLTDLENCLEKYLEQFPVSEIEACTAKLQEQPSFFNRLMKANDKLNQRQIDVLQKQSAAIHNEAYIEMNTLLYRHRREVSIHNRKADYAEKGERIALPFRGLNGITKLPAAVILLPE
RPTHFMKEVLYIPSRIPR

SEQ ID 8185

TTGAATAGGATTCAAAAATATGGTCAAGTAAAGTCCGCTAATTCGGGTATTGAAACAATCCAGCCAAACAATCTATAAAAAATATTTCTCTACTTCAAAATGAAGACAAAGTATGATCATG
TCATCCCTAAATCTAAGGGTGGTCAAGGTACACCTAAAAACGGGCAGGTATTATGACAGGGCTGCAACATTAAGAAGAGTAACAAA

SEQ ID 8186

LNRIQNGQVQKCANCGIETIPAKQSIKNIPTSNERQVDHVIKSKGGQGTPKNGQVLCRGCNIKKSNK

SEQ ID 8187

ATGAAATCGAACTTACTGTCGTCTATTACGATTTGGAAAGCAATATTGCAGAAAGAACTACTGTCAGGAAACATAATGCCTGATGGAATTTTCTTATTCAAGAGATTCTCTTTTCGCAC
CGAATTTGGCTTTAAACGACATTGTTGCCATAGAACGTGAGGATAAGATGCTGTTTTTCGACCACTTGATAAAGCTTCAGGAAATACCCAGATAAACATCGTTGTTTTGGATCATTTCCC
AAAGGATTTTATTGGCAGCCATAGAAAGACACAGTGTGTAATTCAGAAAAATGAGAGAAATATTATTATCGGTAAATTTTCGCCCAAAAAATATATTTCTGATTTAAAGGAATTTTAAAT
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SEQ ID 8188

MKSKLTVVYVYDLESNIAEELISGNIMPDGNFLIQEIPLPAPNLALNDIVAIEREDKMLFPDHLIKASGNTTINIVLDFHPKDLLAAIEHSGKIRKNGENILSVNFPKKYNSDLKGLIN
RYEENILSYREACLGFS

SEQ ID 8189

TTGCCGTACTATCTGTACTGTCTGCGGCTTCGTGCGCTTGTCTGATTTTTGTTAATCCGCTATATTTGTCATTCGGCAGGGAAGCCTGAAGAAGAAATTTCCCGCAAGATGGCCGGCTG
CC

SEQ ID 8190

LPYLYCLRLRLVLIFVNPLYCPFGRESLKKMFPAWPAA

SEQ ID 8191

GTGGAAGGAGCAGGTGTAGGATTTTGAAGAACTTAATTCCTCAATATCTGTTTCAATGAAGAAATAGGTGCTTGAAATTAACACGGTTTCAGACGACCTTTAATCGT

SEQ ID 8192

VEGAGVGLKNLIPNLFQMKIEGRLLIKHGFRRPFNR

SEQ ID 8193

TTGACGGAATGCGCTCTGAAACCTGTGTCGTTTCAGACGGCATTTTGACCAATACGGTACGACGGGCAAAACAGCCGGCTTTCTGTGTTTCATGCTGATGTTTCAACACACA
GGACGGCACATAAAGGCTGCCCCATGTCGCTCC

SEQ ID 8194

LTEMPSETLLSVSDGIL/INTVRRRTAGFSCVSYADVSTHRTAHKASPYVPS

SEQ ID 8195

ATGATGAGTGTAAAGAATTATTCAAAGTCATCTTAGATGAAAAATAAGATTTTCTATTAGAAGATTCACTGACCCCGATGGGATPACTTCCCAACCTGTTGCTTTAAGTATTGTTT
AATATGAAATGACCCGGGATTTTATTGTTTATTGTTGATGAGACCGGTGAGAACAAACGGATACCTTATCATGACACATTAGATTCCGCATTTGAACAGGCTGAATTTGAATTTGGAAT
CAGCAAGAGGAATGGATGCAAAAGTCT

SEQ ID 8196

MMSVKELFKVILDENKDFPIRTIHTFPGILPKFVALSIVQYENDPGFYLYLDETGEQTDYTHDTLDSAFBQAEFEFGISKEEMMQSP

SEQ ID 8197

GTGCTTCATCACTTAGGGAATCGTCCCTTTGAGCCGGGGGGGCAACCGCTACCGGTTTTTGTTAATCCGCCATATCGTCGCAAGATGCGGTTGTTGTTGCAACCCCTTAAAGGAA
AAACCATGAAAAATGTTGTATTGTTCTGTATGCTGTCTCTGCGCTTCTCCCTTGCAGCGGTAAACATCAATGCGGCTTCGACAGCAGGCTGAGGCGCTGCCGGCATAGGCCC
GGCGAAGGCCATTGCGGAATACCGCGCGCAAAACGCGCGTTCAAGTCTGTGGACGATTTGATCAAGGTGAAGGGCATCGTCCGCGGTGCTGGCGAAGCTGAAGAGACCGGCTTCCGTC
GGCGCGCCCGCACCAAAAGGCCGCCAAACCGGTGCTGCTGCGGTTAAAAA

SEQ ID 8198

VILHLRESFPLSRGGATPYRLLIRHIVARCGLLFATLKGKTMKMFVLCMLFSCAPSLAAVNINAASQQLLEALPGIGPAKALAEYRQNGAFKSVDDLKVKIGPAVLAKLKDAQSV
GAPAPKGPAPVLPAPVK

SEQ ID 8199

TTGAACGGAGGACAAAAATGATTACACCGCAACAGGCTATCGAACGATTAAATCAGCAATACAGAGTTGTTTACGATGAAATGACCGACTTGATGCCCAAAATGATGAGCGGAAAGTGC
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CGTGTCCACACAGATTGTCGCGCATTTTTCGCGGCTTCGCAACACTCGGCTCAAAACAGCTTTTGGTCCGTTTCGCGGAGGGCGGTTTGGATGAAATTAACACTGACGGCGCAAAACG
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CGCAGCGGAAGGCATCGATTACAGTAGGGCGAAGCGCAAAAAAGAGAGTTTTCGCTTTTACACGGCAATTCGCC

SEQ ID 8200

INGGQKMTTQQAIERLISNNELFYDEMIDLMRQMSGKVPPEQIAAILTGLRIKVTETVSEITAAAAVHCFASKVPLEDADGLVDIVGTGGDGATYINISTTSMFVAAAAAKVAKHGR
SVSSSGAADVMEQGANLNLTPQLAQSIQTGIGTFAPNHSAMRHVAPVRRSLGRSIPNILGPIITNPAGAPNQLLVFHTDLGILSRVLQQLGSKHVLVCCGEGGLDEITLTGKT
RVAELDKGKISEYDIRPBDPGLSTRNLDEKIVANTQESLLKMNVEILDGEGEARDIVLLNTAALYAGNIAASLSDGI SAAREBGIDSGRAKAKKEFVGTRQFA

SEQ ID 8201

ATGAATACCGTCCCAAAAGCAGGATTCCTGCTCAAACCGTCCCGCAAAAAACACAGCGAAGCCAAAGTCGAAAAATGGCGGAGCTCGTGCAGACACGCTTTCGCGGCGAATGGG
CAGTTCGCGCCAGATTGGCGCAAAACGCTTTACTGAAGACAGATGGAATAATTCGCCAACCTGTTGCGGCAGA

SEQ ID 8202

MNTVPKSRIPVKPLPEKTABAKVEKWRQLQADHGLSGEWAVALRGNGFTBQMENTIANLFGF

SEQ ID 8203

ATGGATGCAAGTCCCTAGACGGCAAAATCAAGATGCCGCTTTATTTTTCAGACGGCATTTCCTGCTCAATAAAAAAGTCGGTATTTGGAGCCCAAAACAGCTTACGCTTCGCCGGATAGGA
TGAAATCTTTAAGAAAAATGATTATAGT

SEQ ID 8204

MDAKSLDGKIKMFLYPSDGLSVNKKVIGIGAQNSLRLAGIMKSLRKNDS

SEQ ID 8205

ATGATTATAGTTGAACATTTAGAACATTTATTTGGGTGAAATCGAAAGCGGTATAAAATGCTTGGATCGACGTTATCATCTCAGCGTTTCCTGCTTCCATCACAAACATATAAAGGGGTAA
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SEQ ID 8206

MITVEHLHYLGEIESGKICLDRHYLSVSVPSPQPYKGVTTFTLGLNRYDLYKSRFELFTCEEMNKENIAAPLSGVAEYLIDNRQPILRGELIQLPRVIIIEGSKMDALVSPFFP
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SEQ ID 8207

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SEQ ID 8208

MYRKLIALPFFALLAACGREPPKALECANPAVLQDIRGSIQETLTQEARSPAREDRQFVDADKI IAAAYGLAFSLHASETQEGGRTFCIADLNTVPSETLADAEANSPLLYGETSLA
DIVQQTGGNVEPKDGLVLAARFLPAKDARTAFIDNTVGMATQTLAALLPYGVKSI VMIDGKAVTTKEDAVRVLGKAREEPEPKPTPEDILEHNAAGDAGVQQAEGAPEPEILHFD
VERADTVTVSRGEVEARVQNRASEITKLWGLDITDVQKELVGEQRKWAQEKI SNCRQAAQADQRYAEVLKQLQCDTRMTREIRIQLRYGSID

SEQ ID 8209

TTGGTAAGGGCTTCTTAAATTTGATTAAAGGTGCTGTAATTAAGCTTGTTTTTCAGATGGTCTTTCCTTCATTGAAGCAGGATATTGAGAAC

SEQ ID 8210

LVRAPNLIKRGLSLPFRWSFLHLKQDIEN

SEQ ID 8211

TTCCTTCCCGGATAAAGCAGGCTTCCTCCGTACTGCTATCTCATCTTACTTTCCTGCCATCGGCTTTTATCTCCCGGTTTACCGTTTTCGCAACTTCGCGGCTTTGGCGGTG
CAATGTTGAAGCGGCTTCGACGCTTTCGCGGCGATTGGGTTGACCGGTACTCATCGCAACCGCAACACGACGCGGTGTTTGTCTTTTCAGCGCTTCGCCGTTTTCGCAAGGTGCT
GCCGTGGAAGGACGAGTG

SEQ ID 8212

LPCKIKQVCLRTVPHIYPPAIGFYLPFGTVFANFAALAVAMLKAASTVSAALGLTRTHPTATRTTFVAFQPSAVLTKVLPWKEQV

SEQ ID 8213

GTGAAGATTAAACCATTAACAATTTCTAACAATAATCACAGATTTTATGTGGACAAAATTTGTGTTACCGAACAGATGTGAACATTTTGGCATCCGACCGAAATATGAATTAATATTTG
AATATTTATTGACAAATAATTCATTTTCAAATAACGAGTGAATCTTATAAGTAATAATTTTCAGAAATTTTATTCGAAATAAAGCAAGAAATTAATTCGATGGGAATCTACTGCAAA
TTATTTTTCGAGATAATAGATGACAGTTATATGAGTGGTTGAAGAAGAAAGTTTGTGTTTTTTGAAAAGAAATATATAAGGCTTATATTTCTTTTTCAGGATTCTGTAATAGAA
GTATCAGCTCGACAGAACCTGTATTTTATCAAAA

SEQ ID 8214

VKIKPLQFSNNHRFPYVDKICVTEQDVNIIASDRNYELNRIEIDNI IHQITDES YKVKFSEYLFENKTENNSDGNPTANYFFBIIIDDSYMDWLKESPGFFEKYKAYIFFSDSVIE
VISSTEPVYSK

SEQ ID 8215

TTGACAAGCCTTAACATTTCCCTAATATCTTCGCGCTTCGCTCCCTTCGCGCGGATATAAAGAAAAACATTTTAGGAGGTCAACAGATATGGAATGGGCGTTTAAACAGTTATTACACCT
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CGGCGGCTGATTCGGAGGGCGGTTGGCGCGCTGATCAACAAATGGGCGCAACCGGTTGAAACCAACAAACAGGATCAGGACGCAACCGGAGCAGCTGTTTCGAGCAGGCAAAA
CGCACCGGCTGATTACGGCGGAATTCGCGTTGAAACGCTTGGCATGTTTGGCGGTGCTGGCGTTTGGCGGAGATTATGGACGGTTTCGCAAAAGAAATACCTGTTGCACTGCCAAAT
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SEQ ID 8216

LTSLNYSNIFALASPSGGYKEKHFRRSNDMEWAFNSYITLIAATLVLVGVKIKILLRDNFPIPEVAGGLIAAIIILFALHEAYGVSFKEKFLQNAFMLIFFTSIGLSADFRLKAG
GLPLVVFATVGGFVLVQNFVGVGLATLGLDLPLIGLITGSVSLTGGHGTSGAGWPNFETQYLVGATGLGIAVTFGLVFGGLIGGPVARRLINMKRKPVENMKQDDNADDVFBQAK
RTRLITAESAVETLAFACLAFAEIMDGFDEYLPDLKPFVNCIFGGVIRNILTAAFKVNMFDRAIDVFGNASLSLFLAMALLNLKLNELTGLAGSVTVILAVQTAVMVLVATPVTVF
MGRDYDAVLAAGHCGFLGATPTAVANMQSVHTFGASHKAPLIVPMVGAFFVDLINAAILTGFVNFPG

SEQ ID 8217

TGACTCGCCTTGCCGCTACTATCTGTACTGTCTGTGGCTTCGTGCGCTTGTCTGATTAAATTTAATCCACTATACAACTATTTTTCACAAACAAATGCGGTC

SEQ ID 8218

LTSLVLSVSVASSPCPDNLNLIHYTTIFIKQNAV

SEQ ID 8219

TTCGCTGCCAACAACTTCGGCAAAATCAAGCCGGCAAGCCCTGCACTCTGTGCCAATCGGAGAAAATGCCGTCTGAAAGCCGAATACCGCTTCAGACGGCATTC

SEQ ID 8220

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SEQ ID 8221

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SEQ ID 8222

LLPTFGNKLKTNILNLIFFIGCRPLQIACQQLRQNGAKPLHPVPIGENAV

SEQ ID 8223

GTGAAGCAATCAAAGCGTCCGACTTCACGACGAACACTTCGGACTGCCGACCATTCTGGACATTCTGTCCGAGCTGGAAAAACCGCAGCCGCAACGGACGCGGCGCAAAACCAAA
CGCAACGAGCGTGTCCAAACCAATTCGGCGATGGCGGATGCGTTTGCAGAGTTGAAGCGTAACTCCGACAGCAGGATGTACAGCGACAGATGACAGCGCGGCTTTTGCCTCCGCTTTT
CTGTATTTCAAATATGCTATTCCCATGATGCCCTC

SEQ ID 8224

VKQIKASDPTDEHFLPTILDILSELEKQPRTDSRPQTTTQRACPNQFDGGCVCEVAVSPTAGMYSRCSGGFCPRFPYFKYVYSHDAV

SEQ ID 8225

ATGGGAATACACATATTGAAATAACAGAAAAAGCGGGGCAAAACCCGCGCTGCATCTGTGCTGTACATCCCTGCTGTGCGGACTTACCGCTTCAACTTCGCAAAACGCATCCGCCATCG
CCGAATTGCTTGGGACACGCTGCTGCGTTGTGTTTGGCGCGGCTGCTGCTGCGGCTGCGGTTTTCAGCTCGGACAGAAATGTCAGAAATGCTGCGGCTCGGAGTGTTCGCTCGG
TGAAGTCGGACGCTTTGATTGCTTACCGCGCTCGCGGTTAACTGCCTAAATATGAAATCTTGGTCTCTCTG

SEQ ID 8226

MGIHIFETEKAGAKPAAASVAVHPCRTYRNFANASAIJELVGRSLRGLRPAVRSRLRFFQLGQNVQNGRQSEVVFVGEVGRFDLLHALAVNCLNMKFLVFL

SEQ ID 8227

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ATGGAAAAACCGCGAGGTTTCGAATATATTGAAAAACGGAAATCTTTTATGTCACAATCTTCGACGCTAGCATTGAAAGCGGATGCGGTAACGGCGGATATGACAGCTATCATGC
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SEQ ID 8228

MFKKFPVLLSFFALVAFWLTGTGIAYEINPRWFLSDTATEVPEPNFVAKLARLPNADRAVVIVKESMRTEESLAGAVDDGFLQSEKDYLAALIRLSRLKEKAKWPHVTEQHEGEVW
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AAARSGGRGLSE

SEQ ID 8229

ATGGGATTTATAGAACCGTTTTCATCAAGCTATACACCTTTATCAGGAGATTATGTACAAGCTGCTACTAACCGAAAAACGACAAACCCCTACTTTCCAAATCGTATATACGCACTCTGGCT
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TTCAATAT

SEQ ID 8230

MGFIEPFLSSYTFPSRDYVQARTNRKQTLKSKIVYTHSGFORSVTENSNIQINFLIKTLVEHPQGLNKKKEIAAMMLVDLKTFFQDDYLITETELNDYFQOGIESGPIERKYNQISYLMNL
LDKLDLKRVDGLYFAEDAQRIFGNLDEITVRKRDPLYHRLYKNQLQEESEHYGNVKMLKLAYPVLIAHKKPFLSDDTFAYPDNNGLLSRLTDLSDLKYISFDDBNMVKSR
LSDDVWRKCDVKLDNLLNKKRSYLAHREMLQEDQEPHI

SEQ ID 8231

ATGCTTTACGCGCTATCTCTCCGAACCTAGCTACCCGGCTATGCACTGGCGTTACAACCGGTACACAGAGGTTCTGCTCACTCCGGTCTCTGCTACTAGGAGCAGCCCGCTCAAACT
TTCCAACGCCCACTGCAGATAGGGAACAACTGTCTACGACGTTTTAAACCCAGCTCAGTACCCTTTAAATGGCGAACACCATACCCCTGGGACCGGACTACAGCCCGCAGGATGTGAT
GAGCCGACATCGAGGTGCAAACTCCGCGTGCATATGAACCTCTGGGCGGAATCAGCCCTGTATCCCGGAGTACCTTTATCCGTTGAGCGATGGCCCTTCCATACAGAACCCCGGAT
CACTATGCTCTGCTTTCCGACCTGCGCCGACTTGTGCTCTCGAGTTAAGCTACCTTTTGCCATTGCATATCAGTCCGATTTCGACCGGACCTAGGTAACTTTCGAATCTCTCGCTTAC
GCTTTGGGAGGAGACCGCCAGTCAAACTGCTTACATGCACGGTCCCGACCGGATGACGGGTCTGGGTAGAACCTCAAAGACACACGGGTGATTTTCAAGGACGACTCCACAGAG
ACTGGGCTCTGCTTCCAAGCTCCACCTATCTTACAG

SEQ ID 8232

MLSALISSELSYPAMQLALQPVHQRVHSGPLVLGAAPVKLPTPTADRDQTVSRFPKPSRTTNGEQPYWDRLOPDVMSRHRGAKLRRRYELLGGISLLSPEYLLSVERWPFHTPEPD
HYVLLSHLPDLVSQSLSYLLPLHYQSDRFDLGNLRTPLRFGRRFPQSNCLPCTVPDIDGSGLEPQRHQGGISRTTPQRLASLLPSLPPILHX

SEQ ID 8233

ATGAATGATGATATTACTTAAATACAAAAAGAAATATTGGTATCGAATATTCTTGAGACAGAGATGAGTAAATACGCCAAACAGCCAAATTTATGAAGATTATTGGGCGTTTACCA
ATGCCTTTACAAATTAACGATCAAAATTTTGTACTGCATCAATATTGTCTTGACTTTATGATGCGAATCAAGACCAGCCATACAGCAACGAATATATGAAGCATTCGACGAAAA
CAATGCCCAAGATTCCGTTATGGCTTCGACAGAGAACAGCAAGGCCATGAATTTGGCGCTCGGTTCGTAGCTATTAATCAATTTG

SEQ ID 8234

MNDRYLLNFKTEYWIYRIFLETESNNQPNISQIYEDYHAFNAFTNYNDQKFTALNICLDFIDANQDPYSNELYEALQONIAQDSVMASQRTSKAMNLASVRELLINLI

SEQ ID 8235

ATGCCGTCTGAAACCGGTTTTTCAGACGGCATTTGGAGAGTCAACCGCTTTTTCGAATGCCGTATATGCCGAACCCGGTTCGCTACAAATTGAAACCAATCCAAAAACGGAATACACA
TTATCAACAAACAAATATAGTGGAT

SEQ ID 8236

MPSETGFTALESQTLFAMPYMPNPFVRYKLTITIQKTEIHIKQTNIVD

SEQ ID 8237

ATGAATAAGAAATATCCGAAATTAATATATCGGTAATAAGAGAAAAAGCTTCTCGGATTTTTGACACGCTTCCGCTGATGTAGATACAGTTGCAGATGTATTAGTGGAGGCTGTT
CCTTTGCTTACGAAGCCAAACACCGCGCTATCTGCTGATTACTAACGATATTTTGGCAATTAATACCAATTTGCTTTAGCAATTAATAGAAAACACCATGAAACATTAATGACGATGA
TGTGCAATGATTTTTTCAGGACGCGCGATGCGGCTTTTATGAGTACGCGTTATTCGCAAAAATCTTATTTTACGATGAATGCCAACCACTTGTATTGTACCGTAAAAATATAGGGAAG
CTGAATAACCACTATAACGTGCTTTTGGCGTTTACTTTAATGCGTCGCGCATGATACGTAATGCGCTTATTCAGATTACAAATTCCTTGGGAAAAAGTTAAACCACTGCGTGATGAAG
AATACAGTTATGCTAAATATGCGCGTTCGACGCGCTTACCAATGAAAGTTTTCAGAGTCAATTTTCGCAAAATTTGATGACTATAACCAAGCTGTTTTCAATAATGGCTGGCGCATCA
CGCTTTAATCAAGATATATTGATTTATTAATCAATATACAGCTGATGCGCTTATTTAGACCCACCTTACACAGGCAGATGAACAAATTTTGGCTTTTACGATTATTTGGACAGT
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AAGCCATAAGGAATCTGTTTTTAGTAGAAAAATACA

SEQ ID 8238

MNKYKPKINYIGNKELASWICDQLPSUVDTVADVPSGSCSFAYEAKRGYRVITNDILAINYQIALALINNHETLNDDDVAMIFSGSPHAGFSQRYSEKPYFHDCEQQLDLRYKNIGK
LNNQYKRALAFTLMRRAMIRKMPYSRFTIPEWKVKQLRDEEYSYAKYGRRRATYHNSQSHPLQLNLDYDQAVFNNGWRHAFNQDIFDLPLNIQADAVYLDPPYTGTMNNYFPGFYGLLDS
VTTSSIFKPFANFMDKKQAVELFKRVINHLKPFKYWLLSYNNASYPNRDELEEMLKNGNRNVQILETPHYVKYTKREKKQSHKEILFVEMT

SEQ ID 8239

ATGAAAGTGAAGAAATATATCAGTATTTTATTTTCCGTTTGTATTTTATTTTTCGAGCGGTTTTTATACGCCAACAGAAAGAAATGATGAATGTTTGTGGATTTGTATTGA
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CCTCTGCATAACGGCTCACCTCTTTTCCAAATCTTCAAGTTCAAAGGAAATCAGGACGCTGTCCTCCCTGTTCTTCTCGCGGATAATCCGCCGCCATCCAAATACCACTGCTGTG
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TCAGTTGCCGTATCGCTCAAAAACCAACCGGATTAATCTCATAGGCAATACCTGTTCCACGCCAAAGCAAAATACAGTGCAAAAAA

SEQ ID 8240

MKVKEYISIFIFRDLFFSERFLYANRKENDELFGVFLINQYIFYTEVFLIGIPSMRMPAAHIKNGKIRWENTVQPSPHNMSTYSGLTKIRRRRAADSTDSTEFIRLVQLHRES
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RMIGLHRRYAIRPQCYRRRLCNKKISVQIIFETLAFPSIVETPIDFLRQTVRIADHKTVRLHPGHQFPHILIKHIARVRCPNVALFAEVPNLLIVIRDIPVPRQIYLGLITPEAH
LINIFDFPAPRRIKRTVRLPNPPIFSCRPIIFPVRSVAHIYKRTIVPIQIFGINKRFRRLRKRNRNQTALADIVIQPNLFPMLLRVYKPRFLFPQTTEPDSERIILLRLQRTVI
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SEQ ID 8241

ATGCACACCACTTACCTATATTGACCTTTCTCAGGAGCAGGAGGCTATCCTTGGGTTTTGAACAAGCCGATTCCAACAAATGCTTTCTGTTGAAATGGAGTCTGATTATTGTGAGA
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CCATTTACGTTCCGAAACAGGTGATATCCGTAATACATCCGTTACAACAGCAACCAACAGCGCTTGTATTACAGGAGATATGCCGAAAGTTTTTCAATGACAGAAATCGGGCTTTAA
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SEQ ID 8242

MHTPLFYIDLPSGAGLSLGFQAGFQQLLSVEMESDYCYTRTNFPRHQLQKDLTTLTEQDLTNCNLNGQSVDLVIGGPPCQGFNAGKIGRTFTDDPRNHLKPEFVRIVKIVQPYFFVM
ENVARLYTHNSKTRIEI IQAFQNIYGSVECKILSAADFGVQJIRSRVPI GRRDKGKISFPEPLQISHQTVGSAIGHFKLAAGESNPHVANHEAMNHSQMLKEMAFVKNNGNRNDIPE
PLRPFKGDRLKYIRYNSNKPAVCITGDMRKVPHYQNRALT VRELAALQSF PDNFIFPGSKIAQQQQVGNVFPFLAKAIAESILKMSENE

SEQ ID 8243

ATGAACGCGTCAAACCTGGAGCGTTTACCTGATATTGTGTGAAACAGCGCGTCTATTGCGGTATCAGCCGGAATCCGCAACAGCGGCTTGCCATCCACAGCCGGAAGGCGCGAAAT
ATACCCGCGTATTCAAACCGGTGGCGATGCGTATCGTTGAGCGCGGATGGATAAGGACATCGCGCTCAAACAGGAAATCGCCGTCAAACAACTGACCGCCGACAAAACCGCAATPTGTG
GGAACAGGCGAAAAAATGCGCTGTGAAC

SEQ ID 8244

MNASNWSVYLILCENSAFYCGISPFPQRLAIHTAGKGAKYTRVFKPVMRI VAGGMDKGTALKEIAVKKLFAAQKRLWEQAEMPSSET

SEQ ID 8245

GTGCGCGCGTAAATCAGGACGGTCATAAACAAACATTCCTTTTACGATTGTATCGGGCAAGATATATCAGTATTATCTTCATCTTTTCCAAACGATTACCCACATTTGCGCGCTCGGCTGTTC
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GACCCGCGCAAGTGTGAAAGCGCGCGAGCTGTGTGAAGTGAAGTGTGGAAGTGCATGCCGACGCAACGCAATCGCGCTGACCATCGCTTGGATGACGAAACCGCGCGCGCAAAAC
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SEQ ID 8246

VPPVIRTVINKHSFQIVSGKVQYLYLHFLQTI THIAPSAVQTSRRQPMNITRILSQELSATTVQINAAIELLDGATVPFFIARYRKEATGGGLDDTQLRQLAERLQYLRLEERKAVVLKS
IEEQKLSDDLRAQTEADNKTALDELVLKPKRRTKAQIAHEHGLQPLADVLLEAQPDVEAAAGYLVNENIPDAKALDGAALIMBQFAEDAELIQLRDLKWEAEIHTQVVEGKE
TEGEKFSDFDRREPVRAMPSTRALAVLRNREGVNLIALKYQDDTPTTQSEYEQI IARRPKVSDGHKWLRTVRLTWRAKIFLSELEALNRLKEAADTDAITVFAARNLKDILLAAPA
GRLTTLGLDGYRNGVKCAVVDOTGLLLDTIVYLHQENMLATLSRLIKQBGVKLIAIGNATSRRETDKIALGELVRGMPESSELEKIVVSEAGASTYSASELAAREFPDLDDVSLRGAVSIA
RRLQDPLAELVKIDPKSIGVQYQHVDVNSRLAKSLDAVVEDCVNAVVDANTASAPILARISGLNQLAQNIVAYRDEWGAFFDSRKLKLVPRLEKTEPQAGFLIRINGGKEPLDASAV
HPEAYFVVKMLAQGITAELIGNRERVQIKASDFTDERFGLPTILDILSELEKPRDRPRAFGQFASFAEGTHEISDLQVMLEBVSNNVNFAGFVDIGVHDLVHISALSNNKFPVQ
DPREVVKAGDVVKVLEVDAAARKRIAL/TMLRDEPGGAKHMPSENRSRERTAGRPQRDRAPTNSAMADAFALR

SEQ ID 8247

TTGCGGGAAGAAATTTGCCCGATAAAACCTGATTTCGATGCGAGTCATCGTTCTGTACAGCAAAACAAAGCCTATTGTAGCAAAATATCGCCCGCTGCTGAAAAATGCCCGCACCGCGC
GCCGCTTTCGCGTTCAATGCAAAATGCCGTC

SEQ ID 8248

LREKICPIKPDFDAVIVRTAKKQKPIVANIARLLKNAATRRFVPMQNAV

SEQ ID 8249

TTGTTTATGACCGTCTGATTACCGCGCGCACCGGCTTTATCGGTTGCGACACCGCGCTCGCTCGTCCAAATCCGGTTACGATGCCGTGATTTCGATAATCTGTGCAACTCGTCTCGCG
CCGTCTCCCGCGCTTTCGCAAAATACCGCGAGAAACATACCGTTTATCAGGCGGACATCCCGGACTGTGAGATTTCGAGGAGGATTTCGAGAACATGAAATCGGATCCGCTATCCA
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GATGGAAGATTTCGCGGTTCGCGTACGCGCAACCCCGCGGATGCGGAT

SEQ ID 8250

LFMTVLITGGTGFIQSHSTAVSLVQSYDAVILDNLCNSSAAVLPRLRQITGRNIPFYQGDIRDQILRQIFSEHEIESVHFAGLKAVGESVAEPTKYGNVNVGSLVLAEMARAGVLKI
VFSSATFYGDAEKVPYTEDMRPGDTANFYGASKAMVERMLTDIQADPRWSVILLRYFNPIGAHESGLIGEOPNGVNNLLPYICQVASGRPLQLSVFGDYPTPDGTGHRDYTHVMDLA
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SEQ ID 8251

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ATCAATTCCTTTGCAAGGCTATCTGATCGAATGGATGGGTTATGTACCGTCTTTTCCGGCTGTGTTTCATACCTTGCCCTGCOCGGGTATGCTGCTGCTGCTGAAAGTTCCGCTTGGAAACGGG
AAAAAACCCAGGATGCAGGCAGA

SEQ ID 8252

MLVCIPTGFGASGLFLYFLINLIPAWLRSSQDLKSGIGMALIGLPTTKFLWSPIMDAVRLPVLGRRRGWMLLTQAGLLAALAAAYAFINPRNHLPIAGLSVLVAFVSASQDIVLDAFREE
ILSDEELGLGNSVHEVNAVRYAALIPGSLSLVADRMPSEVVFVITSLPHLPGLLMTLFLAHEPVLPPSVPKTLKQTVVEPFKEFPMRRGIASAVCVLLFIFLYKLGDSMATALATPFYLLH
GFSKTDIGLIAKNAGLMPAVAAGILGGVWMLKIGVNKALWLCGAVQAITVLGFWLGGFHPDVTGTERLMLAAVIGAEAVGVGLGTAAFVSYMARETNPAFTATQALFTSLSAVPRTV
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SEQ ID 8253

TTGCTACTGAAACCCGACGGTTTACAGCGTGAATAACATTTCAAATTCACGCGGGTCGGCGCCATACGGAATCGCGCGGACATCTTCTCTTTAAAGSGCATGTAGCTGTGATCCAGTCT
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CGCGAGGCACGGTAAAGTGGTGTCTTGCTTTGGTATTCGGTAGGCGCAATTCGACAAAGCGGGCTTGCTTTCTCAATCAATTTACGCGCTTTTAAATGGACATCTTCAGCTGCTGT
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SEQ ID 8254

LLLPLDGLQAVIHFKPQVRVRRHTDAADIFLFGDVAVDVPVFAEHAHQQEFVVGLEGGCKPQRSADGRDERVFFRRQVQVQVIGKVARMDVLNAVQTHGQGGKQCIQVGGRVGETAFD
 AARLAAVHRRDYDGSCTVPGGIGQPGRCFKVRHEAFVGVGGRIQNRVQGGFVDDAADVVERGIGQGLAVACEQVLTVPFNGLDVHTAAVVAHNRPHGHKGGGFAETVGMVLDDVPFHILG
 LVGAFDQSGSETGADFHILAGTDFAVVDGDFDADSFQNVHGGAGQILITAVNRRDGRKVAAPDGGAGVGLTVHMQAACPCRAAFGRDPVTGTFVHVGGFFXYAVEDEEFGPAETIGGVADTGRGQI
 GFGATCDGARVAVVLTVGRVDDVAGDDGNGNIITKRIDEGCGRIGAGLHIGLSNAPFADGRGRKRSVFKPLPGVGFQHDARRHGKVLVLAFGIQAQIDKAGFAFFNQFYGVFNHGLQLL
 KKGNGICGTRRLDAKSARFHYADAV

SEQ ID 8255

ATGCAAAACCGCAGGCAAAAAAACAATCTCTCTGTACCGCGCGGGCGGGTTTTATCGGCTCGGCAGTCTCGGCCATATTTATCCAAAACACCCGAGATTCGGTCGTCAACCTCGACAAAGTTAA
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CAGTCTGTTACCGAAGGTGTGTGTGCGGCGAAACCTACAATATCGCGCGACACCAATGAAAAAACCAATCTCGAAGTGATCAAAACCATCTGCGCCCTCTTGAAGAAGCTCGCCCCGAAAAAC
CGCGCGCGCTGGCACCGGTATGAAGATTTAATTACTTTCTGTACAAGACCGCCCGGCATGATGCGCCCTGATGCGCGGAAATATCAGGCGCGGATTTGGCGTGGCTGCCTTTGGGA
AACTTTTGAATCGCGGCTTCGCGAAAAACCGCAATGATTTTGGACACAAACACCGCGCGCAAAACGCA

SEQ ID 8256

QVVEGVGETYNIGGHNKNTNLEVIKTI CALLEELAPEKPGAVARYEDLITFVQDRPGHDARYAVDAAKIRRDGLWLPLETFESGLKTVQWYLNKKTRQNA

SEQ ID 8257

TGTGTGACAACTCTGCCGTTTGAAGAACTATATTTTCCGGCTTGGAAATTTGACGCAAAACCGGTTTCAGACGGCATCGCGCTGGTAAATCGTGCGCACTTTTGGCTCAAGCCCGCGCGTTCG
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 GCACCACTCTTACCGCTCGCGCACTCTGTGTGTGAAGACCCCGAAGATGTTTGAAGAACCGGCGGCTTTGAGCGGCTGCGGAGCGCTGGAAGAGCATTTGAGCGTTCCGATATG
 CAGTTGCGCCCGATGCGTCCACAGCGTCTGCTGACCTTTTATGATGATCTTACCGTGGCTATTACCTTCGGACTCGCATCGACCTCGGACGCGTTCAGGTTTACGAAACCGCGACCCGCGCT
 CATCTGCAGCTCGCGCGCAAGCCTATTTTGAAATCTTCCGGTATCGGCGACACCGCCTATTTTGGGCCGAAGACCGGAATTTCTCTGCTTCGACGGCGTAGAATTTGAAACCGCATGCAAA
 AACCCGTTACGAAATCAGTTCGCAAGCGCGCGGTGGGCAAGCGCGCTGCTATTTGAGCGGTCAAAACACCGCGCATCGCCGCCGCTCAAGAGCGCGCTACGCGCCGCTCGCGCGGATTTGAC
 TCGGGTCAGAAATTTCGCGCTCCGCCATGTTGAACATTTTGAAGGACTCGGCATCGGAAGTCCGAATTCACCAACAGCGAAGTCGGTACCGCGAGCGCAATGAAATCGGCAACCGTTTCCCA
 CTTTGGTCAAAAGCGCGCAACAAACCAAGATATGAAATACGTCATCAAAACGTTGCCCAAACTTTTCGCGCAAAATTCGCGCAAAACGCCCATTTATGCGCAACCGATATGCGGCAACGCGCAGG
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SEQ ID 8258

SECTID 0230
LTLTLPETPFTISGLEFDAKEFVSDGIGVVKSCRLCVKPPRSAYFAISLQELKMSIKNAVKLIEESEARFVDLRFTDTGKQKHHTVPVPIVLEDPEWFENGPAFDGSSIGGWKIGIASIM
QLRPDASTAFVDPFFYDVTVTVTTCDVIDPADGQGYDRDPRISTARAEAYLKSSGIGDTATYFGEPEFPFVDFGVPEFTIMHKTRYEITSESGAWASGLHMDGQNTGHRPAVKGQYAPVAPID
CQQLRSAMVNTLIEGLGIEVEVHHSEVGTSGSQMEIGTRFATLWKRADQTDQMKYVIQNVAHNFGKATTFMFKPKIMGDNDSGMHVHQSIWKDQGNLPAFGDGYAGLSDTALYYTGGIHKHAKA
LNAITWPNSTNSYKRLVPHFEAPTKLAYSAKNRSASTRIPSVNKSARRIEARFPOTANPYLAFALHAGLGDQNKILHFGPDADKNLYLDLPPEDDALVPTVCASLEALAAALKADHEFL
LRGGVTSQKWDYSYIAFKEKEDVRRIRKAPHELEFETPYSLS

SEQ ID 8259

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CTGCCCACTGTGTGGTTTTGCGGTACGGTTCGAATCAAACCTGAAGCTTAGTGGCTTTTCTGGAAGCGTGGTATCGGTTGCTTCTGTGTCGGTAGACACTCGTCACTCTCTCGGTGTTA
AGAAAACCGGGATTTGGC

SEQ ID 8260

MLAHLQUTFRHRAGVTPYPTSTFVLABCCVFNKQSQPPILCDPPGLTBQVLNLRGHTFSRSYGINLPSSFSRVLSSALEFSSCPPVSVCGTVRFLKLKSGFSWKRIGCFVSDTRHRHFSVL
RKPGFA

SEQ ID 8261

CGACACCCCTGACCAAGATTCTCTGCCAGCTGAATCATAGCATCTTCACTTCGCTGTGGACAGGCGATCCAACGCGGCAACGGCAACAATCGACTGCTTTGCGCGCTCGCCATCGAA
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AATCAAAGGCGAGGTTCGTTTCTTCCGCCAATCGTCCGCGAGCTTTTACCTGTTTCTTCGGTTTCCCGCAATAATCCAGCAGCATCGTCAATAATCGGAATGCGGTACCGACGTA
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GAAATGCACGGGTATATAAAAGTCCCAACCAACACTGCCCGCCGATTCGCGAAGAGATGTTTGGCGTTGCCCGCCACGGCGCAAAATCGCTTTCATCGACGACATCGTCTGCGAGGAG
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GCAT

SEQ ID 8262

RHPDQRFRLQLNHSILHFVAGGQIQRGNGTIDCFARLAYRICQSIRTDIIADFFKIAAICIPQSSTHIVRNLFGLTHQINRQGRFSFRQIVADVFTCFPGFPRIQHI VNNLECRTOV
HTVVFQGLFVPGSFAQNCADLSGSKQFCRFLDDSDILFPGNVRIADVHQLHDLISLGNVGRIRHFNQANTARGNHQLKCTGI * KVANQHCRRIAEQIVCRCPPTAQIAPIDDIVVQE
CGSVDKLDHRCQIQFLVITTDRLTRQNRHNRTOAFARADDICTDLNQCIDILHRTVDDFIDFGKVFRCMSLEIGQLIEH

SEQ ID 8263

TTGTCAACAATATGCTTCGGTTTGTCTGTTCAAAGCGGAATGCCGCCCTTTTGTCCGAATGCCGACAAACAGATGCCGTCTGAAGGCGGTTTCAGACGGCATCGTTCCCATCTTCGCG
CCGCCGTTATAAAA

SEQ ID 8264

LSITCFGLSVQKRNARPFVRMPTKQMPSEGGFRHRHSLRAAVIK

SEQ ID 8265

ATGACCGCCCGCTTTATGGAATATGACTATGCACGCCCTCCCGCTACGCCGTTTTCGGCAACCCCGCGCCACAGCAAAATCGCGCAGATTTCATCAGCAATTTGCCCTTCAGGAAG
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GTTTCATCTGCGCGACGAACATTCGACCGCGCTTTGGCTGCGGTCGCGTCAATACGCTGGTGGTTGGAAGACGCGAGAATACCGCGGACAAATACCGACGGTATCGGTTTGGCCAAC
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AAAATCGCGACGGATGCGTATGCTAGTCTGCTAGGCGCGGCTTCTACGCCCTTTCGCGCGGTTTCAAACCGGACATCCGCCCGCTCATCAACACATGAAAGCCCTG

SEQ ID 8266

MTAPPLMNMTHALPRYAVFGNPAHKSQIHQQFALQEGVDIEYGRICADIGGPAQAVSTFFETGGCGANVTVPFKQEPFLADEHSDRALAAGAVNTLVWLEDGRIRGNDTIGIGLAN
DITQVKNIAIEGKTLILLGAGGAVRGVIVLKEHRPARIVIANRTRAKAEELARLPGEIAPVADVNGGFDIIINGTSGGLSGQLPAVSPKIFRCDRLAYDMVYGEAAKPLDFPARQSGAK
KTADGLGHLVQAAAYALNRGFKPDIRPVIEMKAL

SEQ ID 8267

ATGTTCCGCATCGTCAAAATGGCTGATGCCCTGCCCGTCGGCATCTTTATCTTTTCAATGCCATGTTGTACGGCAACATCATCACTTACCGCGCGCTCGCGCCCATCGGATGCTTTTA
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CTCTTCTCAACGAAGCCGCAACTATCTGCGCAAGGGGAAGAGCGGCCATTACGGCAATGATGGAAGCTGTTACCGACAAAAACAGGATTTTCAACTGTATTTAACTCAATCGAAT
GGCACTACCGGCTTTTCGCGCGGAAGCTGCGTCCCGTATTTTATAAAAAACCGCGCGAGACCTGACCAAAACAGCAGCGCGCGCAAACTGACGGCGCATCGTCCCGCGCCGCTCTACTA
CGCTGACCATCCGAAAGCAACCGCTCGCAACAAAAACCAATATCGTGCTCAGACGATGGGTTTCGCGAGAATTACCCGAAAGCGATACGGAC

SEQ ID 8268

MPRIKWLIALPVGIFIFPNAYVYGNIIITYRAVPHRTAFMSMRKQFEQEGRDVALDYRWVPYNRISTNLKALIASEDVRFAGHGGFDWDGQIQAIRRRNNSGEVKAGGSTISQQLAKN
LFLNESRNYLRKEEAAITAMMEAVTDKNRIFELYLNSEWHYGVFGAASRYFYKPAADLTQKQAAKLTAIVAPPLYADHPKSKRLRNNTNIVLRMGSAELPESDFTD

SEQ ID 8269

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GATTTATTAACCTTGTGCGTTTGTATGCTGGCGGAATCCGCGATATTTTGGTAATTAACGCAACCGAAGACAAACGCTGCCCTTCCAAACGGCTACTCGGCGACGCTCCGACTTCGGCATC
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AATCATTTACGCAACATTTGAAACAGGCGCGCGCAAGACCCAGCGCGCAACCGTATTCGGTTATCGGGTTAAAGACCCGAGCGTTTCGCGCTGGTGAATTTGACGAAAACTTCAACGC
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CCTTCGTCAAACCGTGCAAAATATCCAAACCTGCACATCGCTGCCCTCGAAGAAATCGCTGCGCTAACGCGTGGCTGACGAAAAAGATGTGGAACAACGGGCAAGCCTTTGAAAAA
AACCGCTACGGCAATACCTGCTGCGCTGATCGGCAAA

SEQ ID 8270

MVFGQNPAAKRIKRLPFTLRYGQIVFRQHPDAMPSENFSQRKKEKMGII LAGGSOTRLYPITRGVSKQLLPVYDKPMIYPLSVLMLAGIRDILVITAPEDNAAPQRLLDGSDFGI
RLQYAVQPSFDGLAQAFIIGEEFIGWNVCLILGDNIPYQGSFTYQLKQAAKHTGATVPGYRVKDPERPVGVEFDENFNALSIEEKQPKSDWAVTGLYFDHNRVAFKQLKPSARGE
LEISDLNRMYLEDGSLVQLLGRGFAMLDGTGQESLHBAASFVQVQNIQLMLHIAELIARWNGWLTKKDVEFTRAKPLEKTAYGQVYLLRLIGK

SEQ ID 8271

ATGGACATCATCGACACCGCCCTCCCGACGTAAAACTTTTAAACCGCAAGTCTTCACAGACGGGCGCGGTTTATGGAACATTCGCGCAGGATGTTCAAAGAAAATATTGCCG
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CGTGGCGCGTATGTCGCGGAAGGTTTCGCGACTTTCGGCAATGGCGGGCGCAACCTTTCGCGCGCAAAACCGATACCGAGCTTTGGATACCCGAGGCTTCGCACAGGTTTTCGCGTT
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TACTTTCCGCCAAGACCTTCCCGCAAAACGTGGGCACAGCCGAAAGCTCCGCTTACGCTTTCCCGA

SEQ ID 8272

MDIIDLTPDWLLKLPQVFTDGRGFMETFRDGFKNLADRTFVQENHNSKSGVLRLGLHYQTEWQGLVRIIVVGEVFDVAVDMREGSPTFGKWAGATLSAQNRVQLMIPEGFAHGFCV
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SEQ ID 8273

TTGTTAGAGCAACGAGTTGAAAAATCCGTGTGTCGGCGGTTTCGATTCCGCCCTCTGGCCACCAAAAAACGATTATAAGCGGTATTTTTTTCCTGCCGTTTCGGCAGCAGTCCCGCACCGC
AAATACTTGCCATGCACGACATGGTCTTTGCGGCTGTCCGGCAGGTTAGTGGATTAAACAAAAATCAGGACAAAGCGCAGACAGTACACATAGTACGGCAGGCGGGGTAAC
GCCGTACCGGTTTAAATTTAATCCACTA

SEQ ID 8274

LVEQRIENPCVGGSIPLATKPIISGYFLPAVFGSSPAPQIPAMHDMVFAVQVSGLTIRKTRRSRRQYNIVRQGGVTPYRPFKNPL

SEQ ID 8275

GTGCGTATTAAACAAATTTCCGGACGACACGCAAGCGGATTGTTCGATATTTTTTACCACCGACTAAGTCGATGTTTAAAGTTAAATTAATTCACAGAAAAATAGTCAAAATCGGT
TTTTTTCGGCTTCGTTCCGGCAGTGTCTGCTTTGCAGACGCGAAACGCTTCAATATTTGAAGTTCCTCGCCCAA

SEQ ID 8276

VRIKPNFGTTRKIRICRYFLPNRLSRCPFKLISQKNSANRFFAVRSAMFCFADGKTLQYLKPSFK

SEQ ID 8277

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CCTGGGTGTCGGCTACCTGCCGAGGAAGCCTCGATATTCGCAAAATGACCGTCGAACAAAACATCCGCGCATCTTGAATTCAGAACCAAGATAAAATCAATTCGACAGAGAAATC
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AAATAT

SEQ ID 8278

MSANNSRLVQNLQKSFKKRQVVKSFSLIESGEVIGLGPNGAGKTTGPFYIVGLIAADAGSVMLDGRRLHLP IHERARLVGYLPQASIPKMEVEQNIRAILBIRTKDKNQIDREI
EKLADLNLIGHLRNPAPSLSGGERRRVEIARVLAMKPRFILLDEPFAVDPIAVIDIQIKIIFGLKSRGIVGLITDHNRETLISICDRATYISDGAVALASGKPDVLVNGEJQVRAVYLGENF
KY

SEQ ID 8279

ATGAATAAATCTTTATCCGGTTCCGTAGAAAAATACCGGAAGTACGCTCCGAGGCATGACTCCGGCGCATTTGATCACTGTAATTTTTACTGCGTCTAACGTTTACCTCGGTTTGAAG
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SEQ ID 8280

MNKSLSGSEVKEYRELTLRGMILGALITVIFTASNVLGLKVLTFASSIPAAVISMAVLKPKFSNILENNMVQTQASAGTSLTIIIFVPLGLIMAGYWSGPFQWTTLLCIAGGLILGVP
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PLVAAACGYMAGLVGSSSSPIISGVIVSVIVISLVLLLVGESGGLLADEANRKLALTLFCGSAVICVASISNDNLQDLKTYLLKATPWRQVALIIGCTVGLVISPVLLELYEATGF
TGAMPREGMDAAQALAAQATLMTTIIASGIFAHNLEWAYIPTGIAIGAVLIVVDLVLKSSGGLKALPVLAVGSIYLPSPVNMPIVAGAVLAVALKHIIIGKKAENRERGLKNADRIETLF
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SEQ ID 8281

TTGAAAAATAAAATATTTCACCAACGAACAAAAACAGCGGTATCAGGGAGGTTCCCGGATACGGCTGCTTGTTCGGAACCTTAAATCAATCAACAAATCGCGCAGCTTGTCT

SEQ ID 8282

LKIKTISKRTKFAVSGRFPDPAACFRTLKSIQIAQLV

SEQ ID 8283

ATGAAATACCATCCGACCGCAATCCTGACATAAAGAGCGGAAGAGTTTAAAGAGTACAAAAGCGGTATGAACTTTGTCCGACAAGGAAAGCGTCCATGTACGACCAAGTATG
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SEQ ID 8284

MKYHPDRNPDNKEBERFKEVQKAYETLSDKKRAMYDQYGHAAFEQGGQGGFGGFGGGAQGFDFGDISQMFQGGSGRAQPDYQGEDVQVIGIETLLEAAKGVKKRINIPTYEACDVC
NGSGAKPGASPETCTCKSGTTHIQAIIPRQQTCTCRGAGKHIEPKVCKRGVRNKAIVTVENIIPAGIDGQIRLSGEGGPMHAPAGDLIVYRIIRAKHIFQDGLDLHCELP
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SEQ ID 8285

TGTATAAAGCTTACTGCTTTGTGTGTCTTAATCCTGCTTTTGTGTTTCAGGATTAAGTCGATACATCATCACCAAACTATGTTTGTTCCTTTCTCTTGCAGAGGTTTTTATC
CTTTGCAAAAGATAAAAAACAAACAACTCATTTGTCTTTGTGTTGT

SEQ ID 8286

LILKIFALLCLNPAFCVSGLSRYNHPNTMFVFFSLRAGFYPLQRIKNQKILIVFVC

SEQ ID 8287

ATGCTTTTGTATTACGACAATTACGACAGTTTACTTACAACATCGTCCAGTATTTCCGAGAATTGGGGCAGGAAGTCGCCGTGCGCCGCAACGATGATATTACGTTGGAGGAAATCGAGG
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GCATCAGACGATAGGCGAAGCGTTCGGTGGAGATGTGGTACGGGCAAAAACCTTGATGCACGGTAAGGTGTGCGCCGTGTCCTCATTCGGGCAAGGGTATGTTTAAAGGTTTGGCCCAATCG
GTTACCTGTACCGCTTATCAGCGCTCGTTATCGAACGCGGCACGCTGCCGGATTGCTTGGAAATCAGCGCGTGGACGGAAGACGGCGAAATTATGGCGGTGCGCCATAAGGAATATGCCG
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SEQ ID 8288

MLLFLIDNYDSFTYINIVQYFAELQGEVAVRRNDITLLEIEALNPQYLVIQPGPCSPKEAGISVEAMRHFAGRLLPIMGVCLGHQITIGEPGGDVVRKTLMHGKVPVSHSGKGMFKGLPNP
VTCTRYHSLVIERGTLPDCLLETAWYEDGEIMGVRHKEYAVEGVQFHPREALITERGHDLNINFLVPEQNFQPKI

SEQ ID 8289

ATGAGCACCTTCTTCGCGCAAAACGCCCAAGCCATGACTGCCAAACACATCGGCCCTTCCCGCTATTGGAGTTGGACCAGGTGATTGATTGGCAGCCGATCGAACATACCTGAACCGTC
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SEQ ID 8290

MSPTFRQTAQAMTAKHIGRFLLELDQVIDQPIEQYLNRQKTRYLRDRGRPAYPLSSMFKAVLPQWHSLSDPLEHSLITRIGFNLFCRFDGPGIPGCSTLCRYKFRYARAAYFGLL
KVGAGSHLKAMCLNLLKAAANRLSAPAAA

SEQ ID 8291

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GGGTACGCGTGTCTATCCAGCCTTCAAGCACACAAAAACCGAA

SEQ ID 8292

NIQIKICKLFLVILIVFATSPAFALQSDSRPIQIEADQGSILDQANQSTTFSGNVIIHQGTINISASRVNVTRGGKGESVRAEGSPVRSQTLDDGGKGTVRGQANNVITYSAGSTVVILTGNA
KVQRGGDVAEGAVITYNKTVEVYTINGSTKSGAKSASKTGRVSVVIQPSSTQKTB

SEQ ID 8293

ATGAAAGTAAGATGGCGGTACGGAATTGCGTTCCCATTTGATATTTGGCGGTTGCTTGGCGAGCGTTCGCGCATGTTGGGCGGTATCAGCGAAGTCGAAATCAGGGAAGTCAGGCTCAATC
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SEQ ID 8294

MKVRWRYGLAFLILAVLGSLSAWLGRISSEVIEEVLNDEPQYTMGLDGRRLDEQGYLKEHLSAKGAKQFPENSIDIHFDSPHLVFPQEGRLLYEVGSDEAVYHTENKQVLKNNVVL
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SEQ ID 8295

TGTGTTCTTGTGTTGAAGGGAAATGGCTGGAGAAAGACCTGCGCTATATCGGGGAATGAATCGATGCAAGGAAATGCCGTCTGAACATGCGTTCGGGCAGCGTTTTTATAACAAAACAC
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SEQ ID 8296

LPFWKNGWRRKTCALSGNESMQRKRLNMRSGSVFTIKTLNGWFTYTLSPCVHII

SEQ ID 8297

GTGGTTGTAGGTCATACCGCCGCTGACCGTGCAGCGCGCCATATTTGGAACATGACAGGCGTATCGGTTTGGGCATATTGAGATTTCGGTATCGACGTGCACTTTTTCGGTTTCGACTTTA
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CGGTTTGGCAATA

SEQ ID 8298

VVVGHTARLTVRRAILETDRRIGLILRFGLIDVQFFGDFTRLPPAVGGFGQHNVPFKNLFVFGVNGFIAADPVQQAFLSEHEMRRIKMDVAVFGKLFRTFRAQMFQVSLFVKPPSV
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SEQ ID 8299

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SEQ ID 8300

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SEQ ID 8301

ATGGGAACGCAATTCCTACCGCCATCTTACTTTTATTGATGTACCGCTTCAAAGCGCGCCCAACGTAACCTTTTCGCGCGGATAATCAGGTACACACTTCGCGCACCGCGCCGACCG
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SEQ ID 8302

MTQFPTAILLSDFVQSRARQTFRADNQVTHFAHRARTAGAFNGIIGVLRKPMRVGDGNGRQSAHHHRQIDHVVDKGLGFFQACLRALQFIRGAFVRNAPFVVIYAQLFDADADGG
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SEQ ID 8303

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GGCGCGCCGCAACAAAGCGCCGCAAAACCGGTCTGCTGCGGTTTAAAAA

SEQ ID 8304

VLHHLRESFPLSRGGATPYRFLIRHIVARCGLLPATLKGKTHKMFVLFMLFSCAFSLAAVNINAASQLEALPGIGPAKAIAYRAQNGAFKSVDDLKIKVIGIPAVLAKLKDQASV
GAPAPKGPAPKPVLPVKK

SEQ ID 8305

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SEQ ID 8306

MQAISPELQARAARKILLIDVDGVLTDGRIFIRDDGEIKSFHTLDHGLKMLQASGVTAITGDRAPSVGIRVKQLGINYYFKGISDKRAAYEELRAQAGLEBAECAPVGDVVLDLPV
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SEQ ID 8307

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CTGACCGTGTCCGCTCGGTTTTCCGAGGAACGGCTTGAACCTTTGGGATATTCATTT

SEQ ID 8308

MIVWFFHAKVGHCTPFPKTPGYPGVFALPGKNVGDGATSVRCPVGFAERLETLYGSP

SEQ ID 8309

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SEQ ID 8310

MLSALISSELSYPMQLALQPVHQRVHSGPLVLGAAPVKLPPTADRDQTVSRFPKPSRTTLNGEQYFPWDRLOPQVMSRHRGAKLRRRYELLGGISLSPYLLSVERHPPHTEPPD
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SEQ ID 8311

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CTGCCACCTGTGTCGGTTTGGGTACGGTTCGATTCAAACTGAAGCTTAGTGCTTTCTTGGAAAGCGTGTATCGGTGCTTCGTGTCCTAGACACTGCTCATCACTTCTCGGTGTTA
AGAAAACCGGATTTGCC

SEQ ID 8312

MLAHLQLTFRHRAGVTPYTSTFVLAECVFNKQSQPPLCDPPGLTEQVNLNRGHTFSRSYGINLSSFSRVLSALEFSSCPVSVCGTVRFKLKLSGFSWKRIGICFVSDTRHFSVL
RKQFA

SEQ ID 8313

TTGCTAAGTCTTCCACCTACCGGCTTAAACAAGCTATTCACACAGCTTGCCAACTAACCTTCTCCGTCCCATGCGATTTGAATCAAGTACAGGAATATTAACTGTTTCCCATCGA
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TCGCACTTCTGATACCTCCAGCACATTTACAATGCACCTTCATCAGCTACAGAACGCTCCCTACCATGCCGTAACCGGCATCCGAGCTTCGTTATAGATTGAGCCCCGTACAT
TCTTCCGCGCAGGAGCTCGACAGTGAAGCTATTACGCTTTCTT

SEQ ID 8314

LPKSSTYRLQAIPTACQPNLLRPHAFESSTGILTCFPTSTHFLALGADSPYADERCVGNLGLSAGLPTRFIATHVNI RTSSTLYNAPSSAYRTLPHYAGKPAASAVIDLSPVT
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SEQ ID 8315

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TGTTTCAAGATGCGACAATTTTACCGGCTTTCGATAGACGAAGTATGATACACACCTTAAACCATCTCCGCGAAGCGCTCGCCACCGAAGCGCTGAAAGTATGACGAGCAACCA
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SEQ ID 8316

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VAASNSGESDEITAIIPALKRKDITLVCITARPDSMARHADITHASVQEQACPLGLAPTTSTTAVMALGDALAVVLLRARAFTPDDFALHPAGSLGKRLILLRVADIMHGGGLPAVR
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SEQ ID 8317

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SEQ ID 8318

LYRLNPETQKAGLRHNKAVSFIVKGISSLLF

SEQ ID 8319

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SEQ ID 8320

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EARRLHAATARKNAMIKVPATDAGIDALETLVSDGISVNLTLFSAQTLLKAYAYARGIAKRLAAGQSAHIQVVASPFI SRVDSALDATLPDLRLKGTALALAKAAYQDWEQYFTAPEF
AALEAQGANRVQLLWASTGVKNPAYPDTLYVDSLIGVHTVNTVPDATLKAFIDHGTAKATLTPESADRARLARLALGIDVETLAARLQEDGLKQFEAFKLLAPLV

SEQ ID 8321

TTGTGCTTAATCTGCCCTTTTGTGTTTCAGGATTAAGTCGATACAATCATCAACCAATACTATGTTGTTTCTTTCTCTTGGAAAGGTTTTATCCTTTGCAAGAATAAAAAATC
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SEQ ID 8322

LCLNPAFCVSGLSRYNHPNMFVFFSLAKGFYPLQRIKQNKLIIVFVC

SEQ ID 8323

TTGAAAGCTGATTCAAATAGCGGGCAATTATATCAGCAAGCCATCAGGGTACATCTTTTCAGACGCATATGATTGCCCGAACCGCGCAAACTTTGACAAAAACAGGCAAA

SEQ ID 8324

LKADSNSSQLYQQSHQTSFQYAYDCPNRANFDKTK

SEQ ID 8325

GTGATTAACCTATTGATTTATAATTTGTTTATTATTAACGCAATTTCCGATACCCCATCCATACCCCTTATATCTTAGCGTGCCCGATGCGCCCTCG

SEQ ID 8326

VINLLIYNLFIINCISDTPIHTPLYLVSVPDAPS

SEQ ID 8327

TTGGTAGAGCACTGCTTTGCAAGCAGGGGTCATCGGTTTCGATCCGTTTGCCTCCACCAAACTTTACAAATGAAAGCAAGTTTGTGTTTTTAGCAGCTTATTTGATTTGCGAAGTA
GAATAACGACGCATCGATCTTTAACAATTTGAAAGCCGAATCAACAACAAAGAGACA

SEQ ID 8328

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SEQ ID 8329

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SEQ ID 8330

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SEQ ID 8331

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ACAAAGGAAA

SEQ ID 8332

MPSERLSDGIALITGHSAAVQGSALKILMGKKLMHDI TRQHKRK

SEQ ID 8333

ATGGGCGCAAGCCTGATCCAGCCATGCGCGTGTCTGAAGAAGGCTTCGGGTGTAAGGACTTTTGTGAGGAAAGAAAGCGGTTGCCAATATGCGCGCGCATGACGCTACCTGAAG
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SEQ ID 8334

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SEQ ID 8335

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SEQ ID 8336

LVEHQANRELQIEPSIPSRLLLNMIQLPKSNIMPYMI

SEQ ID 8337

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SEQ ID 8338

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SEQ ID 8339

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SEQ ID 8340

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SEQ ID 8341

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SEQ ID 8318

LYRLNPFQKAGLRHNKAVSFIKVGISLLP

SEQ ID 8319

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SEQ ID 8320

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SEQ ID 8321

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SEQ ID 8322

LCLNPAFCVSGLSRYNHPNTHFVFFSLAKGFYPLQRIKQNKLIIVFC

SEQ ID 8323

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SEQ ID 8324

LKADSNBGLYQSQGSTSFQATYDCPNRANFDTGK

SEQ ID 8325

GTGATTAACCTATTGATTATAATTGTTTATTATTAACGCAATTCGATACCCCATCCATACCCCTTATATCTTAGCGTCCCGATGCGCCCTCG

SEQ ID 8326

VINLLIYNLFILNCISDPTIHTPLYSVPDAPS

SEQ ID 8327

TTGGTAGAGCACTGCTTTGCAAGCAGGGGTCATCGGTTTCGATCCCGTTTGCTCCACCAAACTTTACAAATGAAAGCAAGTTGCTGTTTTAGCAGCTTATTTTGATTGCGAAGTA
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SEQ ID 8328

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SEQ ID 8329

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SEQ ID 8330

LVEHLLCKQGVIGSIPFASTKTLQMKASLLFLAAYFDLRSRITTHRSLTNWKAEINKQEQ

SEQ ID 8331

ATGCGCTGAAAGGCTTTTCAGACGGCATCGCCCTTTGACCGGACACAGTGGCGCATATCAAGGATCCGCCCTAAAAATATTAATGGGCAAGAAGTTAATGCAGACATTACCCGCCAAC
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SEQ ID 8332

MPSERLSGIALITGHSAAVQGSALKILMGKMLMHDITRQHRK

SEQ ID 8333

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SEQ ID 8334

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SEQ ID 8335

TTGGTAGAAATGCAAGCAATGAGAGAAFTGCAGATAGAGCCTTCGATTTTTCTCGCTGCTCTTATGGATGATTCACTACCGAAGAGCAATATAATGCCCTATATGATT

SEQ ID 8336

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SEQ ID 8337

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SEQ ID 8338

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SEQ ID 8339

ATGGCAAAAGCACTCGAAATCATTTACCCGATGAAATTTATTCAGATCTGATTTTTAAGGATCCGGTACCTCCCATACTATATACAGAATTTGATGAAACTGGTTGGTAGAAATGCAG
GCAATGAGAGAAFTGCAGATAGAGCCTTCGATTTTTCTCGCTGCTCTTATGGATGATTCACTACCGAAGAGCAATATAATGCCCTATATGATTTAACCTTGCTTGAAGAGCCCGGAT
GGAAGTGAATAAGATGAGATAACGGCTTTGATTAATAGTCTTAAA

SEQ ID 8340

MAKALEIISPDEIYSDLPKDFVPPHTIYTELKLVGRNAGNERIADRAFDFFSPALMDDSATFEEYNALYDL/LLEEPGMELDKDEITALLINSIK

SEQ ID 8341

ATGCTAAAGCTGACAGAACAGATATTTGAATGGATTGGGCGGGAAGACGATTATATGAATGACGACCACTTTGGCTTTTTTCCGGAATTCGCTGTAAATATGCAAGACGAACTCATCG
AAAACGCTCCGTACACAGGCGCATCTCCAAGAACACGAATCAGCCCCGATCTCGCCGACCGTCCACAGGAAGAGTACGATTGGAACCTCGTACCCGGGATCGGGAACGAA

ACTTCTCAGTAAATACAGGCGACCATCCGCAATATTGATGAAGGGGACTATGGATTCTGTGCCGATACGGGAGAACCTATCGCCTGAAGCGGCTGCTGGCAGCCGACAGCCACTTTA
TCCGTTCAGGCCCAAGAACCOCGAGAGAGGATGAAGAACAGTTTGGCCAC

SEQ ID 8342

MVKLTEDQDILNWIGPEDDYMDHLAFRELLVQMDELLENASVTTGHLQEHESAPDPADRATQEEYALELRTDRERKLLSKIQATIRNIDEGDYGFCADTGEPIGLKRLRLARPTATL
SVEAQERRERMRKQFAD

SEQ ID 8343

ATGTACACAGGACGCTTCGCCCCAGCCGACCCGGGTGCTCCACATCGGCTCTCTGCTGACCCCGCTGCTTCTATGCCGATGCACGTTCAAACCGCGGCAAAATGGCTGGTCCGTATGG
AAGACCTCGATCCGCGCGGCAAAATGCCGGGGCGCAAGCCATATCCTGCACACGCTCGAGGCATTTCGATTCAAGTGGGACGGCGAAGTCACTATCAGAGCCCGCTTACGCCCTGTA
TGAAGAAACCTATACCGTCTGAAGAACCCCGGACTGGTCTATCCTGCCATTGCAACCGCAAGACTGGCAGGCCGGGCAAGCGGGGACAGACGGGTTCGTCTATAACGAGCGCTGC
CGCCACCCCGGCAACGCGCTGCACGCAAGGCAACAGCGCTGCTGGCGCATCCCGCTGCCGACCGGACATCGGCTTTTCAGACGGCATCGTGGCAGTTACGCCCAAAACCTCGCCC
CGGACATCGCGGATTTCGTCTCTGTTCCGTGCGAGCGTTACTGGGCATACCAAGCTCGCGCTGCTGGCGACGATGCCGAACAGGGCGTTACCCACATCGTGGCGGACAGAACCTGCTCTGT
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GCATTGGATTAAACCGCGGCAACAACTTCTCCGCCAAGTGTTCGCTACCTCAAGCTGCCGGAAGCACCAGAACCGACCGCTCGCGAATGCTCGACTGGGCGTGGCACACTGGG
ATATGGACAAGTGGCGAAGACCGCATTACCGCCCC

SEQ ID 8344

MYTGRFAPSPTGLLHIGSLTAVASYADARSNGKWLVRMEDLPPREMPGAASHILHTLEAFGFKWDGEVTTYQSRRYALYEETLYRLKTAGLVYPCHCNKRDWQAGARRGTDGFVYNGRC
RHPGQRPALQKQPSWRIRVPRDIDGFDGIVGSYAQNLRDIDGFLVPRADGYWAYQLAVVADDAEQVTHIVRGDILLVSTPRQIYLQQLGVPTPYAHLPLITNAQGGKMSKQTLAP
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SEQ ID 8345

ATGGCGCTGCCGTTCGCGCGGATTTGGTCAAAACAGGGGATACCGCATCCATATAGCCAACCGTGGTGGGAAAGCGCAACGTTTGGGAAAAGAGTTGGGGTGCAGAACTTCGGCAA
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GTCGGTCGCTACGCTCAGCGTTACCTCGGGGAGCGCGCATTTGTCGGGTTCATCCGAATACACCCGGAATAATCGGCTGGGCGTATCCGCTATGATCCGGAAGCGGAATATCG
GAAACGACGCGCAGGATTGGCATGCAATCATGAATCAGTCGGTTGACCGTTTGGTTGGAAGATGAAGCGCAATGCGACAGCATTACCGGCATCAGCGGACGGCGCGCTTATGCTGT
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AGATTTCGAGAAGCTTCAAAAAATGTAACTGCAAAAGCGGGACAAACCCAGAACCGTGAAGCCTTCAGACGGCATCGTGTGCGGAAGCCATAAGTGAGGGCGTTTGTGCTGTGTG
TCCGTTTCGAGGAAATGGAACGGCAATATCAA

SEQ ID 8346

MAAAVAGGLVKQGGYRIHIANRGAERKRRLKELGVETSATLPELHSDVLLILAVKPDMEAAKNIRTNALVLSVAAGLSVGTLSRYLGGSRIRVMPNTPGKIGLVSGMYAEAEVS
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CRSQEMERQYQ

SEQ ID 8347

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CAGGGGTTGCGCGCAACCGCTTCCGAGCGCTCCGATGG

SEQ ID 8348

MEIRVIKYTATAALFAFTVAGCRLAGWYECSSLSGWCKPRKPAADFDWDIGGESPLSLEDYEIPLSDGNRSVRANEYESAQKSYFYRKIGKPEACGLDWRTRDGLPLVERFKQEGFDCLER
QGLRRNGLSERVW

SEQ ID 8349

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ACAGCCAAAGTCCAATCAAGCGGACCGCGCACAACTCTGCGCCACATTGTCGCCACAGCTCGGGCTGATGACAGGTTTGAAGGCGCGCGGACTTGGCGCGTATGCTTTCGATGC
AACGCTCTTGAAGACAACGACGGCGGCTGATTTCGAAGCGTGAAGAAGTGAACGGCAAAATACCGCGCAA

SEQ ID 8350

MPFELKEENLMINKELIEHKRRRLCVAPMLDWTDRHYRLARQITRNALYSEMNAGAIYVGDKDRFLMPNEGEQPVALLQGGSDPSDLAKAAAEYGYNEVNLNCGCPSPRVQKGA
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VMVGREAYHNPVMRWDRLFYCDNRAPIEYADLVQRLYYSQVQIQAGRGTTILRHIVRHSGLMHLKGARTWRRMLSDATLLKNDNGGLIFEAWEKVERANTRE

SEQ ID 8351

GTGCGAGGCCCAAGGCACTACACTTATCGGTAATCTGTTTGTGTTAAAGAGCTTGCAGAAATATAAAGTATCCCTCCGCTGTCTAAGATATCTCTCGATATTTCGCACTTCGCTGCT
ATACTTTTCAGTTCTGTCGCGCGCTTCGCGCAGCGCGAAGAACCGAATATACGCCCGCAGGGGAAACAGTCAATACTTTCAGCGGGAATTTTTTGGGAAATTCGTCATGCTGCTGCTGCG
A

SEQ ID 8352

VRGPRHSLSVICFVKERCKLIKYPFRLSKISLDISDIPCTTFQVRRPGSGEERNYTPAGENSQYFQDRDFGEIRHVAVG

SEQ ID 8353

TTGATTAAAGAATTGATAAAACAATGGGTTTGAGTGTGATTGTCCTATTTGGCTTCCTGTCGCAATTCAAAAATTTGTATTATATAACATTCGATTTTATATCATAGATTGTA
GAATACTCAGAGGCGATAGGCAAAAGTTTTCAAA

SEQ ID 8354

LIKRIDKTMGLSVICAILASRRISKFCYYITLHFLYHKILRLRGRHQKFPK

SEQ ID 8355

ATGGTGCAAAATGGCAACAATAACCAAGCGCGCAATCTTCCGCGAAACAGTATATCGGGTTCAAGTACGGTTCGGCAAGAAAGGCTATCTGCTTTCATAGAGAGCAGGAGCTTCAGTA
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CGCAACGCTCGAGCGGCTGATTAAAAAGAGCAATGATCGAGCGCAAGCGATATAAAATCCGGGAAG

SEQ ID 8356

MYQMATIKRRNPSETVYRVQVRVVGKGYPAFNRSTPSKKALAVENWKKREARERAGPELLFKRGVRRMTLSEAMRYLNETLAGRSKKNGLRFLMEFFIGIGIDKLKRSDFABEV
MQRRTGPELDIAPLAASTALQELQYIRSVLKHAFYVWGLEIGWQELDFANGLKRSNMVAISAIRDLPTTEELQTLTYFLRQWQSRKSSIPMLHMLLTYTSRRQDEICRLIFDDHE
KNDCTRPVRLKPNPSTGNKKEFDILFALPVDELPEESVRKRLANKGIADSLVPCNGKSVSAWTRACKVLGIKDLRPHDLRHEAATMAEDGFTIPQMQRVTLHDGHNLSQRYVS
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SEQ ID 8357

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SEQ ID 8358

MTVLQERYEVSRIKGLVLQAGREPHSVSLIAVSKTTPSDGIREVYAGQDRDFGENYIQWYKTEELADLTDIVWHVIGDVQSNKTFVFAERAHVHTVCRKLTAVRLSRQRSLPPL
QVCVEVNLAGEAAKHGVAPEEVALAVEAKLPNLVVRGLMCVAKANSSETELKTPQFTWQKLADLNAAGVKADVLNMGSDMPAAIECGATHVIRIGSAIPKRG

SEQ ID 8359

ATGCAGATTACGACTTACTCGCCTTCGGCGCTAAAAACAAAGCATCCGACCTTCACCTGAGTTGGGCATATCCCTTATGATTGGGTTACCGCGACATCGCGGCATCAACCTTCCCG
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SEQ ID 8360

MQITDLAFAGKAKNSDLHLSSGISPMIRVHGMRRINLPMSAEVGNMVTSMVNDHQRIYQNLVDFSPFLPNVARFVNAPNTGRGPAVFRITIPSTVLSLEBKAPSTFQKIARS
PRGMVLVTGPTGSGKSTTLAAMINYNETQPAHILITIEDPIEFVHQSKSLINQRELHQHTLSFANALSSALREDPVLILVGMERDPETIGLALTAETGHLVFGTLHTTGAARTVDRIVD
VFPAGEKEMVRSLSESITAVISQNLKTHDGRVASHEILIANPAVRMLIRENKITQINSVLQTRASGMQTMQSLQSLVRQGLIAPETRRRAQNSSESNSF

SEQ ID 8361

ATGAACATCAGTAAAGCAAGGCGTTTAAATCGCATACGGCGCGCGCGCTATATCCCGCGGAGGGAAGTACACAAAGACTTTTTTGCCATATCGGCTTTAAAGCATCGG
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GGAATATCGGAAATTCGGCTCT

SEQ ID 8362

MNISKEQGLLIAYGGRPYIPPREVHKDPFAHIGFNAFKASGVRCLEFPPIRLSDSRKSEYFVSRELAKAIADKREKAKSEYKPRFS

SEQ ID 8363

TTGCATCAGACCGGAATTTCCGATATTCGATTTCGCTTTTCTCTTGTCTGCGATTGCTTTGCAAGCTCTCGGACGCTGACGAAATATTCGATTTTCGCTGTGCGACAATCGGA
AAATCGGAAACGGAAGCTCGCACCGCACCCCGATGCTTTAAACGCGTTAAAGCGGATATGGGCAAAAAGTCTTTGTGTACTTCCCTCGCGGGATATACGGCGCGCGCGTATGCGAT
TAAAGCCCTTGTCTTACTGATGTCATATATACCTCTTCTGT

SEQ ID 8364

LHQDRNFRYSDFPSSLSAIAFASRTILKYSDFRSLDNKIKNGSSHRTPDALNALKPIWAKSLCTSLGGIYGRPPYAIKSPCSLIIMFYTSFC

SEQ ID 8365

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SEQ ID 8366

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SRESMEYAMQLAQTHLCITFLHANTAPQSLERILNFYKQBHQILIDIALNLFGIICQRLALKDKTGRTAVVDLLINTPAIQDFILKGLMNLISKINETARTDGMQTHDQNLFEYR
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SEQ ID 8367

TTGAGGAGTGGGTTTTCATGTTTACCGGTTTATGTTATGAAAGTGAATAAGTGTGGCAGATGAATGGGCGGATAAAATCATGCCGTGAAACCGGGATGCGGTTTTCAGACGGC
ATTGGGTTTTCGGATCAGGAAA

SEQ ID 8368

LRSGVFMVLPVYCYEVNKVWHMNGADKIMPSENGDAVFRRHVLRIRK

SEQ ID 8369

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SEQ ID 8370

MKTPLLKPLLLITSLPVFASVPTAASIVWQLGEPKLMAMPFVLGI IAGGLVLDLNRLTGRLKNIATVAFLTSSLTAQSTLTGLGFLF ILAMTLMTPGFTILGAVGLKYRTFAFGALAVATYTT
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 TGSGFNWQLQAIRPOLYMSSECFRVAHRLISGLVAACCTIEALNLSGLWYLLTALFVCPQSNYPATKSRVYQRLAGTVLGVIVGSVLFPVTPSVETKMLVILAGTLLTFMTYTKYSFSTFF
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 LKTGYALTGYI SALGAYRSEMHEECS PDPTAQFHLLAEHTAHI FOHL PDMGPPDFQTALDTLRGELGLTRRSSGTSKHILLQOQLIARQLEPPYRAYROI PHROPONAA

SEQ ID 8371

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CGCATCCGCAAAACGCTCCGCCACACCCGGACAAGCCAAAGAACGGACGAAACCCATGACGTTTCAAGGACACAACAACCGTAAAAAGCCGGCGGCTACGCCGAATACATCACGGGCGCG
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SEQ ID 8372

LRQRRLQLQLDRTPQTDGKDPQPHQAQSGSGMRTHIRTCVYHDSGKSGNTASGISGTAAGAABQAPPSAAKTANRSASASANAPPHFDKPKNGRKMPTFGQHNHNRKKAGGYAEYITGG
SLRRLVAAKVRRYCGEHPGVFDGAAGSGQLEQVIEPSPDFRAVEIAEACKALLQNYPAKVYNTSLFLYTDGEPQDCTVMNPPFSIKLKDLSDEKSRIAQEYFWKSGVADEIFVLKGLK
NARRFGFFILFPGIAYRKSQRFREIIGNRLAELNRIONAFEDTPIEVLLLVLDKDKTDGGCTRELYDCKDTLLAADTWQIEPDLNQTVQEPAPPFKEKEDPVILLEHCRDAAAKRIAREL
RFSKMVNEIEGWPHEAFEDFGCDRLCNLIQAEKYGKKHYPPCSLPLFGGAAG

SEQ ID 8373

TTGGGCATTGAGAGAACCGCATCAAAAAATCGAGAAAAAAATGCAAAACAGTAGCAACAAAACCGACGGCAAAACAGATGCTTGC CGCCAAACGCGCGGCGAAGGAATCAACGCGGCAGG
AACGCGCCGTCAAAACGCGCGGGACCGTCAGAAACGTTGACCGGAACCGCGCTGCCGCGCGGTCAAAGCGCAAAAGAAACATCGCCCGGATGTGTCTGCGCGCAAGGTATCGGAAGA
CAAGCCGCTGACGTGCGGCATCATGATCGGGCTGCTCCCTGCAGGATATCGCGCTATCGCTGCAATCAGGAATTAATCAACTTCGCGCGAACATATCTGTCAAACAGGTCGACATCTGGGCCCT
TACTGCAACACTGACGACCCGCGAACCGCGAAGCGGTACTGCTTGGCTGCGCGAAAGATGCGAGCGCGGTGCGCAATGAAGCAATTAAGATTTTGACATTTAAGCCGGAATCGCTGCCCAAC
TCGTGCTGCGTCCGCTGTCAAATCTCTTCGCGCGTACGAAGAATTCTTGAAAGACGCGCTGCACGGCTGATAGCCGAAGTATCGGCATACTCATTGCGCGTGCGGGTGCCAAGAAGC
CATGGCGTTTTTAGAGCTTTGACGCGCGTTTGATTTTGGCGGTTGGCAAAGTCGTCAACGCGCGCGATTTCGCGCGCGGAAGCCCGCGCCTTAAATTCGCGTACGCGGAATTTACAGCGCG
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CATGATGAAAATGCTTGTTCGGAACAAGCGCGCGCTGTGTGCTCGCGCGCTCGGAAGACGTCATCCGGCATTCGCGACAACGCGCGCGGCTTCAGCTGCTTCACTGGAACGA
ACGATTTCAAACGGCGCAAACTCTGATCAGCTCGCTGACGGAACGCGCGCGCA

SEQ ID 8374

IGTIERTASKNRENKMTVATKPTAKQLAAKRAAKESTRQERAVRKAGTVRNVDNRNLSARSKAQKENIARMLSGAKVSEDEALTGCGIMRLSLQDMRYCQNELINFAEHIVKQVQRLGL
YCNTHDPANGESVLPACREASQAQVQWTKDFINLSPNQRLVLRPLSNLPAAYEEFLKDAPARLIAEVSAYSLAVRVAKKAMAFLELDGGLISAVGKVVNGADSRABARRLKMPYAEFTGR
ILHAANLIYDVCGIQADKELSAMYGKPLNPVRPRRI SDVRRPMMKMLVADKGGALVRAVKDSEDVIRHCNGAGGFSCPNTEHFKRTANLISIMHREAAA

SEQ ID 8375

GTGGGCTTGGAAACGGTCAGCGTCGTGGCAAAAGCCGTCCGCGCGCACTTCGGGGCTGCTGCACACTTCGACCGCCCTCCGACAAAATCATCTCCGCGGATACTTTGCGCCAAAAGCCG
TCAACTTGGGCGACGCTTTGGACGGCGTACCGGGCATCCACGCTTCGCAATACGGCGGCGGCGCATCCGCTCCCGTTATTCGCGGTCAAAACGGGCAGACGGATTAAAGTATTGAACCATCA
CGCGAAACCGGCGGATATGGCGGCACTTTTCTCCCGATCAGCGCAATTATGTAGATACCGCTTGTGCGAACAGGTGAAATCCGTGCGGGGCCGGTTACGCTCTGTACAGCTCGGGCAAT
GTGGCGGGGCTGTGTCGATGTTGCCGATGGAATAATCCCGGAAAATAATGCTGAAACCGGGCGATATGGGCGAAGCCGGATTTCGCTTTCAGCAGCGCGCAATTATGAAATAATGACATCCGCAG
GCATCAATATTCGGAAGTGGGCAAAATCTTCGTGCTGCATACCGAAGGCTTGTACCGCAAAATCGGGCGGATTACGCCGTACCCGCTTACCGCAATCTGAAACGCTTGCCCGACAGCCATGCGA
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CACCGCGCATCATCTGCGCAAAATGATTTGATACAAACCAATTTGTGACGCTTATCCGCATCTGTGTACCGAAGAAAGACACATCGATTACGACCAATCCCGGGCTTGAGCTCGGGCTTCCACG
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AAGTTT

SEQ ID 8376

VGLTGVTVSVVGKSRFRATSGSLHTSTASDKIISGDTLRQKAVNLGDALDVGPGIHASQYGGGASAPVIRGQTGRRIKVLVHHGCTGDMADFPSDHAIMVDTALSQQVEILRGPFVTLIYSSGH
VAGLDVDVADGKIEPKMPENGVSAGKALRLSSGNPLSTAGNITGLGNKFNVLHTBGLYRKSVDYAVPRYRNLRKLPDSDHADSQTSGISGLSNVWGKGFIGAAYSDDRRDYGLPASHSEYDDC
HADITWQKSLINKRLYGLPHLLFEEDIDNPLSGCGPHDGAHAHTHNGKWPIDLNRKSGYLRABEWQPPFGFEALRVLHARNDYHDEKAGDAVENFPANKTHNARIELRHQPIGRGL
KGSWGVQYLGQKSSALSAIPETVQOPMLIDANNVRHYSFPGVEQANWDFNLTBGGVYRWEQKASIRYDKALIDRENYQVLPPLDGAHQRTQASFDASISGNWYTPPHKLSLTAHQSERLST
QELYARHGKHAVATWTFEVBGNKHLKERSNNIELALGVBGRDWQYNLAAYRNRPNGNITYAQPLNDGRGPSTIEDDSEHKLVRYNQSGADFPYGAABGEIYFKPTPRYRIGVSGDYVRGRILKNLPS
LPGREDPQYKGRPPYIAQADQNAPRIPAARLGPFLKTSLTDRIANDLDDYRVFAQNKLARYETRTPGHHMLNGLANYRPRYRYGEWNWYVKADNLLNQSVYAHSSFLSDTPTQMGRSFTGCVVY
KF

SEQ ID 8377

CGTTTCGCTCAAAACGGCAGATACCGCTTGAAGACTGATTCAAATAGCGGGCAATTATATCAGCAAAGCCATCAGGGTACATCTTTTCAGACGGCATATGATTGCCCGAAACCGCGAAACTT
TGACAAAACAGGCAGAAATAACAATACAATGCCAATTTCGCACAATGGTGTGGCGGATATTAAACCA

SEQ ID 8378

RFROTADTA*KLIIQIAGNYISKAIRVHLFRRHMIARTAGTLTKQANNNTMPNFAQWCADINH

SEQ ID 8379

ATGCCGCTCTGAAGCCCGAGTTCAGGCGGCATATTCACAAAGGCGCATCAGCCGGAGGAGAAGAGGAGGGGGGGTGTGTGGAGCGCGCGCAGCGTTTGGCGGAGATAAAAAACCTTATC
CGACAGCGACA

SEQ ID 8380

MPSEAPSFRRHIIHKGASAGGEEEGGVVGGGAAFGGDKKPYPTAT

SEQ ID 8381

ATGTCCCGTATCTACCTACCCCTCCTATTTCGGCCCCACATCGTCGAACGGCGCCTTTTGTAATTTTCAGCAGGACAAGGTTTCGGCATGTCCAAAAAATTTCTTAGGGCGTTATTCGGGCGA
AGGTATTTCGATTTCGGAACAATAAT

SEQ ID 8382

MSRIYLPLLFPPIVERGLLYFQODKVRDVQKISLGRYRAKVFDSENY

SEQ ID 8383

TTGTCGATGATGACGATTTCATACGCGCGGCTCCGCCAAGATGGAGGAAATTTTCGGATTTCGGAATCATTTGAAAAAGCCAAGCATTCGGGCGGGCGTTTTCATGAAGGCTGCTGGCTGA
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CAGCGAGGCAAGAGCTAACCGCCACTCGATGAAATCCGTCCGTTCTCAAAATTTTGACCAATACGCGCATGTGGATGGATCGATATTTACAGCGTCAAAAAGAGGGGAAGACAGCGTTTATTT
AGAGAAGATGTATGACAAATCGACAAATTTACCGATTTACCGATTCAGTGGGCT

SEQ ID 8384

LFDDDDFIRAASAKMEETFGFGEIIEKAKHSGGRFYEGCWLMTGNAQYGRVHYGGQRETHLVELTAVGCNAANTIGWESRLFDPLTNAIRPKITRVDIADKFPNGEYSPNQAREDRNKGFLT
CHHVKPKGECGLSDWEEDEAKMTSGKTYGIGRESSKYVRJYEKGQKLGDKTSTWTRFEIETFAKDIVIPFEVLQTPGEYFGGAYPICERFTGSANRIEAVKSKIMIDPPTYIERLKKQI
GRGINASKAVFPDKSKQELFEVLEPKHDFPKLLSFENYDCSEAKLPLLEIPSVLKFDPOYGNMMDRYIOROKRGEORYLEKMYDRYANLPTISA

SEQ ID 8385

ATGAGCTATTGGGAAGATGTAAGAAACGCATTAAAGGGTAATAGATAACTTATGCAAGAAGCATTAAAGAGCCTGAATCGTTAGAGGGTTATATAGACGAAATTAGGGATAAAGCAGACG
AAGCGGATACCTCTTTGGAATTCTAAAGGATGTAATAAATTATGGTATTAGCGATTAAAAATGTAATTGAGGTGTTTGAAGATTGGCTT

SEQ ID 8386

MSYLEDVKNALRVIDNLCKEALKEPESLEGYIDZIRDKADEADTSLEFLKDVINYGISDLKQVIEVFEDCV

SEQ ID 8387

ATGCAGCCTGCGGTTTATATTTTAGCAAGCCAACGTAATGGCAGCTTATACATTGGCGTTACATCTGATTGGTGCAACGTATTACCAACATAGGGAGCAITTTGATTGAAGGATTTACAT
CACGGTACAACGTTACTATGCCGGTTGGTATGAACTCGATCCACGATGGAGAGCGCAATTACTCGGGAAAAACAGTTGAAGAAATGGAACAGGGCTGGAAATGCAACTGATTGAAGA
AAATAATGTTTCTTGGCGGGATTATGGTTTGATATTAAT

SEQ ID 8388

MQPAVYILASQRNGTLYIGVTSDLVQRIYQHREHLIEGFTSRYNVTMPVWYELHPTNESAITREKQKKWNRRANKLQLEENNVSRRDLAFDII

SEQ ID 8389

TTGCTAAAAATATAAACCGCAGGCTGCATATATACCCCTTTTGAATTATTTAAATTTATATTCCCGGAACCACTCCGGTGATTACTTTAAACCTTCGTATATCCCATAGCTTTCCATCAT
TCCCGCAACTCTTCGTATATCCCGCGAAAGCGGAATCCAGGACTCAGGACCTGAGAAACCTTTTATCCCGATAAGTTTCGCGACCGACAGACCCGGATTCCCGCCTGACGCGGAA

SEQ ID 8390

LLKYKPOAAYNTLLNYLNLYSREHHPVITLTLRYPHSFPSFPOLFVIPA KAGIODSGPEKPFYPI SFRTDRPGFPPERE

SEQ ID 8391

TTGGTTTTTCGTTTTTGTAGGAATGATGAAATTTTGAGTTTTTAGGAAATTTATCGGAAAAAACAGAAACCGCTCCGCCGTCATTCCCGCTCAGGCGGGAATCCGGGTCGTGCGGTGCGGAA
CTTATCGGGTAAAAAGGTTTCTCAGGTCC

SEQ ID 8392

LVWFCRNDEILSFNRLSEKTEAPPSFPLRRESGSVGAETVYKVRFLRS

SEQ ID 8393

TTGCTGTTGTCCACGCTCCAGTATCCCGCTCGCGGGGAATGACGCGTTTCATTGCGCCGCCCTCCCGAAAAACGCAAAAAAATGCGTCCGAAGACCTTTCCGACGGCATTTGCGGAA
AAACCGCGCGCGCGGGGTCAGAAGAAGACTTCGCGCCAGCT

SEQ ID 8394

LLLSHVLDRLRGNDAPHLPPPEKRKKMPSELDSDIGCKTGRAGGSEEDFAPA

SEQ ID 8395

ATGACCGCCCTCACACTTACCGGTGCGCGGCAGACGTACAGCGCGCGCTGGATTACTTTGACAGCGAAACCGAGCGGAAGACAGCTGGAAGCGTTATCGGGCAGTTCCGAGGTCA
AAGCGCAATCCGTTATCGCTTATATTAACCAAGAAATACGGAAGAAATGCTTGAAGGGCAGATCAGGCAGATGACCGGGAAGCTCAAGGCGGCAAAAGCGCGGAATCAAGCGCTGAA
AGACTACTTGGCGCGCAATATGACGCGCGCGGCTTACGAAATCAAGCGGATGACGCGACTTTTAAAGCTTCGTTCGCAAAATCGAAGCGCTGCTGATCTTACAGCAAGCAAAATC
CCCGCGAATTTATGCGTGAGGCGTCAAAACCGAACCGGACAAAACCGCATCAGAAAAGCGATTGAAAGCGGTGCGCAAGTAGCAGCGCGAAGATTGAAGGGCGGAAGAAATTCGAGA
TTAGA

SEQ ID 8396

MTALTLYRCAADVQAALDYDFDSETEREDTLEAVIGQFEVKAQSVIAYIKNQBITTEKMLBGHIRQNTGKLKAAKARNQSLKDYLRNMQAAGITEIKADDGTFKAFPRKSEAVVILDEAQI
PAEFMREAVKTEPDKTAIRKAIESGRQVAGAKIEGRKNLQIR

SEQ ID 8397

TTCACCTGCTTCGGACGGCAACAGAGAAAGGAAACAAAAATGGCAACATCGACCTGACCCATGGGACGGGAAAAACCATTTGGCGCGCGCCCAATCCCGAACAGGGATACATCAACA
TCACCATCGCGACGACGACCTATTATCAACATCGAACAGGCATACGCCATACAGCGCGCGTTGGCGAAGCGGTTGCCGAATATGAGGGAGGGGCACAA

SEQ ID 8398

LQLLRATEKGNKKMANIDLFWGDKTIGAAANPEQGYINITIGSDDLFINIBQAYATHAALGEVAEYEGGAQ

SEQ ID 8399

ATGAACGCGCAAAATCTGCCGAGGTAAGTGGGGGAGTCATATTATCAGCGCAAAAAAGACAGGGAGCGCAATTTACCCATACAAATAATTTAAAAATCAGAAGAAACACAATA
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SEQ ID 8400

MNAQNLPEVKGQSYSSAPKDRERQFTHNNFKIRNMTTISFNTDNNVVAQGGIVVFGAATYLPYKGVSGFDTSLKGRGNAVDNMTSTRPGLVGSYENVTCHNNYFAPSRCPEV
YKQPTFGQGLQKAGNKLDIYEDKSRDNPYKLSYDPLVSPNLSSESLLVKEKRNKKIYPFNEVDVQQNSGNPQYKQNLVYTTGDNKYSSRYVQNEHSAIAPYLNKILHLK
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VNSPIVAVGGYLAANDGMVHIFKNGGSDERSYNLKLSTYIPGTPMRKDI ESNDSTLAKELRAFAEKGYVGDYGVGGFVLRRI TDQDQKHFFMFGAMGFGGRGAYALDLSKIDGNY
PAAAPLFDVKNNGDNKMRVKVELGYTVGTPTQIKGTQNGKYAFLASGYAAKNIGSDNKTALVYVDLENGSGSLIKKIEVQGGKGLSSPTLVLDKLDGTVDIAYAGDRGNMYRFLSD
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RTAFVTTISYTGNDKCGAQTALIGINTADGGALTPRSARPIVPDNQVAQYSGHOKMNGKSIPIGCMWKNKTVCPNGYVYDKPVNVRYLDEKRTDDFPVTADGAGSGTTFEGKPKARN
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SEQ ID 8401

ATGGGAAAAACATCAATATGCGGCATAAAGCGCGGTATGGCGGAAACCTGCCCTTTTCAAAGTTTATTCATATTTTATTCCTTAAAGTTTGCTTCGCGGAGCGGCGCGCGGCAAGCGG
GGTTCGG

SEQ ID 8402

MGKHQYGGIKRGAENLFPQSFHILFLKFAFAGRRANAGVR

SEQ ID 8403

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SEQ ID 8404

LLLSVKDESNTKPCPAGSHATCIRIIDLGTQLVEYQNEQKQKILVQWEIDPEGDPEMLPDGRPYLISRRTASLHKSQSLATDLKSWGRDFTPEERDNFDLNLGKPCLLSLAHQ
ESSDGTITYANIPAINSKMKSYPKHPDNAVPAFDLSDPDWANYGLLNEKLREQLAKSPEYAEAVNGRQPPAPPQKQAQAAEGRPEHPQGNAAPEIDIEDIPFN

SEQ ID 8405

TTGCTTTTCGTCTTTCACACTTAAATCAATGACATTTTCGGTCTCTGTATAAGGTCGTTTCGTCTATCGGTCTCGCGCTGTTTATGCTTGGCGGGCGGCTTATC

SEQ ID 8406

LLSSFTLKINDIFGLLLKVVSSIGLALFYALRGVI

SEQ ID 8407

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SEQ ID 8408

VQVSVHMDSSFPRRRESRPWDNSNIQRLSAVVC

SEQ ID 8409

ATGAGCTTCCATCCGAAACCGCTTATAACGGCGCGGAGAAACAGAGCCGTACGGACCAAGCCCCGAAGAAATCAAATACGGCAAGCCCGGAAACCGCGAAACACCGCGGATGACCG
AAAAACAGGCAGAGGCCACATTAAGCATTTATCAGA

SEQ ID 8410

MSFHPETAYNGGGETEPYGPSPPEIKYRQSPETAETRRMTEKQABGHKSIIR

SEQ ID 8411

GTGCGGATATTAAACATAACCTTTATGGAGTTGAGTATGTACCGGTCGTAACCAACGGCGGCAACAGTATAAGTTTCGCTCGCGGAAATTTGAAAGTAGAACAGATACAGCCCAAC
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CGAAAGTCCCGCATCTTCAAATGCGCCCGCAACACATACCAAAAGCCCAAGGCCACCGCCCAAAATTTACCCAAATCGAAATCGTGCAATCGCC

SEQ ID 8412

VRILITITLMLSMYAVVKTGGKQYKVSVEKLVBQIPAQLDSQIELTEVLMADGESVKVGAPFIEGAKVTAKVVAHGRGEKVRIFKMRRRKHVQKRGHRQNTQIEIVAIA

SEQ ID 8413

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GGATGCCGGAACCTGCCGAATTCGTGGATTGCTTCCAGACTTGTGGACACCGAAATTTTAAAGGACAGAAATCTTGATTACCGCAGGTGCGACATTTGAAGCCATTGACCTGTGAG
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SEQ ID 8414

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SEQ ID 8415

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SEQ ID 8416

MQKRHSRHLFIPTSSKHISGLNIHSIPVLKGTGSHSVKSGMSSAQANYQNLPTKNNPVCTKGNPPYRHPFKTAIQHILKIKKSYPOKIPHINIITVLVFKPYLFTITLQNGTA
KRGIFSKN

SEQ ID 8417

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SEQ ID 8418

VHPATGFFFRIQMPLFQPNLGAQFNLRLLSQRHTRCNIGGFSLCRTASASLGESEGLARRQYRQYRELKRNIPCLHFFYFLNLKGFNCAPRPLEMVRTVRRRGYLRLESTKTAAPT
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SEQ ID 8419

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SEQ ID 8420

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DAYEANFDLVFLGADVPYFNKILLENCLPAMRKVAKAVECGIIMPMSASAITFLDGYTTERLPANLLQAQRDYPGAHTYERTDKPRGEFFHTNWTGKGGDTASTTYDI

SEQ ID 8421

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SEQ ID 8422

MPGHFRSVCNNVAVSISAQATIIHKAIGTSFYFLQNKCRPNSSDGISATESNIVGCRSGISALARPVMGKFAARFVGALVSVRAEVVALCLQEVGRQAFGRIVQERNRRSHAGHRDA
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SEQ ID 8423

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SEQ ID 8424

VQDSVRLPVTQSLPHILPRVISFHPPIGAASRRRAVIFHLRPFRLRKPAAFTVSPCRCPALKFDTSSLCAIFGLADIAFGRFVYTKTILALSFKPSFLTVKVKAV

SEQ ID 8425

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GCGA

SEQ ID 8426

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FEKRIGRPRVAVCGSTRVYRGEDEAKLLAAMQYRGDALLAVVPRHEPHTTETAKRPFQVQRSDGLPVEPTDQVWVGSNGELIYAYILCADVAFVGGSLVSGGCGNIIIEPLSCGV
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SEQ ID 8427

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CGCAAGCGCTCAATCACCGCTTTTACTTTTACCGTTAAAAAGACCGCTTAAAGATAAGGCAATGATTGTTTTG

SEQ ID 8428

MNELISKINRVGAREKDGQSLLLKVGIEICRDAGATPTTRKSESINHTAFTTFTVKIDGLKDKAMIVL

SEQ ID 8429

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SEQ ID 8430

MSAYRPFHRLGDSRRASAMLCDAVHARLHLHSAPLAR

SEQ ID 8431

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SEQ ID 8432

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SEQ ID 8450

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SEQ ID 8451

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SEQ ID 8452

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SEQ ID 8453

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SEQ ID 8454

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SEQ ID 8455

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SEQ ID 8456

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SEQ ID 8457

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SEQ ID 8458

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SEQ ID 8459

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SEQ ID 8460

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SEQ ID 8461

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SEQ ID 8462

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VLPDLFDL

SEQ ID 8463

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ACAA

SEQ ID 8464

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SEQ ID 8465

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SEQ ID 8466

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SEQ ID 8467

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TTCAGACGGAATTT

SEQ ID 8468

MPSETKWQTAFLCGGYCALAAHSAGVAATESACSSLLSSWALSPSLIRRWARRALPSNSNETMTAKKWCPSPTSMCSHFATPAIRALTCSGVSVIGSPTWGNAPLYRQIETPSEN
FRNF

SEQ ID 8469

TTGGGTACAGACGTGTCGAGGGGAAAGCCCGCACTTCCTCAGCCTTCACTCTTTTCCGCTCTGAAATATAAAAAATGCGCGCCAGACCTCAATGCTTTTGAAATTCCTCT

SEQ ID 8470

LGYYRVEGKARTSSAFTLLPSENKKIARPDINAFETAP

SEQ ID 8471

TTGGCGGGCGCTTTCAGCATCGCTTTTTAATCAGCGCTGTCTTTCTTCGACAGCGGTTCCTGTCTGCTTCTTCATTTTTTTCCCTTTCCGGTAAATTCGGGATGACTTCCGCTTCAA
TTCGGTTATATCAATTAACATCTGACCCGACGGCTTTTTATTGGGTACAGACGTGTCGAGGGGAAAGCCCGCACTTCCTCAGCCTTCACTCTTTTCCGCT

SEQ ID 8472

LAAAFSIAFLISRLSFFDRRFLSCFPFIFPLSGKLRMTSASIRLYQLTSDPTGFLGLQTCRGESPHFLSLHSFAV

SEQ ID 8473

GAAGCAAACGCTTTGGCGGTAAAGCCTACGGCAACGAGCTGATTCGCCGAGTTCCATCATCGTACGCCAACGCGGTACCAAATTCACGCGAGCGGACAACTAGGTATGGGCAAGAC
ACACTTTGTTTCGCAAAATTCAGCGTTATGTCGAATTCAAAACCAAAGCGCGCTGAACCGTAAACTGTCAGCATCCGCTCTTACACCGGTTCTGAAGAATAATTCACCGGATACCTGAA
GCCGATCTTTTCAGCATGCGGCTTTTACATACCCCATACCCGATTGATACAC

SEQ ID 8474

EAKRLGVKAYGNELIPAGSIIVRQGRKPHAGDNVGMKDHLTFAKIDGYVEPKTKGALNRKTVSIRPYTGSE*FNRYLKPHLFTMRIFTYPIPDLIH

SEQ ID 8475

ATGCCGCCGCCCAACCTTCGCCCTTACGACCCCTGACGCGGGAAGCGGTACCTGCTTTTCCATACCGCTCTTACCTCAAGCCCGAGCAACAGCGGAGCTTGAAAAGCTGTG
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AGCGGTGATCGACGAGCTATTGGAAGATACGGCGGTGACAAAAGGGGAAATGGCGCGGTGTTTCGGCAATATCTGTTGCCGAGATGGTGGACGGGCTGTCCAAATCGCAAAATCAAAATTT
GAAGATCATCGGAACATCAGGCGGAGAGTTTCGCAAACTGATTTCGGCATGACCAAGATGTGCGGTCATCGTTGTCAAATTTGCCAGCCGCTGCACAATATCGGACGCTCGGTT
CGATGCGCCCGGCAAAACGCGCGGATTCGAAGGGAACCTTGAAATCTACGCAAGATTCGCAACCCGATAGGTCTGAATATGCGTATCGGGAGCTTCAGGATTTATCGTTCCAAAT
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AAAGGCGATGATTTCATAGGATACCTGCCGAGCTGTGTTGAAGTCCGATCCGACAGCAGCTGGATCGAGACTGGGAAAAATGAACGGGCAAGCACTACCGGTGTCGGGCTTCAAGTCC
AATCGGAAGACACGAGCTGTTGGCATTAATGGCGCAAGCGATTTCGATTTCCGTTCCGCGGATCAGATCGAGTCCGTCGAAACACCGCTTAAATCCGAGTCCGGAACGGAAGGTTTGTGCGA
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SEQ ID 8476

MPAPQPSAPYDPLTAEARTLLPHTASYLKPEQQAELKAVAYAFRAHDGQTRKSGDPYITHPIAVATQLALHMDIQGLCAGVMHVDLEDVTGVTGEMAAVFGNTVAEMVDGLSKLEKLP
EDHAHQAESFRKLLIANTKDVRIIVKLDRLNHRITLGSMPDKRRRIAREFLEYAQIANRIGLNAYRELQDLSFQNLHPNRYETLKKAMDKSRKNRQDVVGVKVLRAFGRLVIGANI
EAKIRGKELNLYGIHQKMAKRLFAEVMIDYGFVIVNSIPACYAALGTLHTLYQPKPRPKDYLAIPKSNVYQSLHTILVGPYGLPIEVQITREMDAABEGGIVGHSYKSDSETVDQ
AVLHTNQWLNLDLQASSANAIEFLEHVKVDLFNEIYILTPKGLILFLPKGATFPDFAVAVHTDIGHTVAAARVNMVMPRLTKLTKGDSVEIITSEHAKFPNWLNFVSGRSATIR
QYIKNLNRHDAVVLGESLLQKALSSLLPKDVLSDGIEKYLADLNKQTSFEVLYNMGHTLIPYVAMHIAELAGEHFGSEVRLSSIKVDGQESGHIHFAECCHFPVPGDSIRLLLVKG
KGMITHRDCTPTLLKSDPEQLDADWENNGQNYRVGLQVQSDSHGLLALMAQAISDSGADIESVETPSKSQSGTEGFVEFKFLKVKNLQNLQIQLHSPYIRKVRIS

SEQ ID 8477

ATGAACCGCTTTATCCCCACCGATTATCGCCCGTGAGGGCTGGCGGATTATCGCGCGCGTTTGGCTTTGAGCCTGCTGGTGTGATGTGCTCGGCTGGTGGTCTTTGCCGTTTGGG
TGTTTACCGTATTTCAGTTTCAGTTTTCGCCGACCTCGCGGTGAATTCGCAAAATCTGAAAGCGGTGTGAGTCCGGTTGACGGCGGTATCGTGGTGGTTCGAGCGCGCACCGGATCC
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AATGCGGATTGACAAAGCCAGCAGGAAACGAACGCAACGCGGTTTGGCGACTACGGCTTCCGGTCGTGAAATTACTTTTGTTCAGTGGCCGGTCTGGTGGCAGCCGATTTTGT
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AGTAACCGCGTAAACCCGATTGGCGGTTTGGCGCTGACTGATTCCTCAAGCCGATCTGTTTCAAGCTGCTTCGGTGAACAGCGGCAAAACCATCTGCCGAACAGCAGCAATC
GAAGCGCGCGCTAGATTTCAGCGGCTGTGCAAGATGTGTGAAGAT

SEQ ID 8478

MNRLYPHPIIAREGWPIIGGLALSLLVSMCCGWSLPFWVTFVAFQFRDPAREIPQNEAVLSPVDGRIVVVERARDPYRDVDALKISIFMNVFNVHSQKSPADCTVTKVYVYNGKFFV
NADLDKASTENERNAVLATTAAGREITPVQVAGLVARRILCTQAGAKLSRGERYGIRFGRSDMYLVPDQAQVAIGDKVTGVKTVLRLPLTDSQADPVSQAASVETAAANPSAEQQOI
EAAAARIQAADVQDLKD

SEQ ID 8479

ATGAAGAAGCAGGACAGAAACCCCTGTCGAAGAAAGACAGACGGCTGATTAAAGAGCGATGCTGAAGCCGCGCCAAAGGCTGCGATGAGGTTTACAAAATCGCCGCGGTTTGAAG
ACGCTTTGAATTACTTGGAAAGCAGCCGAT

SEQ ID 8480

MKKQDRNRLSKDRRLIKKAMLKAAAKGCDEVYKIAPGLKDGPELLGKQPD

SEQ ID 8481

ATGAGCATCATCACTACTTCTCGCTGCAGTCGAATCCGCGCGCTCCGCACTCAACAGCTTCTCGGCCAACCTTCGGCACACTGCTTACCTCATATAATGCTTGGCGTCGCGATGACCC
TGCCGCTGTTTATGTATCTGGCATCCAAAGCGGGCAAGCGTGTGGGCAAACTCAACAGTTCGCGCAATCAACGCTATATGGAAACCGCGCGCACAAAGCAGCAGCGATACCGT
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CGCAAAAGAAAGAAATCGAAATCAACAACTCTGGTGGCGCGCGCTGCTTATCCGCGCGCTTCTCTTATCAGGCTATGTGGCAGAGTATCTTCTCGCGCGCGTACAGCTTAGGCTT
TGCGGTGGCTGCTCTCTGCGCGCGCGCTTGGTCGATGCCATCTTCAAACTTACGGCTTGAACATCCGCTGGCGTTCTTCTACGTCGCGCAACTCGGCTGGGTGTTTGGCTTCGCTCA
TCGCGTGGCGGCTATTCGCGCGTGGCTTGCACACACACCTGCTGCTTCAAGCCAAAAA

SEQ ID 8482

MSIHYPSLHVESARSALKQLLRQPPGTL/LI/LIMLAVAMTLP/LMYLGIQSGQSVLGLKLNESQITVYMETAAQSDSDTVRSLL/TRDKRLDNIRFIGKEDGLAELQSNLDQNLISMLDGN
PLPDPVFIPTDPATTPAQMQAIYRDIKLPVMSASMDTEWVQLYQINEFIRKILWFLSLU/LMGAFVLVAHNTIRLQILSRKEEIRITKLLGAPASFIRRPFLYQAMWQISFSAVSLGL
CGWLLSAVRPLVDALFKPYGLNIGWRFPYVGEGLVFGFVLALGVFGANLATTQHLCLKK

SEQ ID 8483

GTGAAACCCGTTGCAACGGGTGACGGCAATCGGAAGACGGCTGACCGCCGACAGACGGCGCGCGGATAAAGAAAAACCGCACGGGCGGGTAAATCCCTGAAATTCAGGGAA
CGGCTTCAGGTACCGGCAAGGCGATTA

SEQ ID 8484

VETRLQRDCKSERRLTARTDGRPIKKNPHGAGNPPELQSGSGNGERRL

SEQ ID 8485

ATGCCGCCCTTCTTACAGGACCTCTATGATCCGTTTCAACAAGTTTCCAAACCTATCCCGCGGTTTGAAGCCCTGAAAAACGTGAGCTTCCAGATCAACAAAGGCGAGATGATT
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CCAAATCGGCTTTATGCGCAACACATCGGCATCGTGTTCGAAGACCAACAAATCTCAACGACCGCAATGTCTGCAAAACGTATCTTCCCTTGGCGATTATCGGCTATCCGCGCGC
AAGCCGAAGAACCGCCGATCGCCATCGAAAAAGTCGGCTTGAAGGACGAGAAATGGACGATCCGCTAACCTCTCGGCGGGTGAACAAACACGCTGTGATCGCCCGCGCGCTCG
TCCACCAAGCCCGGCTCTGATGTGCGGACGAACTTCGCAACCTCGACCGCTCGATATTATGGAATTGTTCAAAACCTTCCACGAAGCGGGAACACCGTCACTCGTCGC
CGCATATGACGAACCTGATGCGGACTACGGACACCGCATCTCTCGCTCTCGAAGGACGACTCGCA

SEQ ID 8486

MPFLTGPPMIRFQVSKTYPGFEALKNVSPQINKGEMIFIAHSGSGSKSTVLKLSIGITKPSMGKVLFPNGDLGTLSDNQIGFMRQHIGIVFQDHLILNDRNVLQNVILPLRIIGYPPR
KAERARIAIEKVLKGRELDPPVLSGGEQRLCIRAVVHQPLLIADREPSANLDRAYALDIMEFLKTFHEAGTFTVVAHDETLMDYGHRIILRLSKRLA

SEQ ID 8487

ATGCCGTGCGACTTATCTTCTACTTACCAAGAGCTTATCCGACGCGGTTCTATCCGCTTAAAGGGCAGTACGGCCAAAGACAAGCCGAGAAATGGCGGTATTTCATCCGAACACTTC
ATCAAAACCCGAAGAATCGGAGCAATACCGATAACGAATATTTAATCGGGCTGCTTTCGAAG

SEQ ID 8488

MPDLSPILTKELIRSGSIRLKGSTAKGQAGELAVFIRTLHQKPESEPTINEYILGLLSK

SEQ ID 8489

ATGCCGTAAACGCCGATGCGCTGGAAGCGCTTCAGACGGCAATTTCGCGCCGCGCTTCGGTATCCGCCAACTTATCCACTATCTAAAAACAGCGGAATCTTTATAATCGGTACT
GTCTTACCTATGTGTCAGACGCGATATCCCTGCGGACGCAACCGCCGAACGATATGCCGCCCTTCCCTTACAGGACCTCTA

SEQ ID 8490

MPLNAGCRKLPLQTAFSRPAFGIRQTYPLSKNRRNLNRYLCFYCSDGISLRTQPPETICRPSLDLL

SEQ ID 8491

GTGACGCGCTTGGCGCAGGATAACCGACTTGAAGGACAGGGGCTTCGTGTTTGCAAGCCGCGCATGAAGCGCGCGCGCGGGAAGCCTGTACGCATTATTTCGATTGTCAAAAAAG
GAGCGAAGTA

SEQ ID 8492

VTQLAARITDLEGRGFVFAKPRMKAGGRGKPVTHYSIVKNGAEV

SEQ ID 8493

GTGAAAATTTGATTTCAGACATGACATTTCCCTACTTCTCGACAAATCCCTTATTATCGGCTTACGAGGGTTTACTCAATACCCCGCTCCAAACGCTTACAAACGCTTACAAATACC
CGAATCGACATACAAAGGCAAAACGATGAACGCTTGAATCTCGCCGCAATCGCCCTTGGCGCCACATTTGCCGCACATACCGCTCGGCAGACGAACTGGCCGATGGAAGAGCAATAC
CCGCAAAACCTGCAATCGCTCAAGCCCGCTCGGCATCGCAACCTATGGGCGACTTGGTGGTCCGCTGTCGAAAGAGATGCCCGCATGTCCAAATGGTACAAAGCGCAGAAAAA
GGCAGCGTCGATATGGTTCGCGCATCGCTCGACACATCGCAATATCGGCAATTTCTCAAGCAGACCCCGGTACGCTACCCGATTTGGCGTTACACCGGGCGAACAGCCGAACTTTA
TGAAATCTACGGAACAAATGTGCGGCTACTGCCCTTACCGTCTGTCGAAGCCCGAAATGCGGATACAGGACGACATTACAGGAGAGGTGAACGAGAAAAAGCTGACCGAAGCCGCTCA
ACTGCCCAATCAAAATGCCGT

SEQ ID 8494

VENDFRHDISLLDNPLIIGLRRVLNTPPTVPNGLYPNRHTKDKTMKRLNLAIALAATFAHTASADELAGWKDNTFQNLQSLKAPVRILNLMATWCGPCRKEMPAMSKWYKAQK
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SEQ ID 8495

TTGTTTGTCATTGCGTTTGTGTTTGTGATTCAATAATGCGCTTTTCGCCGTACCTGAACCGCTTCCCTGCAATTTCAGGGGGATTACCGCGCCCGTCGGGGTTTTCTTTATCGGCCCGCCGCTCTG
TCCGGCGCGTCAGCCGCTTTCCGATTTCGCGTCAACCCGTTGCAACCGGGTTTCCACACACGCGCGACGGAG

SEQ ID 8496

LFALRLFLIHNRLSPLPEPLPNSGGLPAPCGFFFIGRPSVRAVSRLSDLPSPRCNRVSTQRPTE

SEQ ID 8497

ATGATGTCGAGGGCTGATGGGGATGGCTTTCAAACGGGATATCCGAGGGGGCAGCGTTTGTGTTTGGTAAAGTTGTGCGCATCGGCCAACGACGATGGCTTGTGTTATCCGTCGCAAGAAA
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CTACCGCATCAACCTGCTCCCTGTTGAAAATGTCTATCGCGAAGCGCGCAAAACGGAAGGCGGCGCGCAGGCAAAAATGTGGGAAGAACCATTGGATTACGAACCTTCGGATTTTGAACCG
TCGGATTACCAACTCTCGAATTTTGAACCTCGGATATCGAACCCTTCGGATTTCGACTGAAGAACCATCAGATTTTGAGCGATGAACCATCAGATTTTGCCTAAGAACCATCAGATTTT
CGCTAAGAACCATCAGATTTTGAGCGCGGAACCATCAGATTTTGCCTAAGAACCATCAGATTT

SEQ ID 8498

MSARLGMMAFKTGPGRQRFVLVKLCDCAANDGLCYPSQETLAEDTGAETAVRQHILKWLKDNFIKSARRQRGRERKSDIYRINVALEKCYAEAAKRKAARQAQKMWEEPLDYEPSDFEP
SDYEPSDFEPSDYEPSDFDAKNHQILSDPEPSDFALRTIRFCAKNHQILSGEPSDFALRTIRF

SEQ ID 8499

TTGAGCGGTGAACCATCAGATTTTGACGGTTCCTTATATGTAGAACCGTCAGTAGAACCGTCAGGATCAAAATGCGCGCGGGCGCGCGCCCTGCCGGACCGCACCCCTGCGAAACCGCAAA
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CGCTCAAGGCAAAACGGCAGCCGTGACGGAACGGCAATGCGCCTGATTTGCCGCCGATGCGGAGAAATGCGGGATGACGGCGCTGCAGGGCGCGGAGTACGCCATCGCCAGCGGCTGGGCC
AGGTTTCGCGCGCGAATGGCTGCAAAACAAACTTTTCGGCGGTCTGAAACCGCGCGGCCCGACGCGCAACCAACCGCCCGCTGCTGGAATGCGGGAAGCTACGGCGATATGCCGACGA
CGGATTTT

SEQ ID 8500

LSGSPDSFDGSLYVPSVPSGSGNARGARAPAGHPAKPQTAPPETAATAAKAKKTRGHETELSLADYGITGQVAADFQVRKAKRQPLTETAMRLIAADAERKCGMTALQAAEYATASGMA
SFRAEWLQNKTFGGSGNRRGGPTHNOTAAVLDAAGSYGDMPTTDF

SEQ ID 8501

ATGTCTGAAATCAAAATTTTCCACAATCCGGCTGTCAGCAAAATCGCGTGCGCCCGTGTCCTATTGGAAGAAGCGGGCAATTGCTGCCAAGCGGTCAAAATATTGGATACGCCGCCCGACT
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GCTGCTGCGTGCCATCGCCGATCATCCGCCCTGTTGGAGCGTCCGATTGTTTGGCAAACGGTAAGCGCGCTGTGCGCAGACCGTTGGAAAAATATCGAAGCGGTATTG

SEQ ID 8502

MSEIKIPHNPRCSKSRAAVSLLEERGIAAEAVKYLDTPDLSLKDIFNKLGLSARGMVRVKDLYKELGLDNPDLNDALLRAIADHPALLERPTVLANGKAAVGRPLNTEAVL

SEQ ID 8503

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CCCGCGGTTTCAGAAACTGCCGGATTGAAAACTACGCGCTCAGCGATTTCGATCCCGGGGATGGCGAGGGCGAAGCGGGCGCGCCGAGATATCGCGCAAACTTCGCCGATGTGTTGCAGACG
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CGGAGTTTGTGTTTCGCTGCTCAACGCGGTCAGCGCGCTGATGTCGCGATCGTGGTCTGACCAACTCTGACGGCGAAGCCTTTCGCGGAAACACCGACGCGCGGATCAGGGACAGCGCTG
CGGACGCGCGCGGCAAGCTGATTCGTTTCGATGCGGAGAGCTACCGTGC

SEQ ID 8504

MALRNASDFLGAYGGGVRRERQCAEHGGYAAKSVLRGVWTCGPACRKLKLEAEMAAAYAEFLRRGAMRDLEKRIGRSGIAPFRNCRNIENAYVSDSIPGMARAKAAAAEYANFADVLQT
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SEQ ID 8505

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TGCCCGCGCCGAATCTGCTCCAGCACACGAAATCGGGCTTACGAAAAATCCCGACCGCCCCCGCTCGCGCGCGCCGCGGAATCTGCTTTCAGCGCTCCGACGATATCGCCCAACCGTGAT
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AATTGTTCGCGCATATCTCGCGCGCGCGGCTTCGCGCTCGCATCTCCCGGATCGAATCTGCTGACGGGTAGTTTTCATCTCGCGAGTTTCTGAAACCGCGGGCGATCGCCGACCGCCGA
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SEQ ID 8506

VSGVWLK SAYLQKKQVSRITVALPVERNQLAAAVPQVPDPRVGVFAEGFRRCVQGHQHRHQPLVPGVDGKQNPVFRFRQTARAEVLVQHQQIGLHENPDRPLRAAAAETVLDPRQPHIAHRD
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AFRVSVAVFRALPPLDPHAAAVSQEIRRVQPSHIRTPPSKIRRRHIAVASRIHQGGGLVVRRAAAVSRPAESFVLQPPGABAGPAAGDGVLRRLQRRHEAPLRIGGNQAHCRFRQRLPFC
LADLQEVRRHLPRDAVVGKQRKQLFVPAGFVFLRRRCGFRRLRFRVRVSRGARAARI

SEQ ID 8507

ATGCGCGAAGGCGGGAATGCGGAAGACGGGCGAAGCATTACCCGGAACCAATCCGTGCGCGCGCGGGCGTTTCAGACGGCATCGGGGCGGCAGTCGCAAAAAGGACGCGCGTCTT
GGGGAATATCCCCCCCCCAATGCGCGCAATT

SEQ ID 8508

MREGAECGRAGEALPANOSVRRRGVSDGIGGGSRKKGANGISPANRRI

SEQ ID 8509

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CGGCGGAAATGGCGAGGATTGGGTGTCGCGGTTATATGCTGCCACGCCGACCACGCGGTTGATCGGGGAAATAGAAAAAATCTTTATGCTGCAAGAGGGGTATGCGTTATCCCT
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SEQ ID 8510

VNKRFLPCSRNGRLKYLLGPGCLSVFPLLLVFASSVWAVYRTGGQVLPVYVRADAALVGLAAWDRKPSVFRFRINHAIALYQSRVVGKIVFTGGRTKKGYMTEAVGRRYALKQGVPARN
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SEQ ID 8511

TTGATACACATTAAAGCTGAAAGTAAAAATCCGCATACACCCCTCCCTGCATATTCTTCAACAACGGGTTTTGATATAATCGCTATCTGTTACAGATAGTTCAAACCGCATTCAAACCT
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CGGACGCGTTTGAAGTTACTCTGATCGAACGCGCCACTGACTGTCTGCAAAATCTCCCTATGACGAGCGGAAATCGCCCTGACCCATTTCCTCCGCGAATATCATGACGCTTTC
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CTGCGGCTTTCCAGCGCGGATATTCTGCAAGCGCAACAGCGCGCTCAAGACTTACGCGCGCTTCTCTGTTGGGAAATATACAGCAGCAAAATATGCTGCTGCAACCGCT
ATCCGCTTTATCAGCGCAACATATGATGCTGAAACTGTTTACCAACGAAACCGCGCGCAAACTGTTGCGCGGTTTGGTATTACGAGCGCGCAACACTTCCCGCGCTGAAAGGCT
GATTACCAACAACTGACCGGT

SEQ ID 8512

LIHILKVKIRIHPPLHISSTTGFDI IAYLLQIVQTA PKPLQMPSEIIGIRLCKGYFMSIHSIDLIVVGAGPAGLSFAELAGSLKVTLIERSPLFVLQNPYPDGREIALTHFSREIMQRL
GMWDKIPENIEYPLDARFVINGSDYQLHFPQTEARGEPADCLGYLISNHNIRRAAYEVVSQLDNVSLITD TAVKEVTSNBAQVFLNGDILTLRLLLAADSRFSQTRRQLGISIDNH
DYSRTHFVCRMKHTLSNQHTYAEFHYGRTIALLPLEKRLTNTVITVDTKINSVQNLSPBELAASVKEQLKRLGDMELVSSIHYPVVGMIKRFYGRKRSALIGDAAVGMPHTAHGPN
IGLSSADILAKLILEAQRGQDIGAASLLEKYSKHLMLHAHPLYHGTNMLKLTNETAPAKLRLGLVLRAGNNFPPLKLLITKQLTG

SEQ ID 8513

GTGGGGATAAGACGGTTCATTTTGTCTACCTTTTATTCAAATATATTAATAGCGCATTTAATACGGAATCCGCGCGCTTCGCGCGCAAAATGCCGCTGTAAGCGCGCTTCAGACGGCATC
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SEQ ID 8514

VGKTVHLSFYSLNLSIDIITESAARQMPSEGRFRHPRKCYNI GFPLFFQAAISIMCNHHPHSHNDTIRIRGARTHNLKNIDLDIPRHLVVTLSGSGKSSLPDFTLYAEGRR
YVESLSAYARQFLQMDKPDVDLIEGLSPAISI EQKSTSHNPRSTVGTVEITHDYLRLLYARVGPYCPHKLPLSSQTVSQMVDVAVLKLPEPTRVMILGPAVREKGEFVDFADLQAG
PARVRVDGEVYQLDEVPLKLEKNKHNDIVDVRVKADIKQRLAESFETALRHGNERALAMEMDSGEHMFSAFACPVCSYSLPELEPRLFSFNPMPGSCPTCDGLGNFTNFPDPEKVA
HPELSATGATDWDKRNQYFQMIQSLAHYKFDVNVAWETLPEKVKVVLHSGKVIDFTYLSERGTFNRSHPFEGIIIPNLERRYRETDSVREKLEQYQNHRAPCSCGGARLKE
ARYVVGGEPLHEVSAWPLTKTRHFFETLDDGNKKQIAEKILKEITERLGLFVGLDYLNLRSRATSLSGGEAQIRLASQIGSGTLGVMTVLDEPSTIGLHQNDRLLATLKLRLDGL
NSVIVVEHDEADREAFVVDMPGAGEHGNVLIADTPENVAKEKSVTGQYLGKKSIAPVSERTFPVNPGRMLVLKARGNNLKNVTELEPLGLITCTIGVSGSGKSLINDTLAKITA
RELNRAQEPAPYDIDRLEHLKVINVDQSPIGRTPRSNPATTTGLFTPIRELFAGVPLSRERGVNVRFSFNVKGRCEACQGDGVKIVEMHFLPDVYVPCVCHGRYRNRELEIQYK
GKNIQSVLDMTVEAREFFDAVPTVSRKLQTLMDVGLYIRLQSATTL SGGEAQIRKLABLSKRDTRGTYLDEPPTGLHFADIALLLVIGRLKGNKNSIVITENHLDVKTADMTV
DLGFBGGDGGKVIKAGSPSEVAKVGSYTGKYLKVVLL

SEQ ID 8515

TTGAAAAACCGGTTAAACGCAAAATTTGAAAGAAATACGGAATGACAGTCCGAAACAGCAACCGGAAACCGTCCGACGGAAGCGCGCGCAACAGAGCGGCAATCAACACCGCGCT
ATTACAAAAACCGCGCTTCGAGTGTGCGGTTTGCAGCAATACCTCAACTTCAACCTCGGCAACGCTTCAAAATACATCTGCGCGCACAGGAAAAAGGCGGCGCGCAAGACTTGAAGAA
AGCCCTGCGGTACTTGAACGCCAACGCGCGCGCGCGCAAGTTCAAGAACTCAACACCGCGCTATGAAAAATGTACGCGGCTGTAAGAGATTGCGGGTTTCAGCGCGCGCAGGAG
GCCGCGCTGCTTGCCTCATCTCCGCGCTTATTACATCCGGGACGCGCAAGCAAAATTTGCGTGGCGCGCGCTGTGTGCAAGATTGTGTAAGAAAAATGCGCGCTGAAGCGCGCGG
CCCCGACCCCTGAAGCCGATGCGCGCTGAAGCGCGCGCGGAGGCAATT

SEQ ID 8516

LKTKLKRKFERKYGTVRNTQTSTVTRTAAPQGGNTNPGYKNRAFCVGFQYLNFLNLGNAFKYIWRHKEKGGREDLEKALRYLERQAGAPKFKLKHRRYERMYAGLKDGCDFDGGTE
AALLAVISAAYIIRDEGNDFWAAACVEDLLEKMPPEAGRAPHPESPMPPETAGGGI

SEQ ID 8517

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GCACCGCTTGTGTTTTCGCGCGGTTTGCCTCCCATCATAAAGCGAATTTTATTGCGTATCGAAGACACCGACTTGGCAGCTTCCACCGCGGAATCCGTCAACATCATCTTTGACCGCAT
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AACCGTCTGCTCCGCTTCAAACCGCTTTTGGACGCGCTTACCAATGGACAGACTTGGTCAAGGGGAAATCTCCATCCCAACGAAGCCCTAGACGACCTGATTTATGCGCGCGGACCG
TACGCGGACCTTACCACTTCTGCGCGCTGGTAGACGACTACGACAGTGGCGTTTACCACATTTATCGCGGGGACGACCATGTGAACCAACCCCGAAACAAATCAACATCTTGAAGCCATC
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CAAAATGGGCAAACTCGTATGCCCTCGCGCTTGTCTGCTGCGGTACGCAAAAAACCCGAGCGTCGATCGCGTGTGGCATTATCAGCAAGAGNAAGTGTGAAGCGCATCCGTGCT

SEQ ID 8518

LMPHKGNKSNAPKDFGADMTVTRFAPSPGYLHIGGVRTALPWFARHHRKEFLRIEDTLARSTAESVNIILDMKRWGLDYDNDNVVYQTRRFDYRKEVIAELLARGDAYYCY
CSKEELAMREKAEKEGTATYDRWRPEAGKTLPEIPAGVQPVVRFKTPLDGVTKWTLVKGESIPNEALDDLIARADGTPTYNFCVAVDDYDMGVTHIRGDEHVNTPKQINILKAI
GANLPEYGHLPMLNBQCKKISKRSQDTVAITDFGAMGILPEAMLNVLARLWAGHDDFFTEPTEQIENFDLKDVSFSPSRMDLKKLYWINGEHIKITPDGLITELVKPRALRDITHEK
PALEDVLALVKDRAQDLNALADECLYFYKQVPAEADVAKHMDDEAARMRFAERLEGLDWNKAITHDLFKPFCDEBGLKNGKLGMPRLRLAVCGTAKTPSVDAVALISKEVILKIRIA

SEQ ID 8519

GTGCGGCAATGCGCTGATGTCGGAATGCGGCTTCAGACGGCATTGACGGAAGTTGAACATGAAAAAATATTGATTTTCTGATGTTGTTTTCACAGCGTATGGCGAGGG
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GCAGGCGGCTCAGCGACATCGCCGTTTGAAGCGAAATCTTCAGCAATGGCCCAAAAGCCCGGAGGCTGAAGAGATGAGGCAATCGGAGTGGCTTTGGACATGCTTTGGAAT
CGGTTTACGCGCGAGGGGAACGAAGCGTTCGGGGAAT

SEQ ID 8520

VRAMPDVCMLRQTAFRRLNKKILYFLMFVSTSVWAGGAEDNLLSIQSGYRALLQKQNNLDGKIIGMSOLEDARRRLQAAQADIARLEAETPAAMAQKARQAEEMRQIGVRLDHAN
AVYGAGERRRRGN

SEQ ID 8521

ATGAATTCCTCTTTGTCGCAACACTGTTTATTACACGGCTGAAAGCCGGCATATCGGAGGTTGGTTACGCGCTGTTTGGAGGAGTGGCAGGATTGAACCGTGGCTTCTGTGG
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AAATTTCCACAGTATGAATATTGGTTGGGCGATGCTTTGTTTACCTGAATATCGCGAAAGGCATTGGCAGGAGGCTGGTCCGCCACTGCATAGGCGCAGCGCTTCGCTGGGATA
AAGTCTCTGTATCTTTATACGCTGATGTGCAAAATATTATGAATCATTCGCTGGGCGGTTGTGCGGCGACATTTCCATAACCGGGAATGGGTTACGGTTATCGGTTTGGATGTGGATA
AGGTT

SEQ ID 8522

MNSLFDVNTVFTRLKAGHIGRLVQALFEEMHGFEPWSSVDKIRAYYGRCLKDDPLAPAAVDSDGTLIGSAAVKRHDMENFPQYEWLGDVFLVPEYRKGIGRLVAHCIGAARSLGI
KFLYLTPDVQIFYESFMAVVGHRHFNHGEWTVVRLLDVVKV

SEQ ID 8523

ATGGGCGATGCGCTGAGCTGTTCCGACGGCATTTTTATGTTTGAATAATTCCTGTGATATAGTGGATTAAACAAAACCGGTACGCGCTTGCCTCCCGCCCGCTCAAAGGGAACGG
TTCC

SEQ ID 8524

MGRCLSCSDGIFVVKFVRYSGLTKTGTALPRPGSKGTVP

SEQ ID 8525

TTGAAATCGCGAAATGCCGTGTAACCGTTTCAGACGGCATTTTTGTATTATGAACCGTTTTCGCTTCCATATCTTGGCAGACGGTTTCAGCAGATTTCGCATACGGCAGATGTTT
CAAGCAGAAAGGAACACAA

SEQ ID 8526

LKTAEMPSETFTQAPLYEYFCGPHILGRRFAADSHADVSSRKETQ

SEQ ID 8527

ATGGCAGCTATTACCAACGAGACTGTACCGGAAAAATTTCAACCATTTTGAACCTGACATTGGTAGCGGCGCGTCGGGCCCCGAGCTTGAATAAGCAATACCGCGCTTGTGGACGATG
TCGCAATTAACACCGACCGTTACCGCTTAAGGAAATCGCAGCGGGCATATCGGTACGGAACCTGTGACGCGCAATAAA

SEQ ID 8528

MARITTEDCTGKLSNHFDLVAARRARQLENGNTPLVDDVRNKPVTALRELAAGHIGTELLTRNK

SEQ ID 8529

ATGATAGATATGCTTGTGCGGTCAAAATATTGTTCAATTTCTATATCCGTTGTTTACTTCAAACCACTTTCAAATACTTCCCGTA

SEQ ID 8530

MIDMLAAVKIIVHFLYPPVVKTFKYPV

SEQ ID 8531

GTGCAATCCGTATCTTAATTTCCGTTGGCGGAGCAGCATCAACCATATGGAATAATCTGTGGATAAATTTATGGCGGATTAAACAAAATCAGGACAAGCGCGCGCGCGCAGGAGTA
CAATGGTACGGAACCGGTTCCCGGCTGCTGGGCGCTTACGGAACCGTTCCCTTTGAGCGGCGCGGCAACCGCTACCGGTTTTGTTAATCCACTATATC

SEQ ID 8532

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SEQ ID 8533

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CGAACAGGTGCGGAAGTCCGCGCGGCAAGGGCCGTTGGAGCGCAAGTCTGTCGATCGTAACGCCCGGACGCTAACCGATTCCGCAATTTAGTGAAGCAAGGAAACCAACCGCATC
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CGAACCCTCCAATGCCATCTGAAGACATTGCCGACATCGAACGTATCGCGCCCGCATCGCGTGGCAATGCCCGCCCGCGGATTGGCATCTTTACGCGACAGTGTGTTCGAGTTG
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SEQ ID 8534

MMQVILGLKAQHTDKLVFYMDFYELFLDDAVEAAKLDDITLTTTRGQMDGVPKIMAGVFPFAAEQVYLARLVKLKSVAIQVQVEVGAGKGFVERKVVIVTPGTITDSALLLEDKETNRI
VAVSPDKYIGLAWASLOSQEFPTKLITADKLINDELARLQAETLLPDSKNAPQLQTAGSVTRINAWQPAADAGEKLLTEYFGCQDLRGFGLDSKEHAVSIGAAGALLNYIRLTQNLMPQH
LDGLSLETDSQYIGMDAATRRNLEITQTLGSKRTPTLPSILDGCATHMGRLLALMLHPLNRRAHTRARQBAVTALESQYEPLQCHLKSTADIETRIARAVGNARPRDLASLRDSLFEL
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ERFIPTELKAFEDKVLTAQDQALALEKQLFDGVLKNLRTALPQLQKAAKAAALDVLSTFSALAKERNFVRPEFADYFVHIEGRHFPVVEQQVRHFTANHTDLDHKRLMLLTGPNMGK
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LKDLCKSVS

SEQ ID 8535

TTGCGCTTTTATGCCGAGGTATTGCTGCATCATTTGGGGAACCGCGGATTGGACATGGGGCTGCCCTATTATTAGGAAACGGTATTGTAGCAAAAGGTTTGTCTTCGACGGAATGAGA
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TTGAAA

SEQ ID 8536

LRFYAEVLLHHWNGGFGHGAALLGKRYCSKRFLRRNETDRKPVNKVVETNRKTAKLSIRIILSQRTSLIICLIQALNSNLFNKKVMKILDICLYTTSRAITKIIKILKSNIECAP
LK

SEQ ID 8537

TTGTTTGACGCGAGTGAATTTGCTATTTCAAAAACGCGCATTCATATTGTGATTTTAAATTTTAAATGATGATTTTGATGATTTGCCGACCTGCTTGTGATATAAG

SEQ ID 8538

LFDAGEFRYPKNAHSIFDFKILMILMIADLLVYK

SEQ ID 8539

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SEQ ID 8540

VECSFISEYNTQIGLYFTTGRNMSIKVAINGFGRIGRLALRQIEKAHGEIYVAVNDLTPAEMLLHLFKYDSTQGRFQTAELKDDAIVVNGREIKVFANPNPEELPWGELGVDVVECTG
FPTNRTKAEAHIRAGARKVVISAPGNDVKTVVYGVNDLIDGSETVISAASCTTNCLAPMAVILQKEPVGVEGLMPTTHAYTGQNTLDAHRRKGLRRARAALNIVPNSTGAARAI
VIPELNGKLDGSAQRVPVATGSLTELVSILRPAATKEINAAMKAASSESYGYNEQIVSSDVVGLIEYSLFATQTRVMTVGGKQLVKTVAVYDNEMSYTCQLVLTLEYFAGKI

SEQ ID 8541

TTGAACAAACGCGTGTGTTTGTTCGCCATAAGCCGCAATATCAAGTTACAGATAAAACATGCCGCTGGAACGCAATGTGTTACAGCGGCAATTTACTTATCCACAGGTTTGTTCAGGCT

SEQ ID 8542

LNRLLFVRHKPYQVTDKQRLNAMCSDGIVLSTGLFKP

SEQ ID 8543

ATGACTTATACCAATACCCCATCGGCACCGCCCGCTCGCCCTACAAACAGAAATTCGGCATCGCCCGCCAGCCCGGTTTGTCTCGCGCGCAAGCCTGCATCGAGCTGAATCCGGAAT
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SEQ ID 8544

MTYTTIPTIGTARSFYKQKFIARQPLVSAAEACIELNPEFTADSVRGLEDPDYVWISFIFHVLDEGNAQMRPRLGGKQKMGVFASTRPHRPNHGLSLKLERIETGKPVRLYCSGS
DLDDGTPTVIDIKPIYPIFIESKPDAAAGSFVSGKPVLEFVWQENI GAENLSANFKNLISQSLAQDPAPAYQNIPIRIYVNIADYEVRFQIEENRATVINISPTPL

SEQ ID 8545

ATGAACCGTTTTCGCGTTTCCATATCTTGGCAGACGGTTTCAGCAGATTTCGATACGGCAGATGTTTCAAGCAGAAAGGAACACAATAAAAAATAAAAAAGCCTCGAACAGTCCGAGG
CTTTCCTTTCAAC

SEQ ID 8546

MNRFAVSISLADGLQIRIRQMFQAEKHNKNKIASQSEALLSN

SEQ ID 8547

TTGGGGGGCGGCGATTTCAGACGGCTTTCCGGATGTATGTGTTTTTCATTTCACAACTGCGACTGCAGCGCGCAGAGTGTGTCCGGCGTCCGTTCCCGCAGAATTTATTTATTCGCGG
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GGCCGTACCAATGTCAAGTCAAAATGGTTGGAAATTTTCCGGTACAGTCTTCGGTGGTATACGTGCCATATTATTGCTTTCTTTCAAAATATTAAATTTGGGAAACCGGATATTTT
CCGGTTTT

SEQ ID 8548

LGGHFRRLSGCMCFIISNRRTARRQSVSACVSGRIYLLRVNSSVPICPAAISLKAVTVGLLLRTSSTSGVLFPSSWRARRAATNVRSKHLEIFPVQSSVIRAILFAFPQKYLNHETGYF
RGF

SEQ ID 8549

TTGTACAAACAAATATGCGACTGGAACAGATTATCTACAATGCGCCAAATTTATGTTGGCAAGGCCGTCCCAAAAGCTGGCGGCAAGCAAGAAATCTGATAATGCGCTAAACCAATCAA
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CACAAATCGAAGCTGCCCTGATTAAATTACACAACTCTATGGAATCTTGTGTCGATGTTTCGGAACACAGCCCCGAAAGAGCCGTACGAAACAGCCAAATCGGATTGGGATGTC
CTTCATAGCGGGCGGTTTGGGCAGATAGGCTAAACGCATACCGAATAGCTATGATGCTCACTTGAAATATCAACACACATTAGAGATAATAAGAGAAAA

SEQ ID 8550

LYKQYADWNRLSYNAPIYVKGAVPKGWRQARNSDNALNQSTELPHRLKEHSRIAASVLDLPSDFHCRFVIFEGAGSDHIGITRAALIKLHKPLHNSVDGPGNHDPCKGRYEQAKSDWDV
LHSGRVHADRLNGIFNSYESILENINTHLEIKRK

SEQ ID 8551

ATGATTGTTTCATTGATGTTGATGCACAAAAACGTTTACGCCACTGTGTCTGACGAACCTGCCCGTGAACGAGGGCGATTGATTGTCGAGGAGTAAATGCCCAAGCCGCTTTGGCGG
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SEQ ID 8552

MIVSIDVDAQKTFPLCPDELNVNEGHLIVBELNAQAALADLRVMTKDAHMAAKVLVDNPDMLKPTGFSADLTWVAHAMVGTGTYELLDLGLPSVKEYDYCVWKGVDPELHPYGACFHD
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SEQ ID 8553

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CGATTAAAAACAGCGCTTCAAGTTTCGCGTATGCAAAAAATGCGCAATATCGCGCAGATTCCGACCGCAGATTGTTGTTTATCAACCGCTGATGATTGTGTTTTCAGCAGATAAAGCC

SEQ ID 8554

MKILLVRLSSMDLIHTLPAIEDLARQCSDELHNLCEAGFAGIARLHPVKKVHVWKWRQWRKHLFQAEWREMGRKQALLQEAFFDVLDSQGLIKSACFAKMAKSPITYGLDKHSAREG
VAALAYDKKYVVPKGRNAVWRNRLFAQVPGYAMPETQVFGLSVPEASRLKNLAQPYAALHATSRSKLMFNMENWRRLQKLNQKQCCNVYLPWGNBAEKVRAEQIADGLPFTTVCANHN
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SEQ ID 8555

ATGAAGCACTGGTCGAGTAAAGCGCGTAGTGGACTACAACGTCAAAGTCCGTGTGAAGCCGATGGTTCCGATGTGGACATCGGCAATGTCAAAATGTCGATGAACCCGTTTGTATGAA
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CGAAGAAACGATTGCGTTGAAATGCTGCGAGTATCAGCGCAGATTTCGCTTGAACGAGCGCGCTTTGTCAAACCTCCCAATATTATGTTGGTGAAGAAAGAAACCTCTGGAAGAACT
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SEQ ID 8556

MKALVAVKRVVDYVNVKRVKADGSDVDIGNVMSMNPFDIAVEAEVRLKEAGKVEIVAVSLGEKKCEETLRTALAMGADRAIHETDVKLEPLAVAKLKAVADKENPQIFPLGKQAD
DDANQVAGMLAALLNAAQGTFFVSKVQIEGDEVQIVREIDGGEETLALKLPAVISADLRINEPRFVKLPNIMVAKKPLEKLSADLATDISPRKTVKFAEPKARQAGVKVASVAELVEKL
KNEAKVI

SEQ ID 8557

ATGAGCGTATTGATTATTCGCGAACACGACAACAAACAGTTGAATCTGCCACTTTGCATGCTGTTGCCGCTGCCGCCAACTGGGCAAGGTGCAATTTATGGTTGTGCGAAACGGCGCAT
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SEQ ID 8558

MSVLIIEAHDNKQINPATLHAAAAAKLKVLDLLVVGNGASSVVEFAKQVAGVEKVLVADAHYAEGLAELAPLVKLAADYRYVAATATTGKMLPRVAALLDVPQISDLTEIVDNTT
FVRPIYAGNAFETQADSEKLVLTFRVTFADVAAGGNAEIVNKTTPAQNLSPVNRQLSHSDRPELTQAKVIVSGRALGSVEKPSVLTPLADVLGAIGASRAAVDAEYAPNDAQV
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SEQ ID 8559

TTGGTATTTTTCATCATCGCCAAATGTCGGAATCGGATAGGCAAAATGCAATAAAACCGCTGCCCTTTATCTTTAAACTCAGCTGCGTCCGGGAAGTAATGGTTTATAAGTCGTAATCATG
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SEQ ID 8560

LVFFHISQCENRIGKCNRTAAFIKLSLRGSGNFIISRNHMFSDLLINKVA

SEQ ID 8561

ATGATTACGACTTATAAAACATTACTTCCCGACGACGAGCTGAGTTAAAGATAAAGCAGCGCTTTATTCATTGCTATCGATTTCGACATTCGGCTGATGTGAAAAATAACCAAT
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SEQ ID 8562

MITTYKTITSPTQAEFKDKGSRFIAFAYPIRTLADVKYQSVKGRAL

SEQ ID 8563

TTTCAGTTTGGTTCTTTGTACTACTGTTTCCGGGCAACCGGATCGAATTTTGTATTCCAGTTTCCGGGCATAGTCCGTTATTTTGGTAGTGGTGTAGAAGTGCCAGTACCT
GCACCGGATTCCAGTTTGTATTTATCGGCAT

SEQ ID 8564

FQFGFFVHYVFAGNRIEFFDFQFAGHSAPIFGSGVEVASTCTGFPDFIAH

SEQ ID 8565

TTGGAAAATATACAGGTAAAAATATGTCGGCTTATCGAAAAGGCAACATCTTTATCATTTCCGGCCGCTTCGGCACGGGCAAAACACGCTGGTGTCCGGCTGTTGGCAAAACATAACG
GTTTGGCGCTTTCGGTGTCCGATACGACGCGCCCGCGCTGAAGGCGAAGCAACCGGCTACATTTATCATTTTCCAAAGAAGAGTTGAATCGCTTATCGCGCAGGAGGCTTTTTT
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AACCGCTGCCGAAGCTGTCCGTATCTTTATCTGCCGCTTCTTTTCGACGTGCTTCCGCGCGCTCAAAGGCGCGGAGCGACAGTCCGGAAGTTATCAAAGGAGGCTGTGGAAG
CAAGCATGAAATCGAACAGTCCGTATTGTTGACATTTGCTGTGTCATGACGACTGGAGAAGCGGAGGGGATTTGCTTCATATTGTGAATGCTGCCGCTGAAAAGGTCGCGCA
ACTGGGATTTATTCAGATTGTTGAAAATTC

SEQ ID 8566

LENIQVKNMSAYRKNIFIIISAASGTGKTLVSRLLANHLNLRVSHHTTRPREGEANGVHYHFVSKKEFESLIAQEAFLYADVFNHYGTSTEGVNALAAAGYDVILEIDVQGAQVR
NALPEAVGIFILPPSFDVLAARLKGRGTDSEVIQRELSKARHEIQSVLDFVVDLEKABGDLHIVNACRLKRSRLGFIADLLENS

SEQ ID 8567

GTGAACGGGATGCGATTTCGCGGCAACGATGATGGAGAGCCACAGGAAGTGTGGCGGCGCAATTTTGGACAGATTGATTCGGTGGTATCACTGATGTTTGGTGGTGGTCCGCT
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ATGTGATATCCGTTTGAATGAAGCAATATGCAATGCCAAATATCAGCGCGATATATTGGAGCAGGATTTCAGTTGGATTCCGATTGACGTAAGTTTGTGCTTGGCAAAATTAT
GAGGCTGTGTTCCGGCTTGGGAAGATACACGCGAGGTTGAAGTAAATACGGAAGGCTTTTGA

SEQ ID 8568

VNGMQFRGNDDEPPGSGRPILGQIDSVGITDVLVVVVYFPGALLGVPLIHAYKEATAQALAEVVEKNIEKTVWLKCEYPLNEAICIAKQYQADILEQDLQLDCRLTVSLSLANY
EACVAAMKNTQREVNTKEPFE

SEQ ID 8569

ATGGACAATTTCTATACCCACGAGTATCAGTGGCCATCAGACTATTGAAGACGGGAGTAAGTGAATTTGCAAAACAGAGGCGAATATAGCATTATGAGTGAAGATGCATTATGGAACG
CGCCGGGCGAATTCATCAATTGGCTTGGCTATATTATGCTCCAGCGTCGATACCTTAGACAGATATACACAAGAAAAT

SEQ ID 8570

MDNFYTHEYQVRHQTIEDGVELNLQTEGEYSIMSEDAWNPAGEFHQLANWLYLCSVDTLDRYTQEN

SEQ ID 8571

GTGTCCTTTTGTGTTGATTTCTACTAAAATTTCTTCAGATGGGACAAAAGTTCCTTTGTATCGAGTTTTCGTTAAAGTACATATTGTCAAGGAGATGGCATGAACTGCTGGTTATCGGTA
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SEQ ID 8572

VVFCLILKFLQMGKFLCIEFSLKVHICQGDGMKLLVINGGREGHALANKLQSPKVTETVFPAGNAGTAIESKLQNLATAYQDLIEFCRKNIVFTVVGPEAPLAGITVDDFRAAGLK
IFGPTQYAAQLESSKDFAKAFVVKYNIPTAQYQTFENADAHDYVNRKAPIVIKADGLVAGKGVIVAMTLEAHAAIDIMLLGNKMGNAGERVVIEDFLQGEASPIVMVDGNHVLPMAT
SQDHKRLLDGDRGPTTGGMGAYSPAPVVTTPAVYERAMNELIETVAGMKAEHETGFLYAGLMIDQSGAPYTIIEFNCRFPDPTQPIMSRLNSDLADLVEAADIGRLDSVKAENPQTAV
GVVLAQNPYETPKKGDVLSGLDDVNRIGKVFFHAGTTVNEKGDVLTNGRILCVVGLGDDVQAQKAKAYGALKELISFGDMQYRKDIADKATNR

SEQ ID 8573

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GCAGCTTTACTTCAATGCGCTCTGAAACATTCAAAACATGCTTAGAAACGAATGCGCTGCTCTTAAGACTTTCTATTGTTGGCTAAATCTGGCGTATTACCTGCGTTCCGCGGGAAG
AGGCGCAGCAAGCTTCGGTTCAGAGTGCCCGATCATACAGGTGCAAGGCGTTTGTGTCAGGCAATGGGTATGCTTTGGTTTCCACTTCAATGATCGCGCGGTAAACCGCGGTTCGGA
CGGAGAGGGAAGTCAGAAAGCAGTTTCGACGCGGATGTGTGATTGTCGCTGGGAGGAATCGGCGAGGCAAAATCGCGAGTCAGATTATCGATGGGGAACAGGTAAACGTTTGGCT

SEQ ID 8574

MTDALQTAIFYIMLPSRIIAASQKRLSVYLLKGGVAYPTESCYGLGCLPTLAKALGLAHLKRPQHKMIVIGNQLQLQPLLQMPSENIQTMLRNEMAPKTFLLLLAKSGVLPAIRCK
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SEQ ID 8575

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TGTATCGGTGTCAAAACAGGCAATTTTGAAGGCTGTGTTGGTTACGGGACGGAGCCGGGAATGTAAAAATGCTTTATCAAAATATGAGGGCGAAGCAGTTTGTGTATCAATGGA
ACAATTTACGTTTGAATAGTAGAGATTGTA

SEQ ID 8576

VKTFLLHTQKRNFLDGLISLHDCYRTAIVKVEGRNVCFDFEDGFVLLNNPNQAGKHLKTFDSRVVLTHENRNAEDDYLVDIFEDIVFLGKRLFTVRKFLDPSLELLEMINAQGYFLEFLYLYE
CIGVKTSDYFLEAVLVTGRSRECKKCFIKIMRASSFVYQWNNLRNLSKIV

SEQ ID 8577

ATGAAACCGTATGCGGAAAAAACTCTGATTTCAACTTATACACAAATTTATCCATAAGCCTTATTTATAAAAAATGCCGTCTGGAATACTGAAATATCAGCAATTCAGACGACATTTTGCCA
TTCCC

SEQ ID 8578

MKPYAGKNSDPNLYTNLSISLIIKMPGILKYQHFRHFALP

SEQ ID 8579

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AACTGAAAAACAATATGAAACCGTATGCGGAAAAAACTC

SEQ ID 8580

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SEQ ID 8581

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CTATTGTTT

SEQ ID 8582

LGNRIFSRPLGIFQOICNKSQLPFPQTAGIHNKQIPLRLQVVIDHDKVQYGLDFMPCLRQPPLDNFPTVRPAFFEARGKHVERRRQDKDITDSFRQRVANLRRALNVDFQNHVIACR
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LLF

SEQ ID 8583

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CATCTGATGGGGTGTGTTGCGGAGAAAGCAGCTGCACAC

SEQ ID 8584

NKSLFISGAGGLAKGLELAGFQHASFIENKDKACNSLRNPNKLVYQGDVDFDLSSQEGIEVIAGGPPCQPPSLGGKHLAHEDRDMPFHAVRYVEYRPAKIFENVKGLLRKSFAD
YFETILLRLTYPNLIGLQNEWKHGLTRLKEIEPNLYKGIKYSYQLLNAADYGVQPKRRERVVIVIGRADLDIDWPKRTHSEDRLNWEKYVTGEYWEKNEPKRPNKDIAEKLQKYG
IFPEPKPWQTVRDTLSDIPHLGNHKITGHEYRDGARIYPGHTGSGIDEPSKTIKAGGHGVPGENMIRYDDGTVRYFTSYEAKLLQTFPEEFVLSGAWGEAMRQIGNAVPVKLSLILK
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SEQ ID 8585

TTGCCGTTTGAGATTGTGCGGATATTTTCCATCGGGCAGACTGTCCGTGTGCTGCGAGCGGTATCAAAATAGGGAGTAAACGAAAGATAGGAAGATTGGCGCATTAGGGTTTCTT
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CGTATGGAGGAATATGCTCTTTTGAAGAGTGTATTATGGATGAACGCCGA

SEQ ID 8586

LPPEIVPIFSHRADLSGVLAQVIKIGSKTKDRKIGRIIVSLIIEIRSFKNLGGGRNAVCEMRQIWEIDAFAVFYVFIYSVWRNMLLLKSVLMMXR

SEQ ID 8587

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SEQ ID 8588

MEEYAAFECCINDLPITVNRFDLPAYAV

SEQ ID 8589

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SEQ ID 8590

LICFRQLMPSEALS DGIYFEVLVVFASDILMV

SEQ ID 8591

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SEQ ID 8592

MVQPRKPEVNVHKKRDIALLSKHQDRETTPEKISTYMHLLFCPHCREYKRLQTIKISLAKTTRTSK

SEQ ID 8593

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AATAACAACGAATTTCAAAAAATCTGCAAGAGTGCCTATACAACCTGCCTGAAACACCGCAGGGTATTACCCCTGAAGGAAATACTCGGTTTTCATCCAACGAAATACACAAATGT
CGGATATCAGCAGCTCAACTACCAACCAATATGACCCGCGCGGAGAATCATGCGCAATGCTGCAAAATCAAAATGGTTCAACCAAGAAAAACCGGAAG

SEQ ID 8594

MPILPDLTDAELMESRRLILHFAQLQPLDHPDLAEDLVQETLSAYSAGDSPOGRALVNSWLPAILKNKIIDLRLQIGRQRKVFALDDELLDEAFESHFSQNGHWTPGEGPQHWNTPKSL
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SEQ ID 8595

TTGCCAAAATTGCCGATTATCAAAACGGTGGCGGAAGGAATACCGCGTGACGCTGAAACCTCCGCCAATACCAGCACCGTTTCTCCCAAGCCATACGCGGGGGCGAAGCCGACAGC
GTCGCGCGAAGACCGATTGAACGCTATATCCGCTGATACGCAACAATATCCACAGCTTTATCGACCGCTGCTATACGAAACGCGGCAATACTTTGACAGCAAGAATGGAGCGCTCT
GAAAGAAGGTTTCGTCGCGACGCGCGTGGCCAAAGCCCTATTTTCAAGAAATCCCGCGGAGTTCCTACAAATATGCGAAAGCCCGCGCTTCAGACGGCATTTTGGCGCTGATGAT
TTTGAATATACCAANTGCTGGCAGAGTTCACAAATTCGGGATATCCCGCATTATTTCAATATGACAGCAAAATACAGCCCTCCCTGCGGCTTTATCCGGCAATATCGATACG
ATGTTACCCATGATTTGACGAAAGCGGAAACAGCCCTTGTAAATATGGCGAAACGCCAGAGATGATGTGATGATACCAACATGGAGCGCTTCGATATGATGCTCTGGAGATAATGGGTT
CTCCGCGCTTCCTTTGACACCCCTCGCCCAACCCCTTGTGCAATTTATGCCATAAGCCGATAATTTGGAATAATATTTTGTCTGGGAAATGGTACGCGTGGATGAACAAAGGATTATCATC
CCCTCTGTGTCGCCATATCCGAAATATGGAAGCAATTCGCCGAGCAAAACCATCTATCCGCA

SEQ ID 8596

LPLKPIIKRVPENFVQPEYSAQYQHRFSQAIIRGGEAADGLPQDRILNVYIRLIRNNIHSFIDRCYTETRYQFDSKWSRLKEGFVRDARAQTPYQEIPEGFQYQCSPPISDGLIALMD
FEYQJLLAEVAQIPDIPDIHYSMSKYTPSPAIFIRQYRVYDTHDLQEAETALLIWRNAEDDVMTQLDGFDMMLLEIMSSALSFDTLAQTLVEFMPKADNWKNNILLGWSGWIQRITII
PSLSAISENMEGNSPQNHLSA

SEQ ID 8597

GTGCCATCCGAACCGGTAAATAATGATTCAACACGCGAGCTTTGGGCTACCGCGCGATTGGCGGAAGACTTTCTCTCGCTTTCCGAAACAGCCCGATATGCTTTATCGAAGCCGAC
CGGAAACTGGCTGAAATGGCGCGCAGGCGCGCAACAGCTTTGACCGTGTGGCGGAACGGCTGCCCTGGCGTTGCGACGATTATCTATGCTGGGCGGACAAGCCCGCTGGATAC
CGATTGATAGACGCGCATCAAGAAATGATGTGCCGTATGACTGACGCTTTTCTCCGATCATTTGAGCTACTGCGACGCGCGGTCTATCTTACGATTGTGTGCCGCTGCCCTTCACT
GAAGAAATGTCATCATACGCGCGCGGTATCCGCGAAGTGAAGACCGCTTTGGGCTGCCGATCCGCGTGAAGAAACAGCTCTACTACCTGCAATCTCCGCTTGGCGAGATGAACGAGG
TCGAGTTCTCTCAACGCGGTTGCCGCTGAAGCCGACTGCGGTATTCATTTGGATGATGAACAAATATTTACGTCACCGCTGTCAATCAGCGCTGCTGTGCGCTGAGGCTTTTATAGAGATGT
GGACGCGAGGCGCGTGTCTACATCCACATCGCCGACGATGCGCAACCCCGAGCTTTTGGATGATACCCACGCGCGCGGCTTTTACCGACCGTTTGGGACTTGTCTGGAATCGCGC
TACACCAAGCTTCCCACTATCCCTCCACCCCTGTGGAACGCGATTCAATTTCCCACTTTTGGCGAACTCGAAGCCGAAGTTGCCAAATTTGCCGATTATCAACACGCGTCCCGGAAAGG
AATACCGCGTGCAGCC

SEQ ID 8598

VPSEPGKMIQHAGLGYRDLAEDFLSLSENSPICFIEAAPENWLMGGRARKQFDRVAERLPLALHGLSMSLGGQAPLDTDLIDGIKEMCRYDCTFFSDHLSYCHDGGHLYDLLPLPT
EEMVHTARRIRREVQDRILGCRILAVENTSYLHSLAEMNEVEFLNAVAREADCGIHLDVNNIYVNAVNHGLLSPEAFLENVDAGRVCYIHLIAGHDAETPELLIDTHGAAVLPTVWDLLELA
YTKLPTIPPTLLERDFNFPFAELEAEVAKIADYQTRAGKEYRRAA

SEQ ID 8599

AGCTTCGCGCGAGCAGCAAAATACGCAATACGACATCAATGCCACTTTTGTGATGTTACGCAATGCAGCGTTGGAAACGCGCAGGCGAAGCCAGCGGTTTCACTTTCTACCCAAAAA
CGAGTGATTGCAAGTTGGGCAAAAAACGCGCTTTGGTTTGTGTTGGCGTGCATACGTTGTGCCGACATCGCGCGCTTACCGGTCACTTTGCAAACTCGTGCCATAATCAGTCTCC
AACTTCTAAATAGTAAACCGGATTATACACGCAAAACATGCCGTTTCAA

SEQ ID 8600

SFAASTQISQYDINAYFVDTQCSVGNQANPAVTFYFKTT*LVGQKTAFGFVGVYVYVAGHRAFTGHFANSCHNQSPNF*NSKTRFIPKTMFQ

SEQ ID 8601

TTGATGTTTTTAACGCCATATTGTAGCCGTGACGCTGCCGCTTGCCAAATCAATCAAAACAATAGCGGCAAAATATGGGCATCGGCAAAATATGAAA

SEQ ID 8602

LMFLTPYCSRPAAQCINQNNSGKIWASAMK

SEQ ID 8603

ATGAACAAAAATATGCTGCCGACTCGCCGCTGCTTTATCCCTGTCTCTGCGCGCGCGCGCTTGGCGCCCAAAACCGGCAAGCAACGCAACAGCGCTTCAAAAAATCCGCCCAAGGCT
CTTGGCGGCATCCAAATCTGCCAAGGTTCTGCGCGCGCATCCAAATCTGCCAAGGTTCTGCGCGCGCGCTGCTTCAAGCAGGCGAAGCAAAATCGCGCGAGGCAAAATCGGTTGC
AACTGTAAAAAGCCCAACACACCAAAAGCATCTAAAGCCAAAGCCAAATCTGCCAAGGCAAAATCGCGCGAAGCAAAATCGCGTTCTAA

SEQ ID 8604

MKNIAAALAGALSLSLAAGAVAHHKPNASNTGVQKSAQSGGASKSAEGSCGASKSAEGSCGAAASKAGBGKCGBGKCGATVKKAHKHTKAKAKAKSAEGKCGBGKCGSK

SEQ ID 8605

ATGAAATCGGAACAACTTGGCAGACGGCATCCGCTATGCTGGTTTTGCGTCTATTTGCGCATATGAATTTTGGAAATCGGGTTTGCAAAAATGGAACGGGGAGAAATGGTTTTTCGAAA
TCAACGATCAGTTTCAATCCCGTTCACTTGTGCGCGGACCGCTTAACTGGAATCTCGCCATGTATGCGGAGCTTTTGTCTGCCGTACTGTGCTTTTGGGTTTGGCAACGCGCTGTC
GCGATTGGGGCTGATGCTGTTACCGCGTCTGCTGGGCTCGGGTTACGCGCGGTTCCGCTTCAATGTCTGCGACAACGGTTATAAAATGGCTTTAATTTATATCGTGGTATTAATCCCG
CTGCTTTTCCAGGCTCGCGCGGATGCTGCTGATACGCTCTGAAAAAAGCTTTTGGCCCCAATGCCGCTGAAACAAGAT

SEQ ID 8606

MKIGTTWQTASAMLVLRPLAAYEFLESLQKNGENWFSEINDQFPFFFNLLPDALNWNLMAYAEILLVLLILGLATRLSALGLNVVTAVANAHVHAGSGYNVCDNGYKMLIYIVVLLP
LLFQAGGWSLDTLLKLLCPKRLKQD

SEQ ID 8607

ATGGAATATGTTAAGCTTTTCAAAATCAGATCATTTTGGCAATCGCGCGCGCGGTTGCTTGGCGCTGCGGTACGCGGGGAAACAATCCGCGCGCAAGCGGTGCAAAACGCCA
AACCGCGCGAGTGGTTCGCTTTGGCACTCGGTGGCGCGCATCTAAAGGATTTGCCATATAGGAATTTGTAAGGTTTTGAAAGAAACCGTATTCCTGTGAAGGTGTTACCGGCACATC
GGCAGGTTGATAGTTCGCGAGCTTTTGGCATCGGGTATGTCGCGGACCGCTCGAATTTGGAAGCCGAGATTAGGTAAACCGGATTAGTCGATTAACTTTGTCACAGCTGCTTT
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TCAATCAAGGGAATGCCGGGCGAGCGGTTCTGCTTCCCGCGCATTTCCCAATGTGTTCCAGCCAGTCATCATCGGACGACAAATATGTTGACGGCGGTCTGTGCGACCGCGTGCCTG
CAGTGCCTCTCGCGCGAGGGGCGAAATTTCTGATGTCGCTGATTTTCCGACGCTCCGAGCAAAATGTCGGTCAAGGTTTCTTCTTATCTGATCAGACGCTGAACGTGATGAGC
GTTTCTGCTTTCGAAACGAGTTGGGCGAGCGGATGCTGTTATCAACCGCAGTTTGGATTTGGGTGCGAGTCGCGGATTCGATACGAAAGCGCGCATCCGCTTGGGCGAGGAGG
CAGCAGTGCCTGCTGAAATCAACGCAAACTGGCGGCTATCCGTTAT

SEQ ID 8608

MENMVTFSKIRSFIAAALLAACGTAGNNAARKPVQTAAPAAVVALALGGGASKGFARIHGIKVLKENGIPVKVVTGTSAGSIVGSLASGMSFDRLEAEILKRTDLVDLT/LSTSGF
IKGEKIQNYINRKYVGRQIQOFFPIKFAAVATDFETGKAVAFNQGNAGQAVRASAIIPNVQPVIIIGREKTVGGLSQPVVPSAARRQGANFVIAVDISARPSKNVGQGF SYLDQTLNVS
VSVLQNELGQADVVIKQVLDLGAAGVFDQKRAIRLGEAARAALPEIKRLAAYR

SEQ ID 8609

GTGTGTTGAGCTGGTGATTACTTCGGCTTCCATGATCTTTCGTTCTTTCAAAATTTTAGGGCGTATGTACGGGATTCGGGTATTTTCTATGGAATGAAGCTTCTCGAAACAG
TTCGGACGGCA

SEQ ID 8610

VLLSWLITSAHLSFQNFGRVLYGIRVFFSMDEAFWKHVRTA

SEQ ID 8611

ATGCCGTTAAACATCAAACTTGGAAACGCAATGCTGCTTCAATCCGAAGCTATGAGTGTCCGGCGGCTTGGCCGACAAATCCGCAAAATCGAAACTGGCCGCAAAAGGCATCTTAT
 TCCACGACATACGCGCTCTGCGAAAGTGCAGAACTACTCCGCTTTTGGTGCATTTGCTGGTTTACCGCTATATGGATCAGAAAAATCGACATCGTTGCGCGCTTGGACGCGCGCGCTT
 CATATCGCGCGGCACTGCGCTACCAGCTCAACGTCGGCTTCGTCCTCCATCCGCAAAAGGCAAGGCTGCTTTTGAACCGTATCGCAAGCTACGCGCTCGAATACGGGGAAGCTCGG
 GTGAAATCAGACCGATGCGCTCAAAACCGGCTCGCGCTCTGCTGCTGATGATTTGGTTGCCACGGCGGCAATGCTTGGCGGGCTGGAACTGATCCGCAAACTCGCGCGGGA
 TTGTCGAAGCGCGCATTTTGAATTTACCGACCTTCAAGCGCGCAAGATATCCGCGCAAGTGGCGGCGCTTATTTACCTGCTTCAAAACGAAGGCTGCATGAAAGGC

SEQ ID 8612

HALKTSHLEHMLVHPEAMSVGALADKIRKIENWPQKILFHDITFVLQSAEYFRLLVDLLVYRYMDQKIDIVAGLDARGFIIGAALAYQLNVGFVPIRKKGLPFETVSQSYALEYGEAA
 VEIHTDAVKPSRVLLVDDLWATGGTMLAGLELIRKLGGETVEAAAILEFTDLQGGKNIRASGAPLFTLLQNEGCMKG.

SEQ ID 8613

AAGAAAAACAGATGTTTTCGCGGGTAAGCGCGCGGAGTCCGCGATCTGCGGAACGTTTGCAGGTGCGGAACAGATGGCGCGGTTATAGCGGATTTCCGGAGCTTCTGCATTCAAAATG
 CCGTCCGACATATTTCCAGTATTTTCAGACGGCATTTCAA

SEQ ID 8614

KNRCCFARVSRPSAASAEIRLQVRNHWGAIADFGSFCIQNAVRTYFYQYQTAFO

SEQ ID 8615

TTGTTGGACTGATGTTTCCAAACGACATTTGGAGCGCTCTGAAAGCACTAGCTTCAACGAAGTTAAAGTTGAAACGGCAAAACCGTCAATCAAGCAACCGCTCGGTACCGCACACCGG
 AGTGGCGGGT

SEQ ID 8616

LLDLHFPNDIGRLKALASTKLKLVETANRQSSNRVETAHTQWAG

SEQ ID 8617

ATGAATATATCGCGCGGACATCTCAAAGGACACCATAGACGCAACATTCATATAAAACAAACGGAAGTATCCATTACATTAATTTAAGAATAATGATGATGGATTAACACGTTTATAGT
 TGTGGATAAAGGGAACAGAATCAGAAAAGTCTATATCGGCATGGAGGCAACAGGCATCTATTACGAAAAGGCAGCAGATATGCTTTCTTCTACTATACGTTTACGTTATCAATCCCTT
 AAAAATCAGGACTACGAAAAAGCAGGTTTAAACCGCACAAACCGACAAAGCAGATTCAAACTGATAGCAGATTACATAAAAGGCATCAAGATACATTGATACCGTATCAGATACCC
 AAAACAAAGCACTGCAAAAATGATTAATCTTAAAAACCAATTACAGAACAGCAGAAACCAATTTAAAAACCAAAACGGAACAATAACCATTACCGCAATCTTCAAAACCATCCGAGCATAGGCAAGA
 TGAATAGATACATACAGGACAGATGGAACAGGTAAAAATAGCCATATCGGAACAAATCAAAAAACAAACGGAACAATAACCATTACCGCAATCTTCAAAACCATCCGAGCATAGGCAAGA
 CACCGCATCAGTTCTTTATGCGCAACTGACAGAAAAACATTTAAAAACCGCAAAACCAATTTGTATCTATGCGCGATTAAAGTCCCGCCATCATCAATCAGGGACAGCGTAAGAGGTGCG
 GCGAGATTGAGCGATACGGAACAGACGATTAAGTACGCTGTATATGCGCGCTTTGTGCTTACCGTTTAAACGCAATTTCCGAAATTAATAATAATCTGAAAAAGCGGTAAGC
 CAAAGATGTTAATATCTGTCATCATGCGCAAACTGGCGAAGCCCGCTATTACATGTTTAAACCGCGCCAGCTTACGATGCGGAAGACACCGATTGAATCAA

SEQ ID 8618

MNIIGPDISKDTIDATLHKTNGSIHYIKFKNDDGLKQFRLWIKGNIRKVIYIMEATGIYYEKAADMLSSYYTVYVINPLKIKDYGKSRFNRTKTDKADSNLIADYIKRHQDTLIPYQIP
 RKNALQKLINLKNLOQQQKQIKNRLHSTEDFIRNIHQDLIDTIQDKMEQVKIAISEQIKRQTTNNHYRNLQTPISIGKDTASVLYAQLPEKHFKTANQFVSYAGLSPALIQSGTSVRGR
 GRLSRYGRRRLKSTLYMPALCAYRFNAPFKLINLKKAGKPKMVIIVAIMRLAKPAYIYVTKGQPYDAERHRLNQ

SEQ ID 8619

TTGCCGCTTTTGGAGATTGCAAAATGGGAGATAAGCAAGGGATGACAAAGCGGTTCGCCGCGTGATGACGGACCGCGCGCGGAGCGGAGAGCCGCAACCGCTTCGAATCTTCCCC
 CCCCTTATCTAACAGGGGGGTACAGAAACCGAAACCGCGCGGCGGGGTCAGGAAGTCTTCAATGTTACGAAACGTACA

SEQ ID 8620

LPVFEDSQMGDKQMTKAVAGVMTDAPADGRKPATASNLPFPLYTGGVQPKRRAGFRKSSNVTKRT

SEQ ID 8621

ATGCCAATAGTTTCCGAATCGAATACCTTCGCGCGATAACGCCCTAAGGAAATTTTGGACATCGCGAACCCTGCTCTGCTGAAAAATACAAAGCGCGCTTCGACGATGTGGGGCGG
 AAATAGGAGGGGTAGGTAGATACGGGACATGGTTTCTTCCAGGAGTTGTTGAAATATGGGGAATTTACTGGTTTGGGCGATGTTTGGGGAGAGGGGTGGGAATTTCTGTTTTCGGAAGT
 GGAAAAAGGTCGTGAAAAATGGGTTTCAGACGACCTTCTGTGAAATGTGCATT

SEQ ID 8622

MPNSFPNRIPSFONALRKFFGHREPCPAENTKGRVRRCGAEIGGVGRYGTWTFASKELLYGFTGLGDVWGEWELFCEVEKGRLLKMGFRFRPFCEMCI

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